

STIC-Biotech/ChemLib

163369

From: Vivlmore, Tracy  
Sent: Monday, August 22, 2005 3:04 PM  
To: STIC-Biotech/ChemLib  
Subject: Sequence search request, application 10/828,394

Hello,

For application 10/828,394 please perform the following sequence searches:

For SEQ ID NO: 1, a score over length search of nucleotides 1-1643 with a length of 8-50 and a cutoff of 80%.

For SEQ ID NO: 5, a length limited search with a maximum length of 50.

Thank you,

Tracy Vivlmore PhD  
Remsen 2B-02, AU 1635  
Mailbox: 2C-18  
Tel: 571-272-2914

\*\*\*\*\*

STAFF USE ONLY

Searcher: \_\_\_\_\_  
Searcher Phone: 2-\_\_\_\_\_  
Date Searcher Picked up: \_\_\_\_\_  
Date Completed: \_\_\_\_\_  
Searcher Prep/Rev. Time: \_\_\_\_\_  
Online Time: \_\_\_\_\_

\*\*\*\*\*

Type of Search

NA#: \_\_\_\_\_ AA#: \_\_\_\_\_  
Interference: \_\_\_\_\_ SPDI: \_\_\_\_\_  
S/L: \_\_\_\_\_ Oligomer: \_\_\_\_\_  
Encode/Transl: \_\_\_\_\_  
Structure#: \_\_\_\_\_ Text: \_\_\_\_\_  
Inventor: \_\_\_\_\_ Litigation: \_\_\_\_\_

\*\*\*\*\*

Vendors and cost where applicable

STN: \_\_\_\_\_  
DIALOG: \_\_\_\_\_  
QUESTEL/ORBIT: \_\_\_\_\_  
LEXIS/NEXIS: \_\_\_\_\_  
SEQUENCE SYSTEM: \_\_\_\_\_  
WWW/Internet: \_\_\_\_\_  
Other(Specify): \_\_\_\_\_

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## SCORE OVER LENGTH SEARCHES

Attached is a score over length search. This search was developed to overcome limitations in most standard search systems which favor large sequences with high scoring, but lesser overall identity over smaller sequences with higher overall identity. This search is especially useful for relatively small nucleic acid or polypeptide target sequences (antisense, fragments, probes, primers, RNAi, epitopes, haptens, etc.) claimed functionally via a form of hybridization and/or identity language and having defined upper and lower polynucleotide and or polypeptide length limits.

The score over length search is performed by first running the query sequence using examiner-specified identity and polynucleotide or protein length limit parameters, and saving 65,000 hits and 0 alignments from each desired database. The resulting output is reformatted using a Microsoft Word macro and is imported into Excel. The summary table data are then sorted by the ratio of score of each hit sequence divided by its length and the accession numbers for all hits below the examiner's desired score over length parameters are deleted. The remaining accession numbers are used to pull the corresponding sequences from the databases into subdatabases enriched for good hits and the query sequence is re-run against these subdatabases to yield the final results.

The score over length cutoff for this search is 80%

Examiner Please Note: This cover sheet should be included when submitting results to be scanned.

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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: September 3, 2005, 15:23:21 ; Search time 128 Seconds  
(without alignments)  
268.452 Million cell updates/sec

Title: US-10-828-394-5

Perfect score: 21

Sequence: 1 cagcagcagagtcctcatcat 21

Scoring table: IDENTITY NUC

Gapop 10.0, Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 1209694

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents NA:\*

1: /cgn2\_6/ptodata/1/ina/5A COMB.seq.\*

2: /cgn2\_6/ptodata/1/ina/5B COMB.seq.\*

3: /cgn2\_6/ptodata/1/ina/6A COMB.seq.\*

4: /cgn2\_6/ptodata/1/ina/6B COMB.seq.\*

5: /cgn2\_6/ptodata/1/ina/PCTUS COMB.seq.\*

6: /cgn2\_6/ptodata/1/ina/backfiles1.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	17.8	84.8	50	4	US-09-485-632B-15
C 2	16.2	77.1	32	4	US-09-410-935B-6
C 3	16.2	77.1	32	4	US-09-784-403A-6
C 4	16	76.2	25	4	US-09-396-196G-7759
C 5	15.4	73.3	45	1	US-07-885-689A-7
C 6	15.2	72.4	22	4	US-09-823-549-46
C 7	14.8	70.5	20	4	US-10-007-010-43
C 8	14.8	70.5	31	2	US-08-467-603-35
C 9	14.8	70.5	31	2	US-08-466-793-35
C 10	14.8	70.5	31	2	US-08-491-861A-35
C 11	14.8	70.5	31	4	US-09-374-671A-35
C 12	14.6	69.5	25	4	US-09-396-196G-10991
C 13	14.6	69.5	25	4	US-09-396-196G-74836
C 14	14.6	69.5	44	3	US-09-110-359A-11
C 15	14.2	67.6	20	2	US-09-205-860-3
C 16	14.2	67.6	20	3	US-09-657-452A-163
C 17	14.2	67.6	24	3	US-09-360-545-57
C 18	14.2	67.6	25	4	US-09-396-196G-103491
C 19	14.2	67.6	30	3	US-09-130-663-10
C 20	14.2	67.6	30	3	US-09-432-335-10
C 21	14.2	67.6	30	3	US-09-254-023B-20
C 22	14.2	67.6	30	3	US-09-614-022-10
C 23	14.2	67.6	47	4	US-09-422-978-3015
C 24	13.8	65.7	18	2	US-09-256-496-15
C 25	13.8	65.7	25	4	US-09-396-196G-35606
C 26	13.8	65.7	25	4	US-09-396-196G-44424
C 27	13.8	65.7	25	4	US-09-396-196G-44425

28	13.8	65.7	25	4	US-09-396-196G-44426	Sequence 44426, A
29	13.8	65.7	25	4	US-09-396-196G-44427	Sequence 44427, A
C 30	13.8	65.7	25	4	US-09-396-196G-108268	Sequence 108268,
C 31	13.8	65.7	28	4	US-09-887-145-35	Sequence 35, Appl
C 32	13.8	65.7	30	4	US-09-586-216C-19	Sequence 19, Appl
C 33	13.8	65.7	37	2	US-08-467-603-54	Sequence 54, Appl
C 34	13.8	65.7	37	2	US-08-466-793-54	Sequence 54, Appl
C 35	13.8	65.7	37	2	US-08-491-861A-54	Sequence 54, Appl
C 36	13.8	65.7	37	4	US-09-374-671A-54	Sequence 4, Appl
C 37	13.8	65.7	41	4	US-09-586-216C-4	Sequence 87, Appl
C 38	13.6	64.8	20	3	US-09-517-467B-87	Sequence 4550, Ap
C 39	13.6	64.8	20	3	US-09-198-452A-4550	Sequence 6, Appl
C 40	13.6	64.8	23	3	US-09-489-085A-6	Sequence 10990, A
C 41	13.6	64.8	25	4	US-09-396-196G-7746	Sequence 68315, A
C 42	13.6	64.8	25	4	US-09-396-196G-10990	Patent No. 5463174
C 43	13.6	64.8	27	6	5463174-1	Patent No. 5463174
C 44	13.6	64.8	27	6	5463174-1	
C 45	13.6	64.8	27	6	5463174-1	

ALIGNMENTS

RESULT 1

US-09-485-632B-15/c

; Sequence 15, Application US/09485632B

; Patent No. 6605280

; GENERAL INFORMATION:

; APPLICANT: NO. 6605280ick, Daniela

; APPLICANT: Dinarello, Charles

; APPLICANT: Rubinstein, Menachem

; APPLICANT: Kim, Soo Hyun

; TITLE OF INVENTION: Interleukin-18 Binding Proteins, their Preparation and

; TITLE OF INVENTION: Use

; FILE REFERENCE: 20993-001

; CURRENT APPLICATION NUMBER: US/09/485,632B

; CURRENT FILING DATE: 2000-10-12

; PRIOR APPLICATION NUMBER: IL98/00379

; PRIOR FILING DATE: 1998-08-13

; PRIOR APPLICATION NUMBER: 125463

; PRIOR FILING DATE: 1998-07-22

; PRIOR APPLICATION NUMBER: 122134

; PRIOR FILING DATE: 1997-11-06

; PRIOR APPLICATION NUMBER: 121869

; PRIOR FILING DATE: 1997-09-29

; PRIOR APPLICATION NUMBER: 121639

; PRIOR FILING DATE: 1997-08-27

; PRIOR APPLICATION NUMBER: 121554

; PRIOR FILING DATE: 1997-08-14

; NUMBER OF SEQ ID NOS: 15

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 15

; LENGTH: 50

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: Chemically synthesized

US-09-485-632B-15

Query Match 84.8%; Score 17.8; DB 4; Length 50;

Best Local Similarity 90.5%; Pred. No. 80;

Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CAGCAGCAGAGTCCTCATCAT.21

Db 42 CAGCAGCAGAGTCCTCATCAT 22

RESULT 2

US-09-410-935B-6

; Sequence 6, Application US/09410935B

; Patent No. 6504083

; GENERAL INFORMATION:

```

; APPLICANT: Barbour, Eric
; APPLICANT: EuClaire Meyer, Terry
; APPLICANT: Eid Saad, Mohammed
; TITLE OF INVENTION: No. 6504083el Maize Promoters
; FILE REFERENCE: 5718-72
; CURRENT APPLICATION NUMBER: US/09/410,935B
; PRIOR FILING DATE: 1999-10-04
; PRIOR APPLICATION NUMBER: US 60/107,201
; PRIOR FILING DATE: 1998-11-05
; PRIOR APPLICATION NUMBER: US 60/103,294
; PRIOR FILING DATE: 1998-10-06
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 32
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Gene specific primer 1 for Gos-2
US-09-410-935B-6

Query Match          77.1%; Score 16.2; DB 4; Length 32;
Best Local Similarity 85.7%; Pred. No. 3.9e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CAGCAGCAGAGTCTTCATCAT 21
    ||||| ||||| ||||| |||||
Db 3 CAGCACCAGAGTCTCAGCAT 23

RESULT 3
US-09-784-403A-6
; Sequence 6, Application US/09784403A
; Patent No. 6670467
; GENERAL INFORMATION:
; APPLICANT: Barbour, Eric
; APPLICANT: EuClaire Meyer, Terry
; APPLICANT: Eid Saad, Mohammed
; TITLE OF INVENTION: No. 6670467el Maize Promoters
; FILE REFERENCE: 35718/208067
; CURRENT APPLICATION NUMBER: US/09/784,403A
; PRIOR FILING DATE: 2001-02-15
; PRIOR APPLICATION NUMBER: US 60/107,201
; PRIOR FILING DATE: 1998-11-05
; PRIOR APPLICATION NUMBER: US 60/103,294
; PRIOR FILING DATE: 1998-10-06
; PRIOR APPLICATION NUMBER: 09/410,935
; PRIOR FILING DATE: 1999-10-04
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 32
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Gene specific primer 1 for Gos-2
US-09-784-403A-6

Query Match          77.1%; Score 16.2; DB 4; Length 32;
Best Local Similarity 85.7%; Pred. No. 3.9e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CAGCAGCAGAGTCTTCATCAT 21
    ||||| ||||| ||||| |||||
Db 3 CAGCACCAGAGTCTCAGCAT 23

RESULT 4
US-09-396-196G-7759/c
; Sequence 7759, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396.196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 7759
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-396-196G-7759

Query Match          76.2%; Score 16; DB 4; Length 25;
Best Local Similarity 100.0%; Pred. No. 4.6e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 AGCAGCAGAGTCTTCA 17
    ||||| ||||| ||||| |||||
Db 16 AGCAGCAGAGTCTTCA 1

RESULT 5
US-07-885-689A-7
; Sequence 7, Application US/07885689A
; Patent No. 5366876
; GENERAL INFORMATION:
; APPLICANT: Cho, Joong M.
; APPLICANT: Lee, Tae H.
; APPLICANT: Chung, Hyun H.
; APPLICANT: Lee, Yong B.
; APPLICANT: Lee, Tae G.
; APPLICANT: Park, Young W.
; APPLICANT: Han, Kyu B.
; TITLE OF INVENTION: Method for Production of Bovine Growth
; TITLE OF INVENTION: Hormone Using a Synthetic Gene.
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Birch, Stewart, Kolash & Birch
; STREET: P.O. Box 747
; CITY: Falls Church
; STATE: Virginia
; COUNTRY: USA
; ZIP: 22040-0747
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/885,689A
; FILING DATE: 19-MAY-1992
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Svensson, Leonard R.
; REGISTRATION NUMBER: 30,330
; REFERENCE/DOCKET NUMBER: 377-144P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-241-1300
; TELEFAX: 703-241-2848
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 45 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; HYPOTHEetical: NO
; FEATURE:

```

APPLICANT: Morgenstern, Jay P.



; TELEPHONE: (617) 227-7400  
; TELEFAX: (617) 742-4214  
; INFORMATION FOR SEQ ID NO: 35:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 31 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; SEQUENCE DESCRIPTION: SEQ ID NO: 35:  
US-09-374-671A-35

Query Match 70.5%; Score 14.8; DB 4; Length 31;  
Best Local Similarity 88.9%; Pred. No. 1.6e+03;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 AGCAGCAGAGTCTTCATC 19  
DB 24 AGGAGCAGGCTTCATC 7

RESULT 12  
US-09-396-196G-10991  
; Sequence 10991, Application US/09396196G  
; Patent No. 6821724  
; GENERAL INFORMATION:  
; APPLICANT: Michael Mittmann  
; APPLICANT: David Mack  
; APPLICANT: David Lockhart  
; APPLICANT: Affymetrix, Inc.  
; TITLE OF INVENTION: Methods of Genetic Analysis  
; FILE REFERENCE: 3101.1  
; CURRENT APPLICATION NUMBER: US/09/396,196G  
; PRIOR FILING DATE: 1999-09-15  
; PRIOR APPLICATION NUMBER: 60/100,678  
; PRIOR FILING DATE: 1998-09-17  
; NUMBER OF SEQ ID NOS: 127806  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 10991  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Mus musculus  
US-09-396-196G-10991

Query Match 69.5%; Score 14.6; DB 4; Length 25;  
Best Local Similarity 81.0%; Pred. No. 1.9e+03;  
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 CACGACGAGTCTTCATCAT 21  
DB 3 CAACAGCAGGCTTCACAT 23

RESULT 13  
US-09-396-196G-74836  
; Sequence 74836, Application US/09396196G  
; Patent No. 6821724  
; GENERAL INFORMATION:  
; APPLICANT: Michael Mittmann  
; APPLICANT: David Mack  
; APPLICANT: David Lockhart  
; APPLICANT: Affymetrix, Inc.  
; TITLE OF INVENTION: Methods of Genetic Analysis  
; FILE REFERENCE: 3101.1  
; CURRENT APPLICATION NUMBER: US/09/396,196G  
; CURRENT FILING DATE: 1999-09-15  
; PRIOR APPLICATION NUMBER: 60/100,678  
; PRIOR FILING DATE: 1998-09-17  
; NUMBER OF SEQ ID NOS: 127806  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 74836  
; LENGTH: 25  
; TYPE: DNA

; ORGANISM: mus musculus  
US-09-396-196G-74836

Query Match 69.5%; Score 14.6; DB 4; Length 25;  
Best Local Similarity 81.0%; Pred. No. 1.9e+03;  
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 CACGACGAGTCTTCATCAT 21  
DB 4 CAGCAGCAGAGCCTGAGCAT 24

RESULT 14  
US-09-110-959A-11  
; Sequence 11, Application US/09110959A  
; Patent No. 6268197  
; GENERAL INFORMATION:  
; APPLICANT: Schulein, Martin  
; APPLICANT: Outtrup, Helle  
; APPLICANT: Jorgensen, Per Lina  
; APPLICANT: Bjornvad, Mads Eskelund  
; TITLE OF INVENTION: Alkaline Xyloglucanase  
; FILE REFERENCE: 5206-200-US  
; CURRENT APPLICATION NUMBER: US/09/110,959A  
; CURRENT FILING DATE: 1998-07-07  
; PRIOR APPLICATION NUMBER: 0822/97  
; PRIOR FILING DATE: 1997-07-07  
; PRIOR APPLICATION NUMBER: 1213/97  
; PRIOR FILING DATE: 1997-10-24  
; PRIOR APPLICATION NUMBER: 60/054,039  
; PRIOR FILING DATE: 1997-07-28  
; PRIOR APPLICATION NUMBER: 60/063,694  
; PRIOR FILING DATE: 1997-10-28  
; NUMBER OF SEQ ID NOS: 14  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 11  
; LENGTH: 44  
; TYPE: DNA  
; ORGANISM: Bacillus sp.  
US-09-110-959A-11

Query Match 69.5%; Score 14.6; DB 3; Length 44;  
Best Local Similarity 81.0%; Pred. No. 2.1e+03;  
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 CACGACGAGTCTTCATCAT 21  
DB 12 CAGCAGCGCGCTTCGICAT 32

RESULT 15  
US-09-205-860-3  
; Sequence 3, Application US/09205860  
; Patent No. 5981732  
; GENERAL INFORMATION:  
; APPLICANT: Lex M. Cowsett  
; TITLE OF INVENTION: ANTISENSE MODULATION OF G-ALPHA-13 EXPRESSION  
; FILE REFERENCE: RTS-0031  
; CURRENT APPLICATION NUMBER: US/09/205,860  
; CURRENT FILING DATE: 1998-12-04  
; NUMBER OF SEQ ID NOS: 87  
; SEQ ID NO 3  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: PCR Primer  
US-09-205-860-3

Query Match 67.6%; Score 14.2; DB 2; Length 20;  
Best Local Similarity 84.2%; Pred. No. 2.8e+03;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CAGCAGCAGAGTCTTCATC 19  
|||  
Db 2 CAGCAGCAGGATCTTCACC 20  
|||

Search completed: September 3, 2005, 16:22:35  
Job time : 131 secs



GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 3, 2005, 15:24:25 ; Search time 603 Seconds  
(without alignments)  
228.072 Million cell updates/sec

Title: US-10-828-394-5

Perfect score: 21

Sequence: 1 cagcagcagatcttcattcat 21

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 733684 seqs, 3274456166 residues

Total number of hits satisfying chosen parameters: 8349320

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications\_NA.\*

- 1: /cgn2\_6/ptodata/1/pubpna/US07\_PUBCOMB.seq.\*
- 2: /cgn2\_6/ptodata/1/pubpna/PCT\_NEW\_PUB.seq.\*
- 3: /cgn2\_6/ptodata/1/pubpna/US06\_NEW\_PUB.seq.\*
- 4: /cgn2\_6/ptodata/1/pubpna/US06\_PUBCOMB.seq.\*
- 5: /cgn2\_6/ptodata/1/pubpna/US07\_NEW\_PUB.seq.\*
- 6: /cgn2\_6/ptodata/1/pubpna/PCTUS\_PUBCOMB.seq.\*
- 7: /cgn2\_6/ptodata/1/pubpna/US08\_NEW\_PUB.seq.\*
- 8: /cgn2\_6/ptodata/1/pubpna/US08\_PUBCOMB.seq.\*
- 9: /cgn2\_6/ptodata/1/pubpna/US09A\_PUBCOMB.seq.\*
- 10: /cgn2\_6/ptodata/1/pubpna/US09B\_PUBCOMB.seq.\*
- 11: /cgn2\_6/ptodata/1/pubpna/US09C\_PUBCOMB.seq.\*
- 12: /cgn2\_6/ptodata/1/pubpna/US09\_NEW\_PUB.seq.\*
- 13: /cgn2\_6/ptodata/1/pubpna/US10A\_PUBCOMB.seq.\*
- 14: /cgn2\_6/ptodata/1/pubpna/US10B\_PUBCOMB.seq.\*
- 15: /cgn2\_6/ptodata/1/pubpna/US10C\_PUBCOMB.seq.\*
- 16: /cgn2\_6/ptodata/1/pubpna/US10D\_PUBCOMB.seq.\*
- 17: /cgn2\_6/ptodata/1/pubpna/US10E\_PUBCOMB.seq.\*
- 18: /cgn2\_6/ptodata/1/pubpna/US10F\_PUBCOMB.seq.\*
- 19: /cgn2\_6/ptodata/1/pubpna/US10G\_PUBCOMB.seq.\*
- 20: /cgn2\_6/ptodata/1/pubpna/US10H\_PUBCOMB.seq.\*
- 21: /cgn2\_6/ptodata/1/pubpna/US10I\_PUBCOMB.seq.\*
- 22: /cgn2\_6/ptodata/1/pubpna/US10\_NEW\_PUB.seq.\*
- 23: /cgn2\_6/ptodata/1/pubpna/US11A\_PUBCOMB.seq.\*
- 24: /cgn2\_6/ptodata/1/pubpna/US11\_NEW\_PUB.seq.\*
- 25: /cgn2\_6/ptodata/1/pubpna/US60\_NEW\_PUB.seq.\*
- 26: /cgn2\_6/ptodata/1/pubpna/US60\_PUBCOMB.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	21	100.0	21	9	US-09-944-326-4
2	21	100.0	21	10	US-09-967-726A-4
3	21	100.0	21	16	US-10-080-794-4
4	21	100.0	21	18	US-10-646-391A-4
5	21	100.0	21	20	US-10-828-394-5
6	21	100.0	21	20	US-10-828-395-5
7	21	100.0	23	18	US-10-646-436-66

Sequence 28, Appli	21	18	95.2	20	95.2	21	18	US-10-646-391A-28	Sequence 28, Appli
Sequence 9, Appli	20	20	95.2	20	95.2	21	18	US-10-646-436-9	Sequence 9, Appli
Sequence 236817,	25	21	90.5	19	90.5	25	21	US-10-956-157-236817	Sequence 236817,
Sequence 42, Appl	19	18	90.5	19	90.5	19	18	US-10-646-391A-42	Sequence 42, Appl
Sequence 43, Appl	19	18	90.5	19	90.5	19	18	US-10-646-391A-43	Sequence 43, Appl
Sequence 67, Appl	19	18	90.5	19	90.5	19	18	US-10-646-436-67	Sequence 67, Appl
Sequence 68, Appl	19	18	90.5	19	90.5	19	18	US-10-646-436-68	Sequence 68, Appl
Sequence 29, Appl	15	19	90.5	15	19	90.5	21	US-10-646-391A-29	Sequence 29, Appl
Sequence 10, Appl	16	19	90.5	16	19	90.5	21	US-10-646-436-10	Sequence 10, Appl
Sequence 15, Appl	17	17.8	84.8	17	17.8	84.8	21	US-09-967-726A-15	Sequence 15, Appl
Sequence 15, Appl	18	17.8	84.8	18	17.8	84.8	21	US-10-080-794-15	Sequence 15, Appl
Sequence 17, Appl	19	17.8	84.8	19	17.8	84.8	21	US-09-790-338A-17	Sequence 17, Appl
Sequence 15, Appl	20	17.8	84.8	20	17.8	84.8	50	US-10-434-583-15	Sequence 15, Appl
Sequence 285427,	25	21	81.0	25	21	81.0	25	US-10-956-157-285427	Sequence 285427,
Sequence 187913,	22	22	78.1	22	22	78.1	22	US-10-719-956-187913	Sequence 187913,
Sequence 217934,	23	22	78.1	23	22	78.1	25	US-10-719-956-217934	Sequence 217934,
Sequence 174230,	24	24	77.1	24	24	77.1	25	US-10-956-157-174230	Sequence 174230,
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Sequence 6, Appli	26	26	77.1	26	26	77.1	32	US-10-690-034-6	Sequence 6, Appli
Sequence 7759, Ap	27	27	76.2	27	27	76.2	25	US-10-809-189-7759	Sequence 7759, Ap
Sequence 190997,	28	28	75.2	28	28	75.2	25	US-10-719-956-190997	Sequence 190997,
Sequence 190998,	29	29	75.2	29	29	75.2	25	US-10-719-956-190998	Sequence 190998,
Sequence 539340,	30	30	73.3	30	30	73.3	25	US-10-719-956-539340	Sequence 539340,
Sequence 562252,	31	31	73.3	31	31	73.3	25	US-10-719-956-562252	Sequence 562252,
Sequence 599108,	32	32	73.3	32	32	73.3	25	US-10-719-956-599108	Sequence 599108,
Sequence 678358,	33	33	73.3	33	33	73.3	25	US-10-719-956-678358	Sequence 678358,
Sequence 46, Appl	34	34	72.4	34	34	72.4	22	US-09-823-549-46	Sequence 46, Appl
Sequence 79840, A	35	35	72.4	35	35	72.4	22	US-10-685-992-46	Sequence 79840, A
Sequence 99916, A	36	36	72.4	36	36	72.4	25	US-10-719-900-79840	Sequence 99916, A
Sequence 516755,	37	37	72.4	37	37	72.4	25	US-10-719-900-99916	Sequence 516755,
Sequence 859600,	38	38	72.4	38	38	72.4	25	US-10-719-900-516755	Sequence 859600,
Sequence 74777, A	39	39	72.4	39	39	72.4	25	US-10-719-900-859600	Sequence 74777, A
Sequence 483005,	40	40	72.4	40	40	72.4	25	US-10-719-956-74777	Sequence 483005,
Sequence 43, Appl	41	41	72.4	41	41	72.4	25	US-10-719-956-483005	Sequence 43, Appl
Sequence 1, Appli	42	42	70.5	42	42	70.5	20	US-10-007-010-43	Sequence 1, Appli
Sequence 2, Appli	43	43	70.5	43	43	70.5	21	US-09-944-326-1	Sequence 2, Appli
Sequence 1, Appli	44	44	70.5	44	44	70.5	21	US-09-944-326-2	Sequence 1, Appli
Sequence 1, Appli	45	45	70.5	45	45	70.5	21	US-09-967-726A-1	Sequence 1, Appli

ALIGNMENTS

RESULT 1  
US-09-944-326-4  
; Sequence 4, Application US/09944326  
; Patent No. US20020128220A1  
; GENERAL INFORMATION:  
; APPLICANT: Gleave, Martin  
; APPLICANT: Rennie, Paul S.  
; APPLICANT: Miyake, Hideaki  
; APPLICANT: Nelson, Colleen  
; TITLE OF INVENTION: TRPM-2 ANTISENSE THERAPY  
; FILE REFERENCE: UBC.P-020-2  
; CURRENT APPLICATION NUMBER: US/09/944,326  
; CURRENT FILING DATE: 2001-08-30  
; PRIOR APPLICATION NUMBER: 60/121,726  
; PRIOR FILING DATE: 1999-02-26  
; PRIOR APPLICATION NUMBER: 09/913,325  
; PRIOR FILING DATE: 2001-08-10  
; NUMBER OF SEQ ID NOS: 14  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 4  
; LENGTH: 21  
; TYPE: DNA  
; ORGANISM: HUMAN  
; FEATURE:  
; OTHER INFORMATION: antisense TRPM-2 ODN  
US-09-944-326-4

Query Match 100.0%; Score 21; DB 9; Length 21;  
Best Local Similarity 100.0%; Pred. No. 3.5;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 1 CAGCAGCAGAGTCTTTCATCAT 21
Db 1 CAGCAGCAGAGTCTTTCATCAT 21

RESULT 2
US-09-967-726A-4
; Sequence 4, Application US/09967726A
; Publication No. US20030158130A1
; GENERAL INFORMATION:
; APPLICANT: Gleave, Martin
; APPLICANT: Rennie, Paul S.
; APPLICANT: Miyake, Hideaki
; APPLICANT: Nelson, Colleen
; APPLICANT: Zellweger, Tobias
; TITLE OF INVENTION: Chemo- and Radiation-Sensitization of Cancer by Antisense TRPM-2
; FILE REFERENCE: UBC.P-022
; CURRENT APPLICATION NUMBER: US/09/967,726A
; CURRENT FILING DATE: 2001-09-28
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 21
; TYPE: DNA
; ORGANISM: human
US-09-967-726A-4

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Best Local Similarity 100.0%; Pred. No. 3.5; Indels 0; Gaps 0;
Matches 21; Conservative 0; Mismatches 0;

Qy 1 CAGCAGCAGAGTCTTTCATCAT 21
Db 1 CAGCAGCAGAGTCTTTCATCAT 21

RESULT 3
US-10-080-794-4
; Sequence 4, Application US/10080794
; Publication No. US20030166591A1
; GENERAL INFORMATION:
; APPLICANT: Gleave, Martin
; APPLICANT: Rennie, Paul S.
; APPLICANT: Miyake, Hideaki
; APPLICANT: Nelson, Colleen
; APPLICANT: Monia, Brett P.
; TITLE OF INVENTION: TRPM-2 ANTISENSE THERAPY USING AN OLIGONUCLEOTIDE
; FILE REFERENCE: UBC.P-020-3
; CURRENT APPLICATION NUMBER: US/10/080,794
; CURRENT FILING DATE: 2002-02-22
; PRIOR APPLICATION NUMBER: 60/121,726
; PRIOR FILING DATE: 1999-02-26
; PRIOR APPLICATION NUMBER: 09/913,325
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: 09/944,326
; PRIOR FILING DATE: 2001-08-30
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 21
; TYPE: DNA
; ORGANISM: HUMAN
; FEATURE:
; OTHER INFORMATION: antisense TRPM-2 ODN
US-10-080-794-4

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Matches 21; Conservative 0; Mismatches 0;

Qy 1 CAGCAGCAGAGTCTTTCATCAT 21
Db 1 CAGCAGCAGAGTCTTTCATCAT 21

RESULT 4
US-10-646-391A-4
; Sequence 4, Application US/10646391A
; Publication No. US20040082534A1
; GENERAL INFORMATION:
; APPLICANT: Gleave, Martin
; APPLICANT: Jansen, Burkhard
; TITLE OF INVENTION: Treatment of Melanoma by Reduction in Clusterin Levels
; FILE REFERENCE: UBC.P-035
; CURRENT APPLICATION NUMBER: US/10/646,391A
; CURRENT FILING DATE: 2003-08-21
; PRIOR APPLICATION NUMBER: US 60/405,193
; PRIOR FILING DATE: 2002-08-21
; PRIOR APPLICATION NUMBER: US 60/319,748
; PRIOR FILING DATE: 2002-12-02
; PRIOR APPLICATION NUMBER: US 60/408,152
; PRIOR FILING DATE: 2002-09-03
; PRIOR APPLICATION NUMBER: US 60/473,387
; PRIOR FILING DATE: 2003-05-20
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4
; LENGTH: 21
; TYPE: DNA
; ORGANISM: human
US-10-646-391A-4

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Matches 21; Conservative 0; Mismatches 0;

Qy 1 CAGCAGCAGAGTCTTTCATCAT 21
Db 1 CAGCAGCAGAGTCTTTCATCAT 21

RESULT 5
US-10-828-394-5
; Sequence 5, Application US/10828394
; Publication No. US20040220131A1
; GENERAL INFORMATION:
; APPLICANT: Jackson, John
; APPLICANT: Burt, Helen
; APPLICANT: Springate, Christopher
; APPLICANT: Gleave, Martin
; TITLE OF INVENTION: Method for Treatment of Cancerous Angiogenic Disorders
; FILE REFERENCE: UBC.P-033
; CURRENT APPLICATION NUMBER: US/10/828,394
; CURRENT FILING DATE: 2004-04-19
; PRIOR APPLICATION NUMBER: US 60/464,159
; PRIOR FILING DATE: 2003-04-18
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 5
; LENGTH: 21
; TYPE: DNA
; ORGANISM: human
US-10-828-394-5

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Best Local Similarity 100.0%; Pred. No. 3.5; Indels 0; Gaps 0;
Matches 21; Conservative 0; Mismatches 0;

Qy 1 CAGCAGCAGAGTCTTTCATCAT 21
Db 1 CAGCAGCAGAGTCTTTCATCAT 21
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US-10-828-395-5
; Sequence 5, Application US/10828395
; Publication No. US20040224914A1
; GENERAL INFORMATION:
; APPLICANT: Jackson, John
; APPLICANT: Burt, Helen
; APPLICANT: Springate, Christopher
; APPLICANT: Gleave, Martin
; TITLE OF INVENTION: Method for Treatment of Angiogenic Disorders
; FILE REFERENCE: UBC.P-032
; CURRENT APPLICATION NUMBER: US/10/828,395
; CURRENT FILING DATE: 2004-04-19
; PRIOR APPLICATION NUMBER: US 60/464,159
; PRIOR FILING DATE: 2003-04-18
; PRIOR APPLICATION NUMBER: US 60/464,160
; PRIOR FILING DATE: 2003-04-18
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 5
; LENGTH: 21
; TYPE: DNA
; ORGANISM: human
US-10-828-395-5

Query Match          100.0%; Score 21; DB 20; Length 21;
Best Local Similarity 100.0%; Pred. No. 3.5;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAGCAGCAGAGTCTTCATCAT 21
Db 1 CAGCAGCAGAGTCTTCATCAT 21

RESULT 7
US-10-646-436-66/c
; Sequence 66, Application US/10646436
; Publication No. US20040096882A1
; GENERAL INFORMATION:
; APPLICANT: Jansen, Burkhard
; APPLICANT: Gleave, Martin
; APPLICANT: Signaevsky, Maxim
; APPLICANT: Beraldi, Eliana
; APPLICANT: Trougakos, Ioannis
; APPLICANT: Gonos, Efstathios
; TITLE OF INVENTION: RNAi Probes Targeting Cancer-Related Proteins
; FILE REFERENCE: UBC.P-030
; CURRENT APPLICATION NUMBER: US/10/646,436
; CURRENT FILING DATE: 2003-08-21
; PRIOR APPLICATION NUMBER: US 60/405,193
; PRIOR FILING DATE: 2002-08-21
; PRIOR APPLICATION NUMBER: US 60/408,152
; PRIOR FILING DATE: 2002-09-03
; PRIOR APPLICATION NUMBER: US 60/473,387
; PRIOR FILING DATE: 2003-05-20
; NUMBER OF SEQ ID NOS: 68
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 66
; LENGTH: 23
; TYPE: DNA
; ORGANISM: human
US-10-646-436-66

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Best Local Similarity 100.0%; Pred. No. 3.5;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAGCAGCAGAGTCTTCATCAT 21
Db 23 CAGCAGCAGAGTCTTCATCAT 3

RESULT 8
US-10-828-395-5
; Sequence 5, Application US/10828395
; Publication No. US20040224914A1
; GENERAL INFORMATION:
; APPLICANT: Jackson, John
; APPLICANT: Burt, Helen
; APPLICANT: Springate, Christopher
; APPLICANT: Gleave, Martin
; TITLE OF INVENTION: Method for Treatment of Angiogenic Disorders
; FILE REFERENCE: UBC.P-032
; CURRENT APPLICATION NUMBER: US/10/828,395
; CURRENT FILING DATE: 2004-04-19
; PRIOR APPLICATION NUMBER: US 60/464,159
; PRIOR FILING DATE: 2003-04-18
; PRIOR APPLICATION NUMBER: US 60/464,160
; PRIOR FILING DATE: 2003-04-18
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 5
; LENGTH: 21
; TYPE: DNA
; ORGANISM: human
US-10-828-395-5

Query Match          100.0%; Score 21; DB 20; Length 21;
Best Local Similarity 100.0%; Pred. No. 3.5;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAGCAGCAGAGTCTTCATCAT 21
Db 1 CAGCAGCAGAGTCTTCATCAT 21

RESULT 9
US-10-646-436-9/c
; Sequence 9, Application US/10646436
; Publication No. US20040096882A1
; GENERAL INFORMATION:
; APPLICANT: Jansen, Burkhard
; APPLICANT: Gleave, Martin
; APPLICANT: Signaevsky, Maxim
; APPLICANT: Beraldi, Eliana
; APPLICANT: Trougakos, Ioannis
; APPLICANT: Gonos, Efstathios
; TITLE OF INVENTION: RNAi Probes Targeting Cancer-Related Proteins
; FILE REFERENCE: UBC.P-030
; CURRENT APPLICATION NUMBER: US/10/646,436
; CURRENT FILING DATE: 2003-08-21
; PRIOR APPLICATION NUMBER: US 60/405,193
; PRIOR FILING DATE: 2002-08-21
; PRIOR APPLICATION NUMBER: US 60/408,152
; PRIOR FILING DATE: 2002-09-03
; PRIOR APPLICATION NUMBER: US 60/473,387
; PRIOR FILING DATE: 2003-05-20
; NUMBER OF SEQ ID NOS: 68
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 9
; LENGTH: 21
; TYPE: DNA
; ORGANISM: artificial
; FEATURE:
; OTHER INFORMATION: RNAi for human clusterin
US-10-646-436-9

Query Match          95.2%; Score 20; DB 18; Length 21;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 AGCAGCAGAGTCTTCATCAT 21
Db 20 AGCAGCAGAGTCTTCATCAT 1

RESULT 9
US-10-646-436-9/c
; Sequence 9, Application US/10646436
; Publication No. US20040096882A1
; GENERAL INFORMATION:
; APPLICANT: Jansen, Burkhard
; APPLICANT: Gleave, Martin
; APPLICANT: Signaevsky, Maxim
; APPLICANT: Beraldi, Eliana
; APPLICANT: Trougakos, Ioannis
; APPLICANT: Gonos, Efstathios
; TITLE OF INVENTION: RNAi Probes Targeting Cancer-Related Proteins
; FILE REFERENCE: UBC.P-030
; CURRENT APPLICATION NUMBER: US/10/646,436
; CURRENT FILING DATE: 2003-08-21
; PRIOR APPLICATION NUMBER: US 60/405,193
; PRIOR FILING DATE: 2002-08-21
; PRIOR APPLICATION NUMBER: US 60/408,152
; PRIOR FILING DATE: 2002-09-03
; PRIOR APPLICATION NUMBER: US 60/473,387
; PRIOR FILING DATE: 2003-05-20
; NUMBER OF SEQ ID NOS: 68
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 9
; LENGTH: 21
; TYPE: DNA
; ORGANISM: artificial
; FEATURE:
; OTHER INFORMATION: RNAi for human clusterin
US-10-646-436-9

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QY 2 AGCAGCAGAGTCTTCATCAT 21
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Publication No. US20050118625A1										
GENERAL INFORMATION:										
APPLICANT: Wyeth										
TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH										
TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES										
FILE REFERENCE: 031896-043000 (AM 101081)										
CURRENT APPLICATION NUMBER: US/10/956,157										
CURRENT FILING DATE: 2004-10-04										
NUMBER OF SEQ ID NOS: 319805										
SOFTWARE: PatentIn version 3.2										
SEQ ID NO 236817										
LENGTH: 25										
TYPE: DNA										
ORGANISM: Probe Sequence										
US-10-956-157-236817										
Query Match										
Best Local Similarity										
Matches										
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DB	25	AGCAGCAGAGTCTTCATCAT 6								
US-10-956-157-236817										
Sequence 42, Application US/10646391A										
Publication No. US20040082534A1										
GENERAL INFORMATION:										
APPLICANT: Jansen, Burkhard										
TITLE OF INVENTION: Treatment of Melanoma by Reduction in Clusterin Levels										
FILE REFERENCE: USC P-035										
CURRENT APPLICATION NUMBER: US/10/646,391A										
CURRENT FILING DATE: 2003-08-21										
PRIOR FILING DATE: 2002-08-21										
PRIOR FILING DATE: 2002-12-02										
PRIOR APPLICATION NUMBER: US 60/408,152										
PRIOR FILING DATE: 2002-09-03										
PRIOR APPLICATION NUMBER: US 60/473,387										
NUMBER OF SEQ ID NOS: 43										
SOFTWARE: PatentIn version 3.2										
SEQ ID NO 42										
LENGTH: 19										
TYPE: RNA										
ORGANISM: artificial										
FEATURE:										
OTHER INFORMATION: RNAi for human clusterin										
US-10-646-391A-42										
Query Match										
Best Local Similarity										
Matches										
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DB	19	GCAGCAGAGTCTTCATCAT 1								
US-10-646-391A-42										
Sequence 43, Application US/10646391A										
Publication No. US20040082534A1										
GENERAL INFORMATION:										
APPLICANT: Jansen, Burkhard										
TITLE OF INVENTION: Treatment of Melanoma by Reduction in Clusterin Levels										
FILE REFERENCE: USC P-035										
CURRENT APPLICATION NUMBER: US/10/646,391A										
CURRENT FILING DATE: 2003-08-21										
PRIOR FILING DATE: 2002-08-21										
PRIOR FILING DATE: 2002-12-02										
PRIOR APPLICATION NUMBER: US 60/408,152										
PRIOR FILING DATE: 2002-09-03										

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Best Local Similarity 73.7%; Pred. No. 31;
Matches 14; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

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Db 1 GCAGCAGAGUCUUCAUCAU 19

Search completed: September 3, 2005, 16:32:54
Job time : 609 secs

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Db 19 GCAGCAGAGTCTTCATCAT 1

RESULT 14

US-10-646-436-68

; Sequence 68, Application US/10646436

; Publication No. US20040096882A1

; GENERAL INFORMATION:

; APPLICANT: Jansen, Burkhard

; APPLICANT: Gleave, Martin

; APPLICANT: Signaevsky, Maxim

; APPLICANT: Beraldi, Eliana

; APPLICANT: Trougakos, Ioannis

; APPLICANT: Gonos, Efsthios

; TITLE OF INVENTION: RNAi Probes Targeting Cancer-Related Proteins

; FILE REFERENCE: USC.P-030

; CURRENT APPLICATION NUMBER: US/10/646,436

; CURRENT FILING DATE: 2003-08-21

; PRIOR APPLICATION NUMBER: US 60/405,193

; PRIOR FILING DATE: 2002-08-21

; PRIOR APPLICATION NUMBER: US 60/408,152

; PRIOR FILING DATE: 2002-09-03

; PRIOR APPLICATION NUMBER: US 60/473,387

; PRIOR FILING DATE: 2003-05-20

; NUMBER OF SEQ ID NOS: 68

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 68

; LENGTH: 19

; TYPE: RNA

; ORGANISM: artificial

; FEATURE:

; OTHER INFORMATION: RNAi fo rhuman clusterin

US-10-646-436-68

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Query Match      90.5%; Score 19; DB 18; Length 19;
Best Local Similarity 73.7%; Pred. No. 31;
Matches 14; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

Qy      3 GCAGCAGAGTCTTCATCAT 21
        | | | | | | | | | | | | |
Db      1 GCAGCAGAGUCUUCAUCAU 19

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RESULT 15
US-10-646-391A-29
; Sequence 29, Application US/10646391A
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; GENERAL INFORMATION:
; APPLICANT: Gleave, Martin
; APPLICANT: Jansen, Burkhard
; TITLE OF INVENTION: Treatment of Melanoma by Reduction in Clusterin Levels
; FILE REFERENCE: UBC P-035
; CURRENT APPLICATION NUMBER: US/10/646,391A
; CURRENT FILING DATE: 2003-08-21
; PRIOR APPLICATION NUMBER: US 60/405,193
; PRIOR FILING DATE: 2002-08-21
; PRIOR APPLICATION NUMBER: US 60/319,748
; PRIOR FILING DATE: 2002-12-02
; PRIOR APPLICATION NUMBER: US 60/408,152
; PRIOR FILING DATE: 2002-09-03
; PRIOR APPLICATION NUMBER: US 60/473,387
; PRIOR FILING DATE: 2003-05-20
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 29
; LENGTH: 21
; TYPE: DNA
; ORGANISM: artificial
; FEATURE:
; OTHER INFORMATION: RNAi for human clusterin
US-10-646-391A-29

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Query Match 90.5%; Score 19; DB 18; Length 21;

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OM nucleic - nucleic search, using sw model

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(without alignments)  
547.369 Million cell updates/sec

Title: US-10-828-394-5

Perfect score: 21  
Sequence: 1 cagcagcagagcttcacat 21

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 1839042

Minimum DB seq length: 0  
Maximum DB seq length: 50

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

GenEmbl: \*  
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2: gb\_hgt: \*  
3: gb\_in: \*  
4: gb\_om: \*  
5: gb\_ov: \*  
6: gb\_pat: \*  
7: gb\_ph: \*  
8: gb\_pl: \*  
9: gb\_pr: \*  
10: gb\_ro: \*  
11: gb\_sta: \*  
12: gb\_sy: \*  
13: gb\_un: \*  
14: gb\_vi: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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C 2	21	100.0	23	6	CQ786178 Sequence
C 3	20	95.2	21	6	CQ786121 Sequence
C 4	20	95.2	21	6	CQ786639 Sequence
C 5	19	90.5	19	6	CQ786179 Sequence
C 6	19	90.5	19	6	CQ786180 Sequence
C 7	19	90.5	19	6	CQ786653 Sequence
C 8	19	90.5	19	6	CQ786654 Sequence
C 9	19	90.5	21	6	CQ786122 Sequence
C 10	19	90.5	21	6	CQ786640 Sequence
C 11	17.8	84.8	50	6	AR374192 Sequence
C 12	16.2	77.1	32	6	AR274120 Sequence
C 13	16.2	77.1	32	6	AR444937 Sequence
C 14	16.2	77.1	48	6	A76301 Sequence 7
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C 17	15.4	73.3	39	6	A12568 fragment of
C 18	15.4	73.3	45	6	A05116 Oligonucleo
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C 23	14.8	70.5	31	6	AR070079	AR070079 Sequence
C 24	14.8	70.5	31	6	AR258163	AR258163 Sequence
C 25	14.8	70.5	31	6	AX670795	AX670795 Sequence
C 26	14.6	69.5	48	6	A76303	A76303 Sequence 9
C 27	14.4	68.6	30	6	BD186389	BD186389 Peptides
C 28	14.4	68.6	39	6	A08490	A08490 oligonucleo
C 29	14.4	68.6	39	6	A08491	A08491 oligonucleo
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C 31	14.4	68.6	39	6	A12570	A12570 fragment of
C 32	14.2	67.6	20	6	AR085567	AR085567 Sequence
C 33	14.2	67.6	20	6	AR221110	AR221110 Sequence
C 34	14.2	67.6	22	6	AX697095	AX697095 Sequence
C 35	14.2	67.6	24	6	AR222129	AR222129 Sequence
C 36	14.2	67.6	26	6	AX697096	AX697096 Sequence
C 37	14.2	67.6	30	6	A70102	A70102 Sequence 20
C 38	14.2	67.6	30	6	AR148235	AR148235 Sequence
C 39	14.2	67.6	30	6	AR204084	AR204084 Sequence
C 40	14.2	67.6	30	6	BD077090	BD077090 Lipocalin
C 41	14.2	67.6	38	6	CQ817644	CQ817644 Sequence
C 42	14.2	67.6	38	6	CQ817645	CQ817645 Sequence
C 43	14.2	67.6	38	6	CQ867639	CQ867639 Sequence
C 44	14.2	67.6	38	6	CQ867640	CQ867640 Sequence
C 45	14.2	67.6	47	6	AR291280	AR291280 Sequence

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RESULT 1  
LOCUS CQ786615 21 bp DNA linear PAT 24-MAR-2004  
DEFINITION Sequence 4 from Patent WO2004018675.  
ACCESSION CQ786615  
VERSION CQ786615.1 GI:45721635  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1  
AUTHORS Jansen,B.  
TREATMENT of melanoma by reduction in clusterin levels  
TITLE Patent: WO 2004018675-A 4 04-MAR-2004;  
JOURNAL The University of British Columbia (CA); Gleave, Martin E. (CA)  
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Db 1 CAGCAGCAGAGCTTCATCAT 21  
RESULT 2  
LOCUS CQ786178/c 23 bp DNA linear PAT 24-MAR-2004  
DEFINITION Sequence 66 from Patent WO2004018676.  
ACCESSION CQ786178  
VERSION CQ786178.1 GI:45721281  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

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REFERENCE
AUTHORS      Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
TITLE        Jansen,B., Gleave,M.E., Signaevsky,M., Beraldi,E., Trougakos,I. and
JOURNAL      Gonos,E.
FEATURES     Rnai probes targeting cancer-related proteins
              Patent: WO 2004018676-A 66 04-MAR-2004;
              The University of British Columbia (CA)
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Db 23 CAGCAGCAGAGTCTTCATCAT 3

RESULT 3
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DEFINITION Sequence 9 from Patent WO2004018676.
ACCESSION CQ786121
VERSION   CQ786121.1 GI:45721224
KEYWORDS  .
SOURCE    synthetic construct
          synthetic construct
          other sequences; artificial sequences.
ORGANISM  Jansen,B., Gleave,M.E., Signaevsky,M., Beraldi,E., Trougakos,I. and
          Gonos,E.
          Rnai probes targeting cancer-related proteins
          Patent: WO 2004018676-A 9 04-MAR-2004;
          The University of British Columbia (CA)
          Location/Qualifiers
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Db 20 AGCAGCAGAGTCTTCATCAT 1

RESULT 4
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DEFINITION Sequence 28 from Patent WO2004018675.
ACCESSION CQ786639
VERSION   CQ786639.1 GI:45721659
KEYWORDS  .
SOURCE    synthetic construct
          synthetic construct
          other sequences; artificial sequences.
ORGANISM  Jansen,B.
          Treatment of melanoma by reduction in clusterin levels
          Patent: WO 2004018675-A 28 04-MAR-2004;
          The University of British Columbia (CA); Gleave, Martin E. (CA)
          Location/Qualifiers
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RESULT 5
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LOCUS      CQ786179 19 bp RNA linear PAT 24-MAR-2004
DEFINITION Sequence 67 from Patent WO2004018676.
ACCESSION CQ786179
VERSION   CQ786179.1 GI:45721282
KEYWORDS  .
SOURCE    synthetic construct
          synthetic construct
          other sequences; artificial sequences.
ORGANISM  Jansen,B., Gleave,M.E., Signaevsky,M., Beraldi,E., Trougakos,I. and
          Gonos,E.
          Rnai probes targeting cancer-related proteins
          Patent: WO 2004018676-A 67 04-MAR-2004;
          The University of British Columbia (CA)
          Location/Qualifiers
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Db 19 GCAGCAGAGTCTTCATCAT 1

RESULT 6
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DEFINITION Sequence 68 from Patent WO2004018676.
ACCESSION CQ786180
VERSION   CQ786180.1 GI:45721283
KEYWORDS  .
SOURCE    synthetic construct
          synthetic construct
          other sequences; artificial sequences.
ORGANISM  Jansen,B., Gleave,M.E., Signaevsky,M., Beraldi,E., Trougakos,I. and
          Gonos,E.
          Rnai probes targeting cancer-related proteins
          Patent: WO 2004018676-A 68 04-MAR-2004;
          The University of British Columbia (CA)
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DEFINITION Sequence 42 from Patent WO2004018675.  
ACCESSION CQ786653  
VERSION CQ786653.1 GI:45721673  
KEYWORDS synthetic construct  
SOURCE synthetic construct  
ORGANISM other sequences; artificial sequences.  
REFERENCE 1  
AUTHORS Jansen, B., Gleave, M.E., Signaevsky, M., Beraldi, E., Trougakos, I. and  
TITLE Rnai probes targeting cancer-related proteins  
JOURNAL Patent: WO 2004018675-A 10 04-MAR-2004;  
The University of British Columbia (CA)  
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DEFINITION Sequence 43 from Patent WO2004018675.  
ACCESSION CQ786654  
VERSION CQ786654.1 GI:45721674  
KEYWORDS synthetic construct  
SOURCE synthetic construct  
ORGANISM other sequences; artificial sequences.  
REFERENCE 1  
AUTHORS Jansen, B.  
TITLE Treatment of melanoma by reduction in clusterin levels  
JOURNAL Patent: WO 2004018675-A 43 04-MAR-2004;  
The University of British Columbia (CA); Gleave, Martin E. (CA)  
FEATURES Location/Qualifiers  
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/note="RNAi for human clusterin"

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Db 1 GCAGCAGAGTCTTCATCAT 19

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LOCUS 19 bp RNA linear PAT 24-MAR-2004  
DEFINITION Sequence 43 from Patent WO2004018675.  
ACCESSION CQ786654  
VERSION CQ786654.1 GI:45721674  
KEYWORDS synthetic construct  
SOURCE synthetic construct  
ORGANISM other sequences; artificial sequences.  
REFERENCE 1  
AUTHORS Jansen, B.  
TITLE Treatment of melanoma by reduction in clusterin levels  
JOURNAL Patent: WO 2004018675-A 43 04-MAR-2004;  
The University of British Columbia (CA); Gleave, Martin E. (CA)  
FEATURES Location/Qualifiers  
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DEFINITION Sequence 29 from Patent WO2004018675.  
ACCESSION CQ786640  
VERSION CQ786640.1 GI:45721660  
KEYWORDS synthetic construct  
SOURCE synthetic construct  
ORGANISM other sequences; artificial sequences.  
REFERENCE 1  
AUTHORS Jansen, B.  
TITLE Treatment of melanoma by reduction in clusterin levels  
JOURNAL Patent: WO 2004018675-A 29 04-MAR-2004;  
The University of British Columbia (CA); Gleave, Martin E. (CA)  
FEATURES Location/Qualifiers  
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VERSION CQ786640.1 GI:45721660  
KEYWORDS synthetic construct  
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REFERENCE 1  
AUTHORS Jansen, B.  
TITLE Treatment of melanoma by reduction in clusterin levels  
JOURNAL Patent: WO 2004018675-A 29 04-MAR-2004;  
The University of British Columbia (CA); Gleave, Martin E. (CA)  
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ACCESSION AR374192  
VERSION AR374192.1 GI:40076792  
KEYWORDS Unknown.  
SOURCE Unknown.  
ORGANISM Unknown.

Unclassified.  
REFERENCE 1 (bases 1 to 50)  
AUTHORS Novick,D., Dinarello,C., Rubinstein,M. and Kim,S.H.  
TITLE Interleukin-18 binding proteins, their preparation and use for blocking the activity of IL-18  
JOURNAL Patent: US 605280-A 15-12-AUG-2003;  
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RESULT 12  
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DEFINITION Sequence 6 from patent US 6504083.  
ACCESSION AR274120  
VERSION AR274120.1 GI:29706097  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 32)  
AUTHORS Barbour,E., Meyer,T.E.C. and Saad,M.E.  
TITLE Maize Goe-2 promoters  
JOURNAL Patent: US 6504083-A 6 07-JAN-2003;  
FEATURES Location/Qualifiers  
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DEFINITION Sequence 6 from patent US 6670467.  
ACCESSION AR444937  
VERSION AR444937.1 GI:42672814  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 32)  
AUTHORS Barbour,E., Meyer,T.E.C. and Saad,M.E.  
TITLE Maize promoters  
JOURNAL Patent: US 6670467-A 6 30-DEC-2003;  
FEATURES Location/Qualifiers  
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ORIGIN  
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DEFINITION Sequence 7 from Patent WO9319173.  
ACCESSION A76301  
VERSION A76301.1 GI:6088388  
KEYWORDS  
SOURCE unidentified  
ORGANISM unidentified  
REFERENCE 1 (bases 1 to 48)  
AUTHORS Maegert,H.  
TITLE DNA CODING FOR APHRODISIN  
JOURNAL Patent: WO 9319173-A 7 30-SEP-1993;  
FORSSMANN WOLF GEORG (DE)  
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DEFINITION DNA sequence coding for human pancreas-2 signal peptide.  
ACCESSION E01067  
VERSION E01067.1 GI:2169326  
KEYWORDS JP 1987000276-A/9.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 48)  
AUTHORS Takiguchi,H., Furukawa,H. and Tani,T.  
TITLE PRODUCTION OF PANCREAS ELASTASE  
JOURNAL Patent: JP 1987000276-A 9 06-JAN-1987;  
SANKYO CO LTD NIPPON SODA CO LTD, NISSAN CHEM IND LTD, TOYO SODA MFG CO LTD  
COMMENT OS homo sapiens (human)  
PN JP 1987000276-A/9  
PD 06-JAN-1987  
PF 25-JUN-1985 JP 1985138494  
PI TAKIGUCHI HIROSHI, FURUKAWA HIDEHIKO, TANI TOKIO PC  
C12N9/66,A61K35/74,A61K37/54,C12N15/00//C07H21/04,(C12N9/66, PC C12R1:19),  
PC (C12N15/00,C12R1:19);  
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CC topology: Linear;  
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CC anti-sense: No;  
CC \*source: tissue\_type=pancreas;

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ORIGIN

Query Match 77.1%; Score 16.2; DB 6; Length 48;
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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

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## SUMMARIES

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16	17.8	84.8	50	2	AAx24790 Interleuk
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30	14.8	70.5	21	12	ADL70404	ADL70404 Antisense
31	14.8	70.5	27	4	AAH40683	AAH40683 SNP speci
32	14.8	70.5	30	2	AAZ12445	AAZ12445 PCR prime
33	14.8	70.5	31	2	AAQ69972	AAQ69972 5' sense 1
34	14.6	69.5	24	6	ABL61345	ABL61345 Naja naja
35	14.6	69.5	33	6	ABK49118	ABK49118 Human tra
36	14.6	69.5	34	4	AAH79384	AAH79384 Plasmodium
37	14.6	69.5	44	2	AAH06964	AAH06964 Bacillus
38	14.4	68.6	30	8	ABZ77331	ABZ77331 Nucleotid
39	14.2	67.6	20	2	AAZ31857	AAZ31857 PCR prime
40	14.2	67.6	20	6	ABK69555	ABK69555 Rat phosph
41	14.2	67.6	20	12	ADH64379	ADH64379 Human glu
42	14.2	67.6	20	12	ADH63983	ADH63983 Human glu
43	14.2	67.6	22	3	AAC58494	AAC58494 Human PRO
44	14.2	67.6	22	3	AAA37208	AAA37208 Human PRO
45	14.2	67.6	22	4	AAF54314	AAF54314 Primer #4

## ALIGNMENTS

## RESULT 1

AAA94226  
ID AAA94226 standard; DNA; 21 BP.

AC AAA94226;

DT 12-JAN-2001 (first entry)

DE Human testosterone-repressed prostate message-2 antisense oligo #2.

KW Human: testosterone-repressed prostate message-2; TRPM-2; clusterin;  
KW sulfated glycoprotein-2; SGP-2; cancer; antisense oligonucleotide; ss.

OS Homo sapiens.

PN WO200049937-A2.

XX 31-AUG-2000.

PF 25-FEB-2000; 2000WO-US004875.

PR 26-FEB-1999; 99US-0121726P.

XX (UYBR-) UNIV BRITISH COLUMBIA.

PI Gleave M, Rennie PS, Miyake H, Nelson C;

DR WPI; 2000-533132/48.

PT Treating prostatic tumors and renal cancers by antisense inhibition of  
PT the testosterone-repressed prostate messenger-2 gene.

PS Claim 3; Page 36; 38pp; English.

XX The present sequence is an antisense oligonucleotide directed at the  
CC human testosterone-repressed prostate message-2 (TRPM-2, also known as  
CC clusterin, sulfated glycoprotein-2 or SGP-2). The sequence was shown to  
CC promote the regression of tumours, and oligonucleotides directed at human  
CC TRPM-2 can be used in the treatment of tumour cells expressing the TRPM-2  
CC gene. These include prostate cancer, renal cell cancer and some breast  
CC cancer cells. In addition to this, they also increase the  
CC chemosensitivity of the cells, meaning that conventional chemotherapy is  
CC more effective

Tue Sep 13 09:41:58 2005

us-10-828-394-5.rng

```
XX SQ Sequence 21 BP; 6 A; 6 C; 4 G; 5 T; 0 U; 0 Other;
Query Match 100.0%; Score 21; DB 3; Length 21;
Best Local Similarity 100.0%; Pred. No. 8.2;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAGCAGCAGAGTCTTCATCAT 21
Db 1 CAGCAGCAGAGTCTTCATCAT 21

RESULT 2
ACF36398
ID ACF36398 standard; DNA; 21 BP.
XX AC ACF36398;
XX DT 18-DEC-2003 (first entry)
XX DE TRPM-2 antisense oligonucleotide.
XX KW TRPM-2; testosterone-repressed prostate message-2; cytosstatic; androgen;
XX KW prostate cancer; anti-apoptotic protein; antisense; ss.
XX OS Synthetic.
XX OS Homo sapiens.
XX PN WO2003072591-A1.
XX PD 04-SEP-2003.
XX PF 20-FEB-2003; 2003WO-US005305.
XX PR 22-FEB-2002; 2002US-00080794.
XX PA (UYBR-) UNIV BRITISH COLUMBIA.
XX PI Gleave M, Rennie PS, Miyake H, Nelson C, Monia BP;
XX WPI; 2003-689981/65.
XX DR New modified antisense oligonucleotide, useful particularly for treating
XX PT prostatic cancer, inhibits the testosterone-repressed prostate message-2.
XX PS Claim 1; Page 25; 44pp; English.
XX CC The invention relates to a compound consisting of an oligonucleotide with
XX CC a phosphorothioate backbone throughout, in which: (a) sugars on
XX CC nucleotide residues 1-4 and 18-21 are 2'-O-methoxyethyl modified, and the
XX CC remaining nucleotides 5-17 are 2'-deoxy; and (b) the cytosines at
XX CC positions 1, 4 and 19 are 5-methylated. Oligonucleotide shown in sequence
XX CC ACF36398 (I) is used: (a) to delay progression of androgen-sensitive
XX CC prostatic cancer cells to the androgen-independent state, in vivo or in
XX CC vitro; (b) to treat prostatic cancer (after initially withdrawing
XX CC androgens to induce apoptosis); and (c) to increase sensitivity of cancer
XX CC cells (prostatic, renal, non-small cell lung, urothelial transitional,
XX CC ovarian and some breast cancer cells) that express abnormal levels of
XX CC TRPM-2 to chemotherapy or radiation. The modifications present in (I)
XX CC increase stability in vivo and activity (both in vivo or in vitro) and
XX CC result in a synergistic increase in effect when (I) is used with
XX CC chemotherapeutic agents or other antisense oligonucleotides directed
XX CC against other antiapoptotic genes. The present sequence represents a
XX CC specific example of an anti-apoptotic protein TRPM-2 (testosterone-
XX CC repressed prostate message-2) antisense oligonucleotide
XX SQ Sequence 21 BP; 6 A; 6 C; 4 G; 5 T; 0 U; 0 Other;
Query Match 100.0%; Score 21; DB 10; Length 21;
Best Local Similarity 100.0%; Pred. No. 8.2;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAGCAGCAGAGTCTTCATCAT 21
Db 1 CAGCAGCAGAGTCTTCATCAT 21

us-10-828-394-5.rng
Db 1 CAGCAGCAGAGTCTTCATCAT 21
RESULT 3
ADM83069
ID ADM83069 standard; DNA; 21 BP.
XX AC ADM83069;
XX DT 03-JUN-2004 (first entry)
XX DE Human TRPM-2 antisense oligonucleotide #4.
XX KW Testosterone-repressed prostate message-2; TRPM-2; chemo-sensitivity;
XX KW radiation-sensitivity; prostate cancer; bladder cancer; ovarian cancer;
XX KW lung cancer; renal cell carcinoma; RCC; antisense gene therapy; human;
XX KW antisense; ss.
XX OS Homo sapiens.
XX OS Synthetic.
XX FH Key Location/Qualifiers
XX FT modified_base 1..21 /*tag= a
XX FT /mod_base= OTHER
XX FT /note= "Phosphorothioate backbone"
XX PN US2003158130-A1.
XX PD 21-AUG-2003.
XX PF 28-SEP-2001; 2001US-00967726.
XX PR 25-FEB-2000; 2000WO-US004875.
XX PR 28-SEP-2000; 2000US-0236301P.
XX PR 10-AUG-2001; 2001US-00913325.
XX PA (GLEA/) GLEAVE M.
XX PA (RENN/) RENNIE P S.
XX PA (MIYA/) MIYAKE H.
XX PA (NELS/) NELSON C.
XX PA (ZELL/) ZELLWEGER T.
XX PI Gleave M, Rennie PS, Miyake H, Nelson C, Zellweiger T;
XX WPI; 2003-778017/73.
XX DR Enhancing the chemo-sensitivity or radiation-sensitivity of cancer cells
XX PT that expresses testosterone-repressed prostate message-2 (TRPM-2)
XX PT comprises administering a composition that inhibits expression of TRPM-2.
XX PS Claim 4; SEQ ID NO 4; 14pp; English.
XX CC The present invention provides a method for treating cancer in which
XX CC cancer cells express testosterone-repressed prostate message-2 (TRPM-2).
XX CC The invention is useful for enhancing the chemo-sensitivity or radiation-
XX CC sensitivity of cancer cells for treating the cancer such as prostate cancer,
XX CC bladder cancer, ovarian cancer, lung cancer and renal cell carcinoma
XX CC (RCC). The invention is also useful in antisense gene therapy. The
XX CC present sequence is human testosterone-repressed prostate message-2 (TRPM
XX CC -2) antisense oligodeoxyribonucleotide (ODN).
XX SQ Sequence 21 BP; 6 A; 6 C; 4 G; 5 T; 0 U; 0 Other;
Query Match 100.0%; Score 21; DB 11; Length 21;
Best Local Similarity 100.0%; Pred. No. 8.2;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAGCAGCAGAGTCTTCATCAT 21
Db 1 CAGCAGCAGAGTCTTCATCAT 21
```

CC	sensitivity to subsequent treatment with cisplatin. A claimed method for
CC	regulating expression of bcl-xL in a subject or cell line comprises
CC	administering an agent effective to modulate the amount of clusterin
CC	expression. In clusterin-expressing cells, expression of bcl-xL is down-
CC	regulated when the effective amount of clusterin is reduced. Such
CC	inhibition is significant because bcl-xL is known to act as an inhibitor
CC	of apoptosis.
XX	
SQ	Sequence 21 BP; 6 A; 6 C; 4 G; 5 T; 0 U; 0 Other;
	Query Match            100.0%; Score 21; DB 12; Length 21;
	Best Local Similarity 100.0%; Pred.No. 8.2;
	Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy	1 CAGCAGCAGAGTCTTCATCAT 21 
Dd	1 CAGCAGCAGAGTCTTCATCAT 21 
RESULT 5	
ADL70521/c	ID ADL70521 standard; cDNA; 23 BP.
XX	AC ADL70521;
XX	DT 20-MAY-2004 (first entry)
XX	Human clusterin target for RNAi.
XX	
KW	RNA interference; RNAi; short interfering RNA; siRNA; human; clusterin;
KW	cytostatic; neuroprotective; nontropic; gene silencing; DNA-RNA hybrid;
ss.	
XX	Homo sapiens.
OS	Synthetic.
XX	
PN	WO2004018676-A2.
XX	
PD	04-MAR-2004.
XX	
PF	21-AUG-2003; 2003WO-CA001277.
XX	
PR	21-AUG-2002; 2002US-0405193P.
PR	03-SEP-2002; 2002US-0408152P.
PR	20-MAY-2003; 2003US-0472387P.
XX	
PA	(UYBR-) UNIV BRITISH COLUMBIA.
XX	
PI	Jansen B, Gleave ME, Signaevsky M, Beraldi E, Trougakos IP;
PI	Gonos ES;
XX	
DR	WPI; 2004-226852/21.
XX	
PT	New RNA molecule less than 49 bases and having a sequence effective to
PT	mediate degradation or block translation of mRNA that is the
PT	transcriptional product of a target gene, useful for treating Alzheimer's
PT	disease or cancer.
XX	
PS	Example 6; SEQ ID NO 66; 63pp; English.
XX	
CC	The present sequence is a human clusterin cDNA target for a double-
CC	stranded short interfering RNA (siRNA) of the invention ADL70522-
CC	ADL70523. It was used in an example from the invention to demonstrate
CC	clusterin gene silencing in PC-3 prostate cancer cells. Clusterin, also
CC	known as testosterone-repressed prostate message-2 (TRPM-2) or sulfated
CC	glycoprotein-2 (SGP-2), is expressed in increased amounts by prostate
CC	tumour cells following androgen withdrawal, and has also been shown to be
CC	critical for neuritic toxicity in mouse models of Alzheimer's disease.
CC	siRNAs of the invention can be used alone or in combination with other
CC	chemotherapy or apoptosis inducing treatments for the treatment of
CC	prostate cancer, sarcomas such as osteosarcoma, renal cell carcinoma,
CC	breast cancer, bladder cancer, lung cancer, colon cancer, ovarian cancer,
CC	anaplastic large cell lymphoma and melanoma, and also for the treatment

CC of Alzheimer's disease.

XX Sequence 23 BP; 5 A; 5 C; 7 G; 6 T; 0 U; 0 Other;

XX Query Match 100.0%; Score 21; DB 12; Length 23;

XX Best Local Similarity 100.0%; Pred. No. 8.3;

XX Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAGCAGCAGAGTCTTCATCAT 21

DB 23 CAGCAGCAGAGTCTTCATCAT 3

RESULT 6

ADL70464/c

ID ADL70464 standard; RNA; 21 BP.

XX AC ADL70464;

XX 20-MAY-2004 (first entry)

XX RNAi for human clusterin.

XX RNA interference; RNAi; short interfering RNA; siRNA; human; clusterin;

XX cytosstatic; neuroprotective; nootropic; gene silencing; DNA-RNA hybrid;

XX ss.

XX Homo sapiens.

XX Synthetic.

XX Key Location/Qualifiers

XX modified\_base 20..21

XX /\*tag= a

XX /mod\_base= OTHER

XX /note= "OTHER= dtGt"

XX WO2004019676-A2.

XX 04-MAR-2004.

XX 21-AUG-2003; 2003WO-CA001277.

XX 21-AUG-2002; 2002US-0405193P.

XX 03-SEP-2002; 2002US-0408152P.

XX 20-MAY-2003; 2003US-0472387P.

XX (UYBR-) UNIV BRITISH COLUMBIA.

XX Jansen B, Gleave ME, Signaevsky M, Beraldi E, Trougakos IP;

XX Gonos ES;

XX WPI; 2004-226852/21.

XX New RNA molecule less than 49 bases and having a sequence effective to

XX mediate degradation or block translation of mRNA that is the

XX transcriptional product of a target gene, useful for treating Alzheimer's

XX disease or cancer.

XX Claim 4; SEQ ID NO 9; 63pp; English.

XX The present sequence is the sense strand of a short interfering RNA

XX (siRNA) targeted to human clusterin. The antisense strand is also

XX provided ADL70465. The siRNA can be used to interfere with the expression

XX of clusterin. Clusterin, also known as testosterone-repressed

XX message-2 (TRPM-2) or sulfated glycoprotein-2 (SGP-2), is expressed in

XX increased amounts by prostate tumour cells following androgen withdrawal,

XX and has also been shown to be critical for neuritic toxicity in mouse

XX models of Alzheimer's disease. siRNAs of the invention can be used alone

XX or in combination with other chemotherapy or apoptosis inducing

XX treatments for the treatment of prostate cancer, sarcomas such as

XX osteosarcoma, renal cell carcinoma, breast cancer, bladder cancer, lung

XX cancer, colon cancer, ovarian cancer, anaplastic large cell lymphoma and

XX melanoma, and also for the treatment of Alzheimer's disease.

XX Sequence 21 BP; 5 A; 4 C; 5 G; 2 T; 5 U; 0 Other;

XX Query Match 95.2%; Score 20; DB 12; Length 21;

XX Best Local Similarity 100.0%; Pred. No. 23;

XX Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 AGCAGCAGAGTCTTCATCAT 21

DB 20 AGCAGCAGAGTCTTCATCAT 1

RESULT 7

ADL70430/c

ID ADL70430 standard; RNA; 21 BP.

XX AC ADL70430;

XX 20-MAY-2004 (first entry)

XX RNAi for human clusterin.

XX Human; clusterin; RNAi; melanoma; cytosstatic; gene silencing;

XX short interfering RNA; siRNA; DNA-RNA hybrid; ss.

XX Homo sapiens.

XX Synthetic.

XX Key Location/Qualifiers

XX modified\_base 20..21

XX /\*tag= a

XX /mod\_base= OTHER

XX /note= "OTHER= TT"

XX WO2004018675-A1.

XX 04-MAR-2004.

XX 21-AUG-2003; 2003WO-CA001276.

XX 21-AUG-2002; 2002US-0405193P.

XX 03-SEP-2002; 2002US-0408152P.

XX 02-DEC-2002; 2002US-0319748P.

XX 20-MAY-2003; 2003US-0472387P.

XX (UYBR-) UNIV BRITISH COLUMBIA.

XX (GLEA/) GLEAVE M E.

XX Jansen B;

XX WPI; 2004-226851/21.

XX Treating melanoma in a mammalian subject comprises administering to the

XX subject a therapeutic agent effective to reduce the effective amount of

XX clusterin in the melanoma cells.

XX Claim 20; SEQ ID NO 28; 32pp; English.

XX The present sequence is that of a short interfering RNA (siRNA) molecule

XX targeted to human clusterin ADL70403. The invention relates to the

XX treatment of melanoma through reduction in the effective amount of

XX clusterin. The therapeutic agent may be an antisense oligonucleotide

XX ADL70404-ADL70421 or short interfering RNA (siRNA) ADL70422-ADL70445

XX targeted to clusterin. The siRNAs molecules direct cleavage of clusterin

XX mRNA. A method for regulating expression of bcl-xL in a subject or cell

XX line comprises administering an agent effective to modulate the amount of

XX clusterin expression. In clusterin-expressing cells, expression of bcl-xL

XX is down-regulated when the effective amount of clusterin is reduced. Such

XX inhibition is significant because bcl-xL is known to act as an inhibitor

XX of apoptosis.

XX Sequence 21 BP; 5 A; 4 C; 5 G; 2 T; 5 U; 0 Other;



```
Query Match      95.2%; Score 20; DB 12; Length 21;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  2 AGCAGCAGAGTCTTCATCAT 21
    |||||
DB  20 AGCAGCAGAGTCTTCATCAT 1

RESULT 8
ADL70522/c
ID  ADL70522 standard; RNA; 19 BP.
XX
AC  ADL70522;
XX
DT  20-MAY-2004 (first entry)
XX
DE  RNAi for human clusterin.
XX
KW  RNA interference; RNAi; short interfering RNA; siRNA; human; clusterin;
KW  cytoskeletal; neuroprotective; nontropic; gene silencing; DNA-RNA hybrid;
KW  ss.
XX
OS  Homo sapiens.
OS  Synthetic.
XX
FH  Key      Location/Qualifiers
FT  modified_base 18..19
FT  /*tag= a
FT  /mod_base= OTHER
FT  /note= "OTHER= dtdt"
XX
PN  WO2004018676-A2.
XX
PD  04-MAR-2004.
XX
PF  21-AUG-2003; 2003WO-CA001277.
XX
PR  21-AUG-2002; 2002US-0405193P.
PR  03-SEP-2002; 2002US-0408152P.
PR  20-MAY-2003; 2003US-0472387P.
XX
PA  (UYBR-) UNIV BRITISH COLUMBIA.
XX
PI  Jansen B, Gleave ME, Signaevsky M, Beraldi E, Trougakos IP;
PI  Gonos ES;
XX
XX  WPI; 2004-226852/21.
XX
PT  New RNA molecule less than 49 bases and having a sequence effective to
PT  mediate degradation or block translation of mRNA that is the
PT  transcriptional product of a target gene, useful for treating Alzheimer's
PT  disease or cancer.
XX
XX  Claim 4; SEQ ID NO 67; 63pp; English.
XX
CC  The present sequence is the sense strand of a short interfering RNA
CC  (siRNA) targeted to a specific portion ADL70521 of human clusterin cDNA.
CC  The antisense strand is also provided ADL70523. The siRNA can be used to
CC  interfere with the expression of clusterin. Clusterin, also known as
CC  testosterone-repressed prostate message-2 (TRPM-2) or sulfated
CC  glycoprotein-2 (SGP-2), is expressed in increased amounts by prostate
CC  tumour cells following androgen withdrawal, and has also been shown to be
CC  critical for neuritic toxicity in mouse models of Alzheimer's disease.
CC  siRNAs of the invention can be used alone or in combination with other
CC  chemotherapy or apoptosis inducing treatments for the treatment of
CC  prostate cancer, sarcomas such as osteosarcoma, renal cell carcinoma,
CC  breast cancer, bladder cancer, lung cancer, colon cancer, ovarian cancer,
CC  anaplastic large cell lymphoma and melanoma, and also for the treatment
CC  of Alzheimer's disease. In an example from the invention, the present
CC  siRNA was used to examine the effects of clusterin gene silencing in PC-3
CC  prostate cancer cells. A reduction in clusterin transcript was observed.
XX
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Sequence 19 BP; 5 A; 4 C; 5 G; 0 T; 5 U; 0 Other;
Query Match      90.5%; Score 19; DB 12; Length 19;
Best Local Similarity 100.0%; Pred. No. 64;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  3 GCAGCAGAGTCTTCATCAT 21
    |||||
DB  19 GCAGCAGAGTCTTCATCAT 1

RESULT 9
ADL70523
ID  ADL70523 standard; RNA; 19 BP.
XX
AC  ADL70523;
XX
DT  20-MAY-2004 (first entry)
XX
DE  RNAi for human clusterin.
XX
KW  RNA interference; RNAi; short interfering RNA; siRNA; human; clusterin;
KW  cytoskeletal; neuroprotective; nontropic; gene silencing; DNA-RNA hybrid;
KW  ss.
XX
OS  Homo sapiens.
OS  Synthetic.
XX
FH  Key      Location/Qualifiers
FT  modified_base 18..19
FT  /*tag= a
FT  /mod_base= OTHER
FT  /note= "OTHER= dtdt"
XX
PN  WO2004018676-A2.
XX
PD  04-MAR-2004.
XX
PF  21-AUG-2003; 2003WO-CA001277.
XX
PR  21-AUG-2002; 2002US-0405193P.
PR  03-SEP-2002; 2002US-0408152P.
PR  20-MAY-2003; 2003US-0472387P.
XX
PA  (UYBR-) UNIV BRITISH COLUMBIA.
XX
PI  Jansen B, Gleave ME, Signaevsky M, Beraldi E, Trougakos IP;
PI  Gonos ES;
XX
XX  WPI; 2004-226852/21.
XX
PT  New RNA molecule less than 49 bases and having a sequence effective to
PT  mediate degradation or block translation of mRNA that is the
PT  transcriptional product of a target gene, useful for treating Alzheimer's
PT  disease or cancer.
XX
XX  Claim 4; SEQ ID NO 68; 63pp; English.
XX
CC  The present sequence is the antisense strand of a short interfering RNA
CC  (siRNA) targeted to a specific portion ADL70521 of human clusterin cDNA.
CC  The sense strand is also provided ADL70522. The siRNA can be used to
CC  interfere with the expression of clusterin. Clusterin, also known as
CC  testosterone-repressed prostate message-2 (TRPM-2) or sulfated
CC  glycoprotein-2 (SGP-2), is expressed in increased amounts by prostate
CC  tumour cells following androgen withdrawal, and has also been shown to be
CC  critical for neuritic toxicity in mouse models of Alzheimer's disease.
CC  siRNAs of the invention can be used alone or in combination with other
CC  chemotherapy or apoptosis inducing treatments for the treatment of
CC  prostate cancer, sarcomas such as osteosarcoma, renal cell carcinoma,
CC  breast cancer, bladder cancer, lung cancer, colon cancer, ovarian cancer,
CC  anaplastic large cell lymphoma and melanoma, and also for the treatment
CC  of Alzheimer's disease. In an example from the invention, the present
CC  siRNA was used to examine the effects of clusterin gene silencing in PC-3
CC  prostate cancer cells. A reduction in clusterin transcript was observed.
XX
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CC prostate cancer cells. A reduction in clusterin transcript was observed.

Sequence 19 BP; 5 A; 5 C; 4 G; 0 T; 5 U; 0 Other;

Query Match 90.5%; Score 19; DB 12; Length 19;  
Best Local Similarity 73.7%; Pred. No. 64;  
Matches 14; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

Qy            3 GCAGCAGAGTCTTCATCAT 21  
               |||||:::||:  
Db            1 GCAGCAGAGUCUUAUCAU 19

RESULT 10	
ADL70444/c	
ID	ADL70444 standard; RNA; 19 BP.
XX	
XX	
AC	ADL70444;
XX	
XX	
DT	20-MAY-2004 (first entry)
XX	
DE	RNAi for human clusterin.
XX	
XX	
KW	Human; clusterin; RNAi; melanoma; cytostatic; gene silencing;
KW	short interfering RNA; siRNA; DNA-RNA hybrid; ss

XX	Homo sapiens.
OS	Synthetic.
OS	
XX	
FH	Key
FT	modified_base
FT	Location/Qualifiers
FT	18..19
FT	/tag= a
FT	/mod_base= OTHER
FT	/note= "OTHER= TT"

XX PN WO2004018675-A1.

04-MAR-2004.

21-AUG-2003: 2003WO-CA001276.

21-AUG-2002: 2002US-0405193P.

03-SEP-2002; ZVUZUS-V#V813ZE  
02-DEC-2002; 2002US-0319748P.

FR 20-MAY-2003; 200305-04/238/F.  
XX

PA (UIBR-) UNIV BRITISH COLUMBIA.  
PA (GLEA/) GLEAVE M E.

XX Jansen B:  
PI

XX  
DR  
WPI: 2004-226851/21

PT Treating

PT subject a therapeutic clusterin in the mel

XX  
PS  
Claim 20: SEQ ID NO 42: 32pp: English.

The present sequence is that of a short interfering RNA (siRNA) molecule targeted to human clusterin ADL70403. The invention relates to the treatment of melanoma through reduction in the effective amount of clusterin. The therapeutic agent may be an antisense oligonucleotide ADL70404-ADL70421 or short interfering RNA (siRNA) ADL70422-ADL70445 targeted to clusterin. The siRNAs molecules direct cleavage of clusterin mRNA. A method for regulating expression of bcl-xL in a subject or cell line comprises administering an agent effective to modulate the amount of clusterin expression. In clusterin-expressing cells, expression of bcl-xL is down-regulated when the effective amount of clusterin is reduced. Such inhibition is significant because bcl-xL is known to act as an inhibitor of apoptosis.

Sequence 19 BP; 5 A; 4 C; 5 G; 0 T; 5 U; 0 Other;

Query Match 90.5%; Score 19; DB 12; Length 19;  
Best Local Similarity 100.0%; Pred. No. 64;  
Matches 19; Conservative 0; Mismatches 0; Indels

Qy 3 GCAGCAGAGTCTTCATCAT 21  
|||  
pb 19 GCAGCAGAGTCTTCATCAT 1

RESULT 11  
ADL70445  
ID ADL70445 standard; RNA; 19 BP.

AC ADL70445;

DT 20-MAY-2004 (first entry)

XX RNAi for human clusterin.  
KW Human; clusterin; RNAi; melanoma; cytostatic; gene silencing;  
KW short interfering RNA; siRNA; DNA-RNA hybrid; ss.  
XX

XX	Homo sapiens.	Location/Qualifiers
OS	Synthetic.	18..19
OS		/tag= a
XX		/mod_base= OTHER
PH	Key	/note= "OTHER= TT"
FT	modified_base	
FT		
FT		
FT		

AA WO2004018675-A1.

04-MAR-2004.

21-AUG-2003; 2003WO-CA001276.

PR 21-AUG-2002; 2002US-0405193P.

PR 02-DEC-2002; 2002US-0319748P.

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PA (GLEA/) GLEAVE M E.

PI Jansen B;

DR WPI; 2004-226851/21

PT  
Treating

PT clusterin in the mel

PS Claim 20; SEQ ID NO 43; 32pp; English.

The present sequence is that of a short interfering RNA (siRNA) molecule targeted to human clusterin ADL70403. The invention relates to the treatment of melanoma through reduction in the effective amount of clusterin. The therapeutic agent may be an antisense oligonucleotide ADL70404-ADL70421 or short interfering RNA (siRNA) ADL70422-ADL70445 targeted to clusterin. The siRNAs molecules direct cleavage of clusterin mRNA. A method for regulating expression of bcl-xL in a subject or cell line comprises administering an agent effective to modulate the amount of clusterin expression. In clusterin-expressing cells, expression of bcl-xL is down-regulated when the effective amount of clusterin is reduced. Such inhibition is significant because bcl-xL is known to act as an inhibitor of apoptosis.

SQ Sequence 19 BP; 5 A; 5 C; 4 G; 0 T; 5 U; 0 Other;

Query Match	90.5%	Score 19;	DB 12;	Length 19;
Best Local Similarity	73.7%	Pred. No. 64;		

Matches 14; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 3 GCAGCAGAGTCTTCATCAT 21  
|||||:|:|:|:|:  
Db 1 GCAGCAGAGUCUUCAU 19

## RESULT 12

ADL70465  
ID ADL70465 standard; RNA; 21 BP.  
XX  
AC ADL70465;  
XX  
DT 20-MAY-2004 (first entry)  
XX  
DE RNAi for human clusterin.  
XX  
DE RNA interference; RNAi; short interfering RNA; siRNA; human; clusterin;  
KW cytotostatic; neuroprotective; nontropic; gene silencing; DNA-RNA hybrid;  
KW ss.  
XX  
OS Homo sapiens.  
OS Synthetic.  
XX  
FH Key Location/Qualifiers  
FT modified\_base 20..21  
FT /\*tag= a  
FT /mod\_base= OTHER  
FT /note= "OTHER= dTdT"  
XX  
PN WO2004018676-A2.  
XX  
PD 04-MAR-2004.  
XX  
PF 21-AUG-2003; 2003WO-CA001277.  
XX  
PR 21-AUG-2002; 2002US-0405193P.  
PR 03-SEP-2002; 2002US-0408152P.  
PR 20-MAY-2003; 2003US-0472387P.  
XX  
XX (UYBR-) UNIV BRITISH COLUMBIA.  
XX  
XX Jansen B, Gleave ME, Signaevsky M, Beraldi E, Trougakos IP;  
PI Gonos ES;  
XX  
XX WPI; 2004-226852/21.

XX New RNA molecule less than 49 bases and having a sequence effective to  
PT mediate degradation or block translation of mRNA that is the  
PT transcriptional product of a target gene, useful for treating Alzheimer's  
PT disease or cancer.

XX Claim 4; SEQ ID NO 10; 63pp; English.

XX The present sequence is the antisense strand of a short interfering RNA  
CC (siRNA) targeted to human clusterin. The sense strand is also provided  
CC ADL70464. The siRNA can be used to interfere with the expression of  
CC clusterin. Clusterin, also known as testosterone-repressed prostate  
CC message-2 (TRPM-2) or sulfated glycoprotein-2 (SGP-2), is expressed in  
CC increased amounts by prostate tumour cells following androgen withdrawal,  
CC and has also been shown to be critical for neuritic toxicity in mouse  
CC models of Alzheimer's disease. siRNAs of the invention can be used alone  
CC or in combination with other chemotherapy or apoptosis inducing  
CC treatments for the treatment of prostate cancer, sarcomas such as  
CC osteosarcoma, renal cell carcinoma, breast cancer, bladder cancer, lung  
CC cancer, colon cancer, ovarian cancer, anaplastic large cell lymphoma and  
CC melanoma, and also for the treatment of Alzheimer's disease.

XX Sequence 21 BP; 5 A; 5 C; 4 G; 2 T; 5 U; 0 Other;

Query Match 90.5%; Score 19; DB 12; Length 21;

Best Local Similarity 73.7%; Pred. No. 65;

Matches 14; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 3 GCAGCAGAGTCTTCATCAT 21  
|||||:|:|:|:|:  
Db 1 GCAGCAGAGUCUUCAU 19

## RESULT 13

ADL70431  
ID ADL70431 standard; RNA; 21 BP.  
XX  
AC ADL70431;  
XX  
DT 20-MAY-2004 (first entry)  
XX  
DE RNAi for human clusterin.  
XX  
DE Human; clusterin; RNAi; melanoma; cytotostatic; gene silencing;  
KW short interfering RNA; siRNA; DNA-RNA hybrid; ss.  
KW  
XX  
OS Homo sapiens.  
OS Synthetic.  
XX  
FH Key Location/Qualifiers  
FT modified\_base 20..21  
FT /\*tag= a  
FT /mod\_base= OTHER  
FT /note= "OTHER= TT"  
XX  
PN WO2004018675-A1.  
XX  
PD 04-MAR-2004.  
XX  
PF 21-AUG-2003; 2003WO-CA001276.  
XX  
PR 21-AUG-2002; 2002US-0405193P.  
PR 03-SEP-2002; 2002US-0408152P.  
PR 02-DEC-2002; 2002US-0319748P.  
PR 20-MAY-2003; 2003US-0472387P.  
XX  
XX (UYBR-) UNIV BRITISH COLUMBIA.  
XX  
XX (GLEA/) GLEAVE M E.  
XX  
XX Jansen B;  
XX  
XX WPI; 2004-226851/21.

XX Treating melanoma in a mammalian subject comprises administering to the  
PT subject a therapeutic agent effective to reduce the effective amount of  
PT clusterin in the melanoma cells.

XX Claim 20; SEQ ID NO 29; 32pp; English.

XX The present sequence is that of a short interfering RNA (siRNA) molecule  
CC targeted to human clusterin ADL70403. The invention relates to the  
CC treatment of melanoma through reduction in the effective amount of  
CC clusterin. The therapeutic agent may be an antisense oligonucleotide  
CC ADL70404-ADL70421 or short interfering RNA (siRNA) ADL70422-ADL70445  
CC targeted to clusterin. The siRNAs molecules direct cleavage of clusterin  
CC mRNA. A method for regulating expression of bcl-xL in a subject or cell  
CC line comprises administering an agent effective to modulate the amount of  
CC clusterin expression. In clusterin-expressing cells, expression of bcl-xL  
CC is down-regulated when the effective amount of clusterin is reduced. Such  
CC inhibition is significant because bcl-xL is known to act as an inhibitor  
CC of apoptosis.

XX Sequence 21 BP; 5 A; 5 C; 4 G; 2 T; 5 U; 0 Other;

Query Match 90.5%; Score 19; DB 12; Length 21;

Best Local Similarity 73.7%; Pred. No. 65;

Matches 14; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 3 GCAGCAGAGTCTTCATCAT 21  
|||||:|:|:|:|:

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Db      1 GCAGCAGAGUCUUAU 19

RESULT 14
ACF36409
ID      ACF36409 standard; DNA; 21 BP.
XX
XX
AC      ACF36409;
XX
XX
DT      18-DEC-2003 (first entry)
XX
DE      DNA sequence of a TRPM-2 mismatch control oligonucleotide.
XX
KW      TRPM-2; testosterone-repressed prostate message-2; cytostatic; androgen;
KW      prostate cancer; anti-apoptotic protein; antisense; ss.
XX
XX      Synthetic.
OS
PN      WO2003072591-A1.
XX
XX      04-SEP-2003.
PD
XX
XX      20-FEB-2003; 2003WO-US005305.
PF
XX
XX      22-FEB-2002; 2002US-00080794.
PR
XX
XX      (UYBR-) UNIV BRITISH COLUMBIA.
PA
PI      Gleave M, Rennie PS, Miyake H, Nelson C, Monia BP;
XX
XX      WPI; 2003-689981/65.
DR
XX
XX      New modified antisense oligonucleotide, useful particularly for treating
PT      prostatic cancer, inhibits the testosterone-repressed prostate message-2.
XX
XX      Example 13; Page 20; 44pp; English.
XX
XX      The invention relates to a compound consisting of an oligonucleotide with
XX      a phosphorothioate backbone throughout, in which: (a) sugars on
XX      nucleotide residues 1-4 and 18-21 are 2'-O-methoxyethyl modified, and the
XX      remaining nucleotides 5-17 are 2'-deoxy; and (b) the cytosines at
XX      positions 1, 4 and 19 are 5-methylated. Oligonucleotide shown in sequence
XX      ACF36398 (I) is used: (a) to delay progression of androgen-sensitive
XX      prostatic cancer cells to the androgen-independent state, in vivo or in
XX      vitro; (b) to treat prostatic cancer (after initially withdrawing
XX      androgens to induce apoptosis); and (c) to increase sensitivity of cancer
XX      cells (prostatic, renal, non-small cell lung, urothelial transitional,
XX      ovarian and some breast cancer cells) that express abnormal levels of
XX      TRPM-2 to chemotherapy or radiation. The modifications present in (I)
XX      increase stability in vivo and activity (both in vivo or in vitro) and
XX      result in a synergistic increase in effect when (I) is used with
XX      chemotherapeutic agents or other antisense oligonucleotides directed
XX      against other antiapoptotic genes. The present sequence represents a
XX      mismatch control oligonucleotide, used in antisense assays of anti-
XX      apoptotic protein TRPM-2 (testosterone-repressed prostate message-2)
XX
XX      Sequence 21 BP; 7 A; 4 C; 4 G; 6 T; 0 U; 0 Other;
SQ
      Query Match      84.8%; Score 17.8; DB 10; Length 21;
      Best Local Similarity 90.5%; Pred. No. 2.3e+02;
      Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      1 GCAGCAGAGTCCTTCATCAT 21
      |||||
Db      1 GCAGCAGAGTATTATCAT 21

RESULT 15
ADM83080
ID      ADM83080 standard; DNA; 21 BP.
XX
XX      ADM83080;
AC
XX

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DT      03-JUN-2004 (first entry)
XX
XX      Control TRPM-2 mismatch oligonucleotide.
DE
XX
XX      Testosterone-repressed prostate message-2; TRPM-2; chemo-sensitivity;
KW      radiation-sensitivity; prostate cancer; bladder cancer; ovarian cancer;
KW      lung cancer; renal cell carcinoma; RCC; antisense gene therapy; ss.
XX
XX      Unidentified.
OS
XX      US2003158130-A1.
PN
XX      21-AUG-2003.
PD
XX
XX      28-SEP-2001; 2001US-00967726.
PF
XX
XX      25-FEB-2000; 2000WO-US004875.
PR      28-SEP-2000; 2000US-0236301P.
PR      10-AUG-2001; 2001US-00913325.
XX
XX      (GLEA/) GLEAVE M.
PA      (RENN/) RENNIE P S.
PA      (MIYA/) MIYAKE H.
PA      (NELS/) NELSON C.
PA      (ZELL/) ZELLWEGER T.
XX
XX      Gleave M, Rennie PS, Miyake H, Nelson C, Zellweger T;
PI      WPI; 2003-778017/73.
XX
XX      Enhancing the chemo-sensitivity or radiation-sensitivity of cancer cells
PT      that expresses testosterone-repressed prostate message-2 (TRPM-2)
PT      comprises administering a composition that inhibits expression of TRPM-2.
XX
XX      Disclosure; SEQ ID NO 15; 14pp; English.
XX
XX      The present invention provides a method for treating cancer in which
XX      cancer cells express testosterone-repressed prostate message-2 (TRPM-2).
XX      The invention is useful for enhancing the chemo-sensitivity or radiation-
XX      sensitivity of cancer cells for treating cancer such as prostate cancer,
XX      bladder cancer, ovarian cancer, lung cancer and renal cell carcinoma
XX      (RCC). The invention is also useful in antisense gene therapy. The
XX      present sequence is control testosterone-repressed prostate message-2
XX      (TRPM-2) mismatch oligonucleotide. The oligonucleotide is used in the
XX      exemplification of the invention.
XX
XX      Sequence 21 BP; 7 A; 4 C; 4 G; 6 T; 0 U; 0 Other;
SQ
      Query Match      84.8%; Score 17.8; DB 11; Length 21;
      Best Local Similarity 90.5%; Pred. No. 2.3e+02;
      Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      1 GCAGCAGAGTCCTTCATCAT 21
      |||||
Db      1 GCAGCAGAGTATTATCAT 21

Search completed: September 3, 2005, 14:58:27
Job time : 435 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 3, 2005, 14:58:36 ; Search time 3027 Seconds  
(without alignments)  
264.073 Million cell updates/sec

Title: US-10-828-394-5

Perfect score: 21

Sequence: 1 cagcagcagcttctcatc 21

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 159776

Minimum DB seq length: 0  
Maximum DB seq length: 50

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : EST:\*  
1: gb\_est1:\*  
2: gb\_est2:\*  
3: gb\_hic:\*  
4: gb\_est3:\*  
5: gb\_est4:\*  
6: gb\_est5:\*  
7: gb\_est6:\*  
8: gb\_gss1:\*  
9: gb\_gss2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	14.8	70.5	46	1	AA916352 oh80e11.s
2	14.6	69.5	44	7	W25663 zc64e08.r1
3	14	66.7	50	8	BH861678 SALK_0877
4	13.6	64.8	42	9	CC7941149 SALK_0439
5	13.4	63.8	50	9	CG869035 AB0164.Sa
6	13	61.9	21	8	AZ802584 2M0061105
7	13	61.9	41	8	BH908888 SALK_0510
8	13	61.9	43	1	AA973632 oo48504.s
9	13	61.9	48	9	AL948370 Arabidops
10	12.8	61.0	50	1	AU107924 AU107924
11	12.8	61.0	50	1	AU107925 AU107925
12	12.8	61.0	50	1	AU107928 AU107928
13	12.8	61.0	50	1	AU107929 AU107929
14	12.6	60.0	39	9	AL760945 Arabidops
15	12.6	60.0	43	1	AI766391 wh61d04.x
16	12.6	60.0	46	1	AA581123 v141c01.r
17	12.6	60.0	46	6	CB213634 OML03914
18	12.6	60.0	47	9	CL212422 G040810.G
19	12.6	60.0	50	1	AU105963 AU105963
20	12.6	60.0	50	1	AU105967 AU105967
21	12.6	60.0	50	1	AU105968 AU105968
22	12.6	60.0	50	1	AU105972 AU105972
23	12.6	60.0	50	1	AA566984 1038 Lob1
24	12.4	59.0	37	8	AZ797149 2M0053009

C 25	12.2	58.1	35	8	AZ332831	AZ332831 1M0061C05
C 26	12.2	58.1	36	9	AJ587667	AJ587667 Arabidops
C 27	12.2	58.1	43	8	AZ610505	AZ610505 1M0435N18
C 28	12.2	58.1	46	1	AA109083	AA109083 mp37b05.r
C 29	12.2	58.1	49	1	AA052336	AA052336 mb35b02.r
C 30	12.2	58.1	49	1	AA864073	AA864073 vx88f02.r
C 31	12.2	58.1	50	1	AU104442	AU104442 AU104442
C 32	12.2	58.1	50	9	CR155807	CR155807 Reverse s
C 33	12.2	57.1	33	8	AZ305164	AZ305164 1M0005M08
C 34	12.2	57.1	33	8	AZ318599	AZ318599 1M0037N24
C 35	12.2	57.1	34	1	AA116347	AA116347 mc70g12.r
C 36	12.2	57.1	34	4	BI246596	BI246596 602988318
C 37	12.2	57.1	34	9	AG201385	AG201385 Pan trogl
C 38	12.2	57.1	35	9	BX285461	BX285461 Arabidops
C 39	12.2	57.1	40	8	BH910804	BH910804 SALK_0626
C 40	12.2	57.1	40	9	CG774406	CG774406 1123018G0
C 41	12.2	57.1	41	8	BZ586362	BZ586362 3590.1.16
C 42	12.2	57.1	46	6	CA964065	CA964065 CILL02a07
C 43	12.2	57.1	46	7	H92446	H92446 yt89b09.r1
C 44	12.2	57.1	46	7	T74174	T74174 yc60b12.s1
C 45	12.2	57.1	47	8	AZ772648	AZ772648 1M0583N12

#### ALIGNMENTS

RESULT 1  
AA916352 46 bp mRNA linear EST 14-APR-1998  
LOCUS oh80e11.s1 NCI CGAP Co8 Homo sapiens cDNA clone IMAGE:1473356 3'  
DEFINITION similar to TR:Q15347 Q15347 RAGA. [1] ; mRNA sequence.  
ACCESSION AA916352  
VERSION AA916352.1 GI:3055744  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
REFERENCE 1 (bases 1 to 46)  
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
TITLE NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
JOURNAL National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
COMMENT Unpublished (1997)  
Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-r@mail.nih.gov  
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.  
Emmert-Buck, M.D., Ph.D.  
cDNA Library Preparation: M. Bento Soares, Ph.D.  
DNA Sequencing: Greg Lennon, Ph.D.  
Cloning: Washington University Genome Sequencing Center  
Clone distribution: NCI-CGAP clone distribution information can be  
found through the I.M.A.G.E. Consortium/LINL at:  
www.bio.llnl.gov/bbrp/image/image.html

Trace considered overall poor quality  
Seq primer: -40mi3 fwd. ET from Amersham  
High quality sequence stop: 1.

#### FEATURES

Location/Qualifiers  
1..46  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:1473356"  
/tissue\_type="adenocarcinoma"  
/lab\_host="DH10B"  
/clone\_lib="NCI-CGAP\_Co8"  
/note="Organ: colon; Vector: pTT73D-Pac (Pharmacia) with a modified polylinker; 1st strand cDNA was prepared from colon adenocarcinoma, and was then primed with a Not I - oligo(dT) primer. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pTT73 vector. Library is normalized. Library was constructed by

```

ORIGIN
Query Match          70.5%; Score 14.8; DB 1; Length 46;
Best Local Similarity 88.9%; Pred. No. 4.2e+04;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CAGCAGCAGAGTCTTCAT 18
    ||||| ||||| |||||
Db 20 CAGCAGCTTAGTCTTCAT 37

RESULT 2
W25663/c
LOCUS
DEFINITION
z64e08.r1 Soares_fetal_heart_NbHL19W Homo sapiens cDNA clone
IMAGE:327110 5' similar to gb:X15183_cds1 HEAT SHOCK PROTEIN HSP
90-ALPHA (HUMAN) ; mRNA sequence.

ACCESSION
W25663
VERSION
W25663.1 GI:1303517
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
REFERENCE
1 (bases 1 to 44)
AUTHORS
Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
Holman,M., Hultman,M., Kucaba,T., Le.M., Lennon,G., Marra,M.,
Parsons,J., Rifkin,L., Kohlfing,T., Soares,M., Tan,F.,
Trevasakis,E., Waterston,R., Williamson,A., Wohlmann,P. and
Wilson,R.
The WashU-Merck EST Project
TITLE
Unpublished (1995)
JOURNAL
COMMENT
Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LML; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Trace considered overall poor quality
Insert length: 596 Std Error: 0.00
Seq primer: mob.REGA+ET
High quality sequence stop: 1.
FEATURES
source
1..44
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="GDB:1261312"
/db_xref="taxon:9606"
/clone="IMAGE:327110"
/sex="unknown"
/dev_stage="19 weeks"
/lab_host="DH10B (ampicillin resistant)"
/clone_lib="Soares_fetal_heart_NbHL19W"
/note="Organ: heart; Vector: p7T3D (Pharmacia) with a
modified polylinker; Site 1: Not 1; Site 2: Eco RI; 1st
strand cDNA was primed with a Not I - oligo(dT) primer [5',
TGTTACCAATCTGAAGTGGGCGCGCATCTTTTTTTTTTTT 3'],
double-stranded cDNA was size selected, ligated to Eco RI
adapters (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of a modified p7T3 vector
(Pharmacia). Library went through one round of
normalization to a Cot = 5. Library was constructed by
M.Fatima Bonaldo. This library was constructed from the
same fetus as the fetal lung library. Soares fetal lung
NbHL19W."

ORIGIN
Query Match          69.5%; Score 14.6; DB 7; Length 44;
Best Local Similarity 81.0%; Pred. No. 5.2e+04;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Bento Soares and M. Fatima Bonaldo. "

QY 1 CAGCAGCAGAGTCTTCAT 21
    ||||| ||||| |||||
Db 26 CAGCAGTAGGTTCATCTTCAT 6

RESULT 3
BH861678/c
LOCUS
DEFINITION
BH861678 Arabidopsis thaliana TDNA insertion lines Arabidopsis
thaliana genomic clone SALK_087727, genomic survey sequence.

ACCESSION
BH861678
VERSION
BH861678.1 GI:22097004
KEYWORDS
GSS.
SOURCE
Arabidopsis thaliana (thale cress)
ORGANISM
Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1 (bases 1 to 50)
AUTHORS
Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R.,
Gadrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L.,
Shinn,P., Zimmermann,J. and Ecker,J.R.
A Sequence-Indexed Library of Insertion Mutations in the
Arabidopsis Genome
Unpublished (2001)
CONTACT: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (SIGnAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6379
Email: ecker@salk.edu
This is single pass sequence recovered from the left border of
TDNA.
FEATURES
source
1..50
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/ecotype="Col-0"
/db_xref="taxon:3702"
/clone="SALK_087727"
/clone_lib="Arabidopsis thaliana TDNA insertion lines"
/note="PCR was performed on Arabidopsis thaliana lines
each of which contains one or more TDNA insertion
elements. The resultant fragment for each line was
directly sequenced to determine the genomic sequence at
the site of insertion. Details of the protocols used can
be found at http://signal.salk.edu/tdna_protocols.html"

ORIGIN
Query Match          66.7%; Score 14; DB 8; Length 50;
Best Local Similarity 100.0%; Pred. No. 9.8e+04;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GCAGCAGAGTCTTC 16
    ||||| ||||| |||||
Db 41 GCAGCAGAGTCTTC 28

RESULT 4
CC794149/c
LOCUS
DEFINITION
SALK_043910.30.25.x Arabidopsis thaliana TDNA insertion lines
Arabidopsis thaliana genomic clone SALK_043910.30.25.x, genomic
survey sequence.

ACCESSION
CC794149
VERSION
CC794149.1 GI:32389372
KEYWORDS
GSS.
SOURCE
Arabidopsis thaliana (thale cress)
ORGANISM
Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

```

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsids. 1 (bases 1 to 42)

#### REFERENCE AUTHORS

Alonso, J.M., Leisse, T.J., Barajas, P., Chen, H., Cheuk, R., Gadriab, C., Jecke, A., Karnes, M., Kim, C.J., Parker, H., Prednis, L., Shinn, P., Zimmerman, J., and Ecker, J.R.

#### TITLE

A Sequence-Indexed Library of Insertion Mutations in the Arabidopsis Genome

#### JOURNAL

Unpublished (2001)

#### COMMENT

Contact: Joseph R. Ecker

Salk Institute Genomic Analysis Laboratory (SIGnAL)

The Salk Institute for Biological Studies

10010 N. Torrey Pines Road, La Jolla, CA 92037, USA

Tel: 858 453 4100 x1752

Fax: 858 558 6379

Email: ecker@salk.edu

This is single pass sequence recovered from the left border of TDNA.

Class: TDNA tagged.

#### FEATURES

source

Location/Qualifiers

1..42

/organism="Arabidopsis thaliana"

/mol\_type="genomic DNA"

/ecotype="Col-0"

/db\_xref="taxon:3702"

/clone="SALK\_043910.30.25.x"

/clone\_lib="Arabidopsis thaliana TDNA insertion lines"

/notes="PCR was performed on Arabidopsis thaliana lines

each of which contains one or more TDNA insertion

elements. The resultant fragment for each line was

directly sequenced to determine the genomic sequence at

the site of insertion. Details of the protocols used can

be found at [http://signal.salk.edu/tdna\\_protocols.html](http://signal.salk.edu/tdna_protocols.html)"

#### ORIGIN

Query Match 64.8%; Score 13.6; DB 9; Length 42;  
Best Local Similarity 80.0%; Pred. No. 1.5e+05;  
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 AGCAGGAGCTCTTCATCAT 21

Db 29 AGAAACGAGTCATCATCAT 10

#### RESULT 5

CG869035/c

LOCUS

DEFINITION AB0164 Sanger Institute Gene Trap Library pGT01xr Mus musculus

CDNA, mRNA sequence.

CG869035

CG869035.1 GI:38532715

GSS.

Mus musculus (house mouse)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 50)

Sanger Institute Gene Trap Resource - SIGTR.

<http://www.sanger.ac.uk/PostGenomics/genetrap/>

Unpublished (2003)

Contact: Sanger Institute Gene Trap Resource - SIGTR

Wellcome Trust Sanger Institute

Email: [info.genetrap@sanger.ac.uk](mailto:info.genetrap@sanger.ac.uk)

Sequence tag generated by 5' RACE of total RNA from gene trap ES

cell line. ES cell lines harboring insertion mutation of target

gene are available upon request from Sanger Institute Gene Trap

Resource. Annotation information available from

<http://www.sanger.ac.uk/PostGenomics/genetrap/>

Class: Gene Trap.

#### FEATURES

source

Location/Qualifiers

1..50

/organism="Mus musculus"

/mol\_type="mRNA"

ORIGIN

Query Match 63.8%; Score 13.4; DB 9; Length 50;  
Best Local Similarity 93.3%; Pred. No. 1.8e+05;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 CAGAGTCTTCATCAT 21

Db 48 CAGAGTCTTCATCAT 34

#### RESULT 6

AZ802584

LOCUS

DEFINITION

2M0061105R Mouse 10kb plasmid UUGC1M library Mus musculus genomic

clone UUGC2M0061105 R, genomic survey sequence.

ACCESSION AZ802584

VERSION AZ802584.1

KEYWORDS GI:12954907

SOURCE

ORGANISM

Mus musculus (house mouse)

Mus musculus

Mammalia; Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi;

1 (bases 1 to 21)

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,

Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,

Reilly, M., Rose, R., Rose, R., Stokes, R., Tingey, A., von

Niederhausern, A. and Wright, D., Weiss, R.

Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts

Unpublished (2000)

Contact: Robert B. Weiss

University of Utah Genome Center

University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: [ddunn@genetics.utah.edu](mailto:ddunn@genetics.utah.edu)

Insert Length: 10000

Std Error: 0.00

Plate: 0061 row: 1 column: 05

Seq primer: CACACAGGAACAGCTATGACC

Class: plasmid ends

High quality sequence stop: 21.

Location/Qualifiers

1..21

/organism="Mus musculus"

/mol\_type="genomic DNA"

/strain="C57BL/6J"

/db\_xref="taxon:10090"

/clone="UUGC2M0061105"

/sex="Male"

/lab\_host="E. Coli strain XL10-Gold, TI-resistant, F-"

/clone\_lib="Mouse 10kb plasmid UUGC1M library"

/note="Vector: PWD42nv; Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource

(<http://www.jax.org/resources/documents/dnares/>). The DNA

was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA

was blunt end-repaired with T4 DNA polymerase and T4

polynucleotide kinase. Adaptor oligonucleotides were

ligated to the blunt ends in high molar excess. The

adapted DNA was purified and size-selected for a 9.5 to

10.5 kb range using preparative agarose gel

electrophoresis. Vector DNA was prepared from a derivative

of pWD42 (GI:4732114|gb|AF129072.1), a copy-number

inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

## ORIGIN

Query Match 61.9%; Score 13; DB 8; Length 21;  
Best Local Similarity 76.2%; Pred. No. 2.5e+05;  
Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 CAGCAGCAGAGTCTTCATCAT 21

Db 1 CAGCAGCAGCATACATCAT 21

## RESULT 7

BH908888 41 bp DNA linear GSS 04-SEP-2002

LOCUS SALK\_051042.25.80.x Arabidopsis thaliana TDNA insertion lines

DEFINITION Arabidopsis thaliana genomic clone SALK\_051042.25.80.x, genomic

survey sequence.

ACCESSION BH908888

VERSION BH908888.1 GI:22721821

KEYWORDS GSS.

SOURCE Arabidopsis thaliana (thale cress)

ORGANISM Arabidopsis thaliana

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

1 (bases 1 to 41)

REFERENCE Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R.,

Gadrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L.,

Shinn,P., Zimmerman,J., and Ecker,J.R.

A Sequence-Indexed Library of Insertion Mutations in the

Arabidopsis Genome

Unpublished (2001)

Contact: Joseph R. Ecker

Salk Institute Genomic Analysis Laboratory (SIGNAL)

The Salk Institute for Biological Studies

10010 N. Torrey Pines Road, La Jolla, CA 92037, USA

Tel: 858 453 4100 x1752

Fax: 858 558 6379

Email: ecker@salk.edu

This is single pass sequence recovered from the left border of

TDNA. This sequence lies within an annotated exon of At5g58140.

Class: TDNA tagged

Location/Qualifiers

1..41

/organism="Arabidopsis thaliana"

/mol\_type="genomic DNA"

/ecotype="Col-0"

/db\_xref="taxon:3702"

/clone="SALK\_051042.25.80.x"

/clone\_lib="Arabidopsis thaliana TDNA insertion lines"

/note="PCR was performed on Arabidopsis thaliana lines

each of which contains one or more TDNA insertion

elements. The resultant fragment for each line was

directly sequenced to determine the genomic sequence at

the site of insertion. Details of the protocols used can

be found at [http://signal.salk.edu/tdna\\_protocols.html](http://signal.salk.edu/tdna_protocols.html)

Query Match 61.9%; Score 13; DB 8; Length 41;

Best Local Similarity 76.2%; Pred. No. 2.7e+05;

Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 CAGCAGCAGAGTCTTCATCAT 21

Db 19 CAGCAGGGGATTCCTTACCAT 39

## RESULT 8

AA973632

LOCUS

DEFINITION

AA973632

43 bp mRNA linear

EST 17-JUN-1998

OO48B04.s1 NCI CGAP Lu5 Homo sapiens cDNA clone IMAGE:1569391 3'

similar to SW:XP\_CERA P33194 POSSIBLE DNA-REPAIR PROTEIN XP-E ;

mRNA sequence.

AA973632

AA973632.1 GI:3148812

EST.

VERSION

KEYWORDS

SOURCE

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 43)

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov

Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.

Emmert-Buck, M.D., Ph.D.

cDNA Library Preparation: M. Bento Soares, Ph.D.

cDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

[www-bio.llnl.gov/bbrp/image/image.html](http://www-bio.llnl.gov/bbrp/image/image.html)

Trace considered overall poor quality

Insert Length: 703 Std Error: 0.00

Seq primer: -40ml3 fwd. ET from Amersham

High quality sequence stop: 1.

Location/Qualifiers

1..43

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="IMAGE:1569391"

/tissue\_type="carcinoid"

/lab\_host="DH10B"

/clone\_lib="NCI-CGAP Lu5"

/note="Organ: lung; Vector: pT7T3D-Pac (Pharmacia) with a

modified polylinker; 1st strand cDNA was prepared from

neuroendocrine lung carcinoid, and was then primed with a

Not I - oligo(dT) primer. Double-stranded cDNA was ligated

to Eco RI adaptors (Pharmacia), digested with Not I and

cloned into the Not I and Eco RI sites of the modified

pT7T3 vector. Library is normalized. Library was

constructed by Bento Soares and M. Fatima Bonaldo. "

Query Match 61.9%; Score 13; DB 1; Length 43;

Best Local Similarity 76.2%; Pred. No. 2.8e+05;

Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 CAGCAGCAGAGTCTTCATCAT 21

Db 1 CAACATAGAGTCTTCATCAT 21

RESULT 9

AL948370/c

LOCUS

DEFINITION

AL948370

Arabidopsis thaliana T-DNA flanking sequence GK-311H09-015792,

genomic survey sequence.

AL948370.1 GI:24404992

GSS.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Arabidopsis thaliana (thale cress)

Arabidopsis thaliana

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;



rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

1 Li, Y., Rosso, M.G., Strizhov, N., Viehoever, P. and Weisshaar, B.  
GABI-Kat Simplesearch: a flanking sequence tag (FST) database for  
the identification of T-DNA insertion mutants in Arabidopsis  
thaliana  
Bioinformatics 19 (11), 1441-1442 (2003)  
22755829  
12874060

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
MEDLINE  
PUBMED  
REFERENCE  
AUTHORS

Rosso, M.G., Li, Y., Strizhov, N., Reiss, B., Dekker, K. and  
Weisshaar, B.  
An Arabidopsis thaliana T-DNA mutagenized population (GABI-Kat) for  
flanking sequence tag-based reverse genetics  
Plant Mol. Biol. 53 (1-2), 247-259 (2003)  
23117147  
14756321

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
MEDLINE  
PUBMED  
REFERENCE  
AUTHORS

Strizhov, N., Li, Y., Rosso, M.G., Viehoever, P., Dekker, K.A. and  
Weisshaar, B.  
High-throughput generation of sequence indexes from T-DNA  
mutagenized Arabidopsis thaliana lines  
Biotechniques 35 (6), 1164-1168 (2003)  
14682050

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
MEDLINE  
PUBMED  
REFERENCE  
AUTHORS

Strizhov, N., Rosso, M.G., Li, Y. and Weisshaar, B.  
Submitted (31-MAR-2004) Weisshaar B., Max-Planck-Institut fuer  
Zuechtungsforschung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany  
This sequence has been recovered from the left border of the T-DNA.  
It indicates an insertion close to or within gene Atg34110.  
Details on the protocols used for generation of the sequence are  
described in References 1-3. The sequences are generated at the MPI  
for Plant Breeding Research in the context of the GABI-Kat project.  
GABI-Kat is part of the German Plant Genomics program designated  
"GABI". Information on line availability can be found at:  
<http://www.mpiz-koeln.mpg.de/GABI-Kat/>.

FEATURES  
Location/Qualifiers  
1..48  
/organism="Arabidopsis thaliana"  
/mol\_type="genomic DNA"  
/strain="Columbia 0"  
/db\_xref="taxon:3702"  
/clone="GK-311H09-015792"  
/lib="Arabidopsis thaliana T-DNA insertion lines"  
/ecotype="Col-0"  
/note="PCR was performed on DNA from Arabidopsis thaliana  
plants (Ti) which were transformed with the T-DNA from  
vector pAC161 (GenBank accession number: AJ537514). The  
lines contain one or more T-DNA insertions. The DNA  
fragment(s) resulting from the PCR were directly sequenced  
to determine the genomic sequence flanking the insertion.  
T-DNA derived sequences were removed."

ORIGIN  
Query Match 61.9%; Score 13; DB 9; Length 48;  
Best Local Similarity 76.2%; Pred. No. 2.8e+05;  
Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 CAGCAGCAGGCTTCATCAT 21  
|||||  
DB 37 CAGCAGCAGGAGGATTTTCAT 17  
|||||

RESULT 10  
AU107924  
LOCUS  
DEFINITION  
AU107924 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone  
HRC02185, mRNA sequence.  
ACCESSION  
AU107924  
VERSION  
AU107924.1 GI:13557446  
KEYWORDS  
Homo sapiens (human)

ORGANISM  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 50)

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
MEDLINE  
PUBMED  
COMMENT

Suzuki, Y., Taira, H., Teunoda, T., Mizushima-Sugano, J., Sese, J.,  
Hata, H., Oca, T., Isogai, T., Tanaka, T., Morishita, S., Okubo, K.,  
Sakaki, Y., Nakamura, Y., Suyama, A. and Sugano, S.  
Diverse transcriptional initiation revealed by fine, large-scale  
mapping of mRNA start sites  
EMBO Rep. 2 (5), 388-393 (2001)  
21270072  
11375929

Contact: Yutaka Suzuki  
Department of Virology  
Institute of Medical Science, University of Tokyo  
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan  
Email: ysuzuki@ims.u-tokyo.ac.jp  
Suzuki, Y., Yoshitomo-Nakagawa, K., Maruyama, K., Suyama, A. and  
Sugano, S.  
Construction and a 5'-end-enriched cDNA library. Gene 200 (1-2),  
149-156 (1997).

FEATURES  
Location/Qualifiers  
1..50  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="HRC02185"  
/clone\_lib="Sugano Homo sapiens cDNA library"

ORIGIN  
Query Match 61.0%; Score 12.8; DB 1; Length 50;  
Best Local Similarity 87.5%; Pred. No. 3.5e+05;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 AGCAGCAGAGTCTTCA 17  
|||||  
DB 27 AGCAGCAGAGTCCGCA 42  
|||||

RESULT 11  
AU107925  
LOCUS  
DEFINITION  
AU107925 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone  
HSI06916, mRNA sequence.  
ACCESSION  
AU107925  
VERSION  
AU107925.1 GI:13557447  
KEYWORDS  
Homo sapiens (human)  
ORGANISM  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 50)

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
MEDLINE  
PUBMED  
COMMENT

Suzuki, Y., Taira, H., Teunoda, T., Mizushima-Sugano, J., Sese, J.,  
Hata, H., Oca, T., Isogai, T., Tanaka, T., Morishita, S., Okubo, K.,  
Sakaki, Y., Nakamura, Y., Suyama, A. and Sugano, S.  
Diverse transcriptional initiation revealed by fine, large-scale  
mapping of mRNA start sites  
EMBO Rep. 2 (5), 388-393 (2001)  
21270072  
11375929

Contact: Yutaka Suzuki  
Department of Virology  
Institute of Medical Science, University of Tokyo  
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan  
Email: ysuzuki@ims.u-tokyo.ac.jp  
Suzuki, Y., Yoshitomo-Nakagawa, K., Maruyama, K., Suyama, A. and  
Sugano, S.  
Construction and a 5'-end-enriched cDNA library. Gene 200 (1-2),  
149-156 (1997).

FEATURES  
Location/Qualifiers  
1..50  
/organism="Homo sapiens"  
/mol\_type="mRNA"



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REFERENCE 4 (bases 1 to 39)
AUTHORS Strizhov,N., Rosso,M.G., Li,Y. and Weisshaar,B.
TITLE Direct Submission
JOURNAL Submitted (31-MAR-2004) Weisshaar B., Max-Planck-Institut fuer
Zuechtungsforschung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany
COMMENT This sequence has been recovered from the left border of the T-DNA.
It indicates an insertion within the locus defined by BAC clone
t10j7. Details on the protocols used for generation of the sequence
are described in References 1-3. The sequences are generated at the
MPI for Plant Breeding Research in the context of the GABI-Kat
project. GABI-Kat is part of the German Plant Genomics program
designated 'GABI'. Information on line availability can be found
at: http://www.mpiz-koeln.mpg.de/GABI-Kat/.

FEATURES
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            /ecotype="Col-0"
            /note="PCR was performed on DNA from Arabidopsis thaliana
plants (Ti) which were transformed with the T-DNA from
vector pAC161 (GenBank accession number: AJ537514). The
lines contain one or more T-DNA insertions. The DNA
fragment(s) resulting from the PCR were directly sequenced
to determine the genomic sequence flanking the insertion.
T-DNA derived sequences were removed."

ORIGIN
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    Best Local Similarity 78.9%; Pred. No. 4.2e+05;
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Db 38 AGCGGCAGAGTGTCTCCA 20

RESULT 15
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LOCUS wh61d04.x1 NCI CGAP Kid11 Homo sapiens cDNA clone IMAGE:2385223 3'
DEFINITION similar to SW:COX2_HUMAN P00403 CYTOCHROME C OXIDASE POLYPEPTIDE II
:mRNA sequence.
ACCESSION AI766391
VERSION AI766391.1 GI:5232900
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 43)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgaps-r@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LINL at:
www-bio.llnl.gov/bbrp/image/image.html

Trace considered overall poor quality
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Seq primer: -40UP from Gibco
High quality sequence stop: 1.

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## FEATURES

source

## Location/Qualifiers

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/clone_lib="NCI CGAP Kid11"
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a modified polylinker; Site 1: Not 1; Site 2: Eco RI;
Plasmid DNA from the normalized library NCI CGAP Kid3 was
prepared, and ss circles were made in vitro. Following HAP
purification, this DNA was used as tracer in a subtractive
hybridization reaction. The driver was PCR-amplified cDNAs
from a pool of 5,000 clones made from the same library
(cloneIds 1322376-1323911, 1456007-1456775, and
1500552-1502855). Subtraction by Bento Soares and M.
Fatima Bonaldo."

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## ORIGIN

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    Best Local Similarity 78.9%; Pred. No. 4.2e+05;
    Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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Db 32 CATCATCATAGTCTTCATC 14

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Job time : 3031 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 13, 2005, 10:44:45 ; Search time 4 Seconds  
(without alignments)  
2.954 Million cell updates/sec

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Perfect score: 1643  
Sequence: 1 gaattccgcgcgtaccgag.....taaaactgtctgtgagctg 1643

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 0.5

Searched: 198 seqs, 3596 residues

Total number of hits satisfying chosen parameters: 396

Minimum DB seq length: 8  
Maximum DB seq length: 50

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 198 summaries

Database : rmidb:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

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C 5	25	1.5	25	1	US-09-225-928-748
C 6	25	1.5	25	1	US-09-225-928-748
C 7	23	1.4	23	1	US-09-659-791A-5
8	21.8	1.3	25	1	US-09-396-196G-31760
9	21	1.3	21	1	US-08-410-540-21
10	21	1.3	21	1	US-09-659-791A-6
11	21	1.3	21	1	US-09-459-749D-14
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13	20.6	1.3	21	1	US-09-657-472-2422
14	20.6	1.3	21	1	US-09-657-472-2423
15	20.6	1.3	21	1	US-09-657-472-2424
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C 25	20	1.2	20	1	US-09-659-791A-22
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; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Field, Bret E.
; REGISTRATION NUMBER: 37,620
; REFERENCE/DOCKET NUMBER: 09096/002001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-322-5070
; TELEFAX: 415-854-0875
; INFORMATION FOR SEQ ID NO: 748:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; MOLECULE TYPE: DNA
; FEATURE:
; OTHER INFORMATION: oligonucleotide primer
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; Sequence 748, Application US/09225928
; Patent No. 6352829
; GENERAL INFORMATION:
; APPLICANT: Chenchik, Alex
; ;
; ; Bibilashvilli, Robert
; ;
; TITLE OF INVENTION: METHOD OF ASSAYING DIFFERENTIAL
; EXPRESSION
;
; NUMBER OF SEQUENCES: 1375
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 2200 Sand Hill Road, Suite 100
; CITY: Menlo Park
; STATE: CA
; COUNTRY: US
; ZIP: 94025
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSEQ for Windows Version 2.0
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; FILING DATE: 05-Jan-1999
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/859,998
; FILING DATE: 21-MAY-1997
; NAME: Field, Bret E.
; ATTORNEY/AGENT INFORMATION:
; REGISTRATION NUMBER: 37,620
; REFERENCE/DOCKET NUMBER: 09096/002001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-322-5070
; TELEFAX: 415-854-0875
; INFORMATION FOR SEQ ID NO: 748:
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; STRANDEDNESS: single
; MOLECULE TYPE: DNA
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; OTHER INFORMATION: oligonucleotide primer
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; US-09-225-928-748
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; Best Local Similarity 100.0%; Pred. No. 3;
; Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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; RESULT 6
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; Sequence 748, Application US/09225201B
; Patent No. 6489455
; GENERAL INFORMATION:
; APPLICANT: Chenchik, Alex
; ;
; ; Johhadze, George
; ; Bibilashvilli, Robert
; ;
; TITLE OF INVENTION: METHOD OF ASSAYING DIFFERENTIAL
; EXPRESSION
;
; NUMBER OF SEQUENCES: 1375
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 2200 Sand Hill Road, Suite 100
; CITY: Menlo Park
; STATE: CA
; COUNTRY: US
; ZIP: 94025
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/225,201B
; FILING DATE: 05-Jan-1999
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/859,998
; FILING DATE: 21-MAY-1997
; NAME: Field, Bret E.
; ATTORNEY/AGENT INFORMATION:
; REGISTRATION NUMBER: 37,620
; REFERENCE/DOCKET NUMBER: 09096/002001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-322-5070
; TELEFAX: 415-854-0875
; INFORMATION FOR SEQ ID NO: 748:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; MOLECULE TYPE: DNA
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; FEATURE:
; OTHER INFORMATION: oligonucleotide primer
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; US-09-225-928-748
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; Best Local Similarity 100.0%; Pred. No. 3;
; Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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RESULT 7
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; Sequence 5, Application US/09659791A
; Patent No. 6383808
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Susan M. Freier
; TITLE OF INVENTION: ANTISENSE MODULATION OF CLUSTERIN EXPRESSION
; FILE REFERENCE: RTS-0156
; CURRENT APPLICATION NUMBER: US/09/659,791A
; CURRENT FILING DATE: 2000-09-11
; NUMBER OF SEQ ID NOS: 90
; SEQ ID NO 5
; LENGTH: 23
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: PCR Primer
US-09-659-791A-5

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Best Local Similarity 100.0%; Pred. No. 5.4;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 23 CTTGAGATGATACACAGGCTCA 1

RESULT 8
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; Sequence 31760, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 31760
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-396-196G-31760

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Best Local Similarity 92.0%; Pred. No. 10;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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RESULT 9
US-08-410-540-21
; Sequence 21, Application US/08410540
; Patent No. 5807678
; GENERAL INFORMATION:
; APPLICANT: Miller, Walter L.
; APPLICANT: Lin, Dong

QY 1354 AGAAGCGCTGCAGGAATACC 1374
DB 1 AGAAGCGCTGCAGGAATACC 21

Query Match 1.3%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 9.2;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 10
US-09-659-791A-6
; Sequence 6, Application US/09659791A
; Patent No. 6383808
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Susan M. Freier
; TITLE OF INVENTION: ANTISENSE MODULATION OF CLUSTERIN EXPRESSION
; FILE REFERENCE: RTS-0156
; CURRENT APPLICATION NUMBER: US/09/659,791A
; CURRENT FILING DATE: 2000-09-11
; NUMBER OF SEQ ID NOS: 90
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; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: PCR Probe
US-09-659-791A-6

Query Match 1.3%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 9.2;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 766 TCCACGCCATGTTCAGCCCT 786
```

```
Db      1  TCCAGCCATGTTCCAGCCT 21
|||||
RESULT 11
US-09-459-749D-14
; Sequence 14, Application US/09459749D
; Patent No. 6464975
; GENERAL INFORMATION:
; APPLICANT: Millis, Albert J. T.
; TITLE OF INVENTION: Compositions and Methods For Altering Cell Migration
; FILE REFERENCE: 0794.016A
; CURRENT APPLICATION NUMBER: US/09/459,749D
; CURRENT FILING DATE: 1999-12-10
; PRIOR APPLICATION NUMBER: 60/111,856
; PRIOR FILING DATE: 1998-12-11
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 14
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: primer bind
; OTHER INFORMATION: synthetic sense primer based on porcine clusterin
US-09-459-749D-14

Query Match      1.3%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 9.2; Mismatches 0; Indels 0; Gaps 0;
Matches 21; Conservative 0;

Qy      274  AAGCCAAGAGAAAGAAAGG 294
|||||
Db      1  AAGCCAAGAGAAAGAAAGG 21
|||||

RESULT 12
US-09-657-472-2421
; Sequence 2421, Application US/09657472
; Patent No. 6727063
; GENERAL INFORMATION:
; APPLICANT: Lander, Eric S.
; APPLICANT: Cargill, Michele
; APPLICANT: Ireland, James S.
; APPLICANT: Bolk, Stacey
; APPLICANT: Daley, George Q.
; APPLICANT: McCarthy, Jeanette J.
; TITLE OF INVENTION: SINGLE NUCLEOTIDE POLYMORPHISMS IN GENES
; CURRENT APPLICATION NUMBER: US/09/657,472
; CURRENT FILING DATE: 2000-09-07
; PRIOR APPLICATION NUMBER: US 60/153,357
; PRIOR FILING DATE: 1999-09-10
; PRIOR APPLICATION NUMBER: US 60/220,947
; PRIOR FILING DATE: 2000-07-26
; PRIOR APPLICATION NUMBER: US 60/225,724
; PRIOR FILING DATE: 2000-08-16
; NUMBER OF SEQ ID NOS: 2551
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2421
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-657-472-2421

Query Match      1.3%; Score 20.6; DB 1; Length 21;
Best Local Similarity 95.2%; Pred. No. 11; Mismatches 1; Indels 0; Gaps 0;
Matches 20; Conservative 1;

Qy      1050  GAGAGGTTGACCAGGAATAC 1070
|||||
Db      1  GAGAGGTTGAYCAGGAATAC 21
|||||

RESULT 13
US-09-657-472-2422
; Sequence 2422, Application US/09657472
; Patent No. 6727063
; GENERAL INFORMATION:
; APPLICANT: Lander, Eric S.
; APPLICANT: Cargill, Michele
; APPLICANT: Ireland, James S.
; APPLICANT: Bolk, Stacey
; APPLICANT: Daley, George Q.
; APPLICANT: McCarthy, Jeanette J.
; TITLE OF INVENTION: SINGLE NUCLEOTIDE POLYMORPHISMS IN GENES
; FILE REFERENCE: 2825.1027-001
; CURRENT APPLICATION NUMBER: US/09/657,472
; CURRENT FILING DATE: 2000-09-07
; PRIOR APPLICATION NUMBER: US 60/153,357
; PRIOR FILING DATE: 1999-09-10
; PRIOR APPLICATION NUMBER: US 60/220,947
; PRIOR FILING DATE: 2000-07-26
; PRIOR APPLICATION NUMBER: US 60/225,724
; PRIOR FILING DATE: 2000-08-16
; NUMBER OF SEQ ID NOS: 2551
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2422
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-657-472-2422

Query Match      1.3%; Score 20.6; DB 1; Length 21;
Best Local Similarity 95.2%; Pred. No. 11; Mismatches 1; Indels 0; Gaps 0;
Matches 20; Conservative 1;

Qy      999  CCCTCCAGGCTAGCTCGG 1019
|||||
Db      1  CCCTCCAGGCTAGCTCGG 21
|||||

RESULT 14
US-09-657-472-2423
; Sequence 2423, Application US/09657472
; Patent No. 6727063
; GENERAL INFORMATION:
; APPLICANT: Lander, Eric S.
; APPLICANT: Cargill, Michele
; APPLICANT: Ireland, James S.
; APPLICANT: Bolk, Stacey
; APPLICANT: Daley, George Q.
; APPLICANT: McCarthy, Jeanette J.
; TITLE OF INVENTION: SINGLE NUCLEOTIDE POLYMORPHISMS IN GENES
; FILE REFERENCE: 2825.1027-001
; CURRENT APPLICATION NUMBER: US/09/657,472
; CURRENT FILING DATE: 2000-09-07
; PRIOR APPLICATION NUMBER: US 60/153,357
; PRIOR FILING DATE: 1999-09-10
; PRIOR APPLICATION NUMBER: US 60/220,947
; PRIOR FILING DATE: 2000-07-26
; PRIOR APPLICATION NUMBER: US 60/225,724
; PRIOR FILING DATE: 2000-08-16
; NUMBER OF SEQ ID NOS: 2551
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2423
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-657-472-2423

Query Match      1.3%; Score 20.6; DB 1; Length 21;
Best Local Similarity 95.2%; Pred. No. 11; Mismatches 1; Indels 0; Gaps 0;
Matches 20; Conservative 1;

Qy      1170  CTCACGAAGCGAAGACCAG 1190
|||||
```

Db 1 CTCACGCAAGCGAAGACCAG 21  
|||||:|||||

RESULT 15  
US-09-472-2424  
; Sequence 2424, Application US/09657472  
; Patent No. 6727063  
; GENERAL INFORMATION:  
; APPLICANT: Lander, Eric S.  
; APPLICANT: Cargill, Michele  
; APPLICANT: Ireland, James S.  
; APPLICANT: Bolk, Stacey  
; APPLICANT: Daley, George Q.  
; APPLICANT: McCarthy, Jeanette J.  
; TITLE OF INVENTION: SINGLE NUCLEOTIDE POLYMORPHISMS IN GENES  
; CURRENT APPLICATION NUMBER: US/09/657,472  
; CURRENT FILING DATE: 2000-09-07  
; PRIOR APPLICATION NUMBER: US 60/153,357  
; PRIOR FILING DATE: 1999-09-10  
; PRIOR APPLICATION NUMBER: US 60/220,947  
; PRIOR FILING DATE: 2000-07-26  
; PRIOR APPLICATION NUMBER: US 60/225,724  
; PRIOR FILING DATE: 2000-08-16  
; NUMBER OF SEQ ID NOS: 2551  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 2424  
; LENGTH: 21  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-657-472-2424

Query Match 1.3%; Score 20.6; DB 1; Length 21;  
Best Local Similarity 95.2%; Pred. No. 11;  
Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1105 TCACACCTTCCTCTGTGG 1125  
|||||:|||||

Db 1 TCACACCTTCCTCTGTGG 21

RESULT 16  
US-09-396-196G-31758  
; Sequence 31758, Application US/09396196G  
; Patent No. 6821724  
; GENERAL INFORMATION:  
; APPLICANT: Michael Mitmann  
; APPLICANT: David Mack  
; APPLICANT: David Lockhart  
; APPLICANT: Affymetrix, Inc.  
; TITLE OF INVENTION: Methods of Genetic Analysis  
; FILE REFERENCE: 3101.1  
; CURRENT APPLICATION NUMBER: US/09/396,196G  
; CURRENT FILING DATE: 1999-09-15  
; PRIOR APPLICATION NUMBER: 60/100,678  
; PRIOR FILING DATE: 1998-09-17  
; NUMBER OF SEQ ID NOS: 127806  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 31758  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Mus musculus  
US-09-396-196G-31758

Query Match 1.2%; Score 20.2; DB 1; Length 25;  
Best Local Similarity 88.0%; Pred. No. 18;  
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1171 TCACGAGGCGAAGACCAAGTACTA 1195  
|||||:|||||

Db 1 TCACGAGGCGAAGACCAAGTACTA 25

RESULT 17  
US-09-659-791A-14/c  
; Sequence 14, Application US/09659791A  
; Patent No. 6383808  
; GENERAL INFORMATION:  
; APPLICANT: Brett P. Monia  
; APPLICANT: Susan M. Freier  
; TITLE OF INVENTION: ANTISENSE MODULATION OF CLUSTERIN EXPRESSION  
; FILE REFERENCE: RTS-0156  
; CURRENT APPLICATION NUMBER: US/09/659,791A  
; CURRENT FILING DATE: 2000-09-11  
; NUMBER OF SEQ ID NOS: 90  
; SEQ ID NO 14  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Antisense Oligonucleotide  
US-09-659-791A-14

Query Match 1.2%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 12;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 TGACCGAGCGTGCAAGAC 32  
|||||:|||||

Db 20 TGACCGAGCGTGCAAGAC 1

RESULT 18  
US-09-659-791A-15/c  
; Sequence 15, Application US/09659791A  
; Patent No. 6383808  
; GENERAL INFORMATION:  
; APPLICANT: Brett P. Monia  
; APPLICANT: Susan M. Freier  
; TITLE OF INVENTION: ANTISENSE MODULATION OF CLUSTERIN EXPRESSION  
; FILE REFERENCE: RTS-0156  
; CURRENT APPLICATION NUMBER: US/09/659,791A  
; CURRENT FILING DATE: 2000-09-11  
; NUMBER OF SEQ ID NOS: 90  
; SEQ ID NO 15  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Antisense Oligonucleotide  
US-09-659-791A-15

Query Match 1.2%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 12;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 21 GCGTGCAAGACTCCAGAAT 40  
|||||:|||||

Db 20 GCGTGCAAGACTCCAGAAT 1

RESULT 19  
US-09-659-791A-16/c  
; Sequence 16, Application US/09659791A  
; Patent No. 6383808  
; GENERAL INFORMATION:  
; APPLICANT: Brett P. Monia  
; APPLICANT: Susan M. Freier  
; TITLE OF INVENTION: ANTISENSE MODULATION OF CLUSTERIN EXPRESSION  
; FILE REFERENCE: RTS-0156  
; CURRENT APPLICATION NUMBER: US/09/659,791A  
; CURRENT FILING DATE: 2000-09-11  
; NUMBER OF SEQ ID NOS: 90  
; SEQ ID NO 16  
; LENGTH: 20

```
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-659-791A-16

Query Match          1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 39 ATTGAGGCGATGATGAC 58
Db 20 ATTGAGGCGATGATGAC 1

RESULT 20
US-09-659-791A-17/c
; Sequence 17, Application US/09659791A
; Patent No. 6383808
; GENERAL INFORMATION:
; APPLICANT: Susan M. Freier
; TITLE OF INVENTION: ANTISENSE MODULATION OF CLUSTERIN EXPRESSION
; FILE REFERENCE: RTS-0156
; CURRENT APPLICATION NUMBER: US/09/659,791A
; CURRENT FILING DATE: 2000-09-11
; NUMBER OF SEQ ID NOS: 90
; SEQ ID NO 17
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-659-791A-17

Query Match          1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 77 GCTGCTGCTGACCTGGGAGA 96
Db 20 GCTGCTGCTGACCTGGGAGA 1

RESULT 21
US-09-659-791A-18/c
; Sequence 18, Application US/09659791A
; Patent No. 6383808
; GENERAL INFORMATION:
; APPLICANT: Susan M. Freier
; TITLE OF INVENTION: ANTISENSE MODULATION OF CLUSTERIN EXPRESSION
; FILE REFERENCE: RTS-0156
; CURRENT APPLICATION NUMBER: US/09/659,791A
; CURRENT FILING DATE: 2000-09-11
; NUMBER OF SEQ ID NOS: 90
; SEQ ID NO 18
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-659-791A-18

Query Match          1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 101 GCAGGTCCTGGGGACCAGA 120
Db 20 GCAGGTCCTGGGGACCAGA 1
```

```
RESULT 22
US-09-659-791A-19/c
; Sequence 19, Application US/09659791A
; Patent No. 6383808
; GENERAL INFORMATION:
; APPLICANT: Susan M. Freier
; TITLE OF INVENTION: ANTISENSE MODULATION OF CLUSTERIN EXPRESSION
; FILE REFERENCE: RTS-0156
; CURRENT APPLICATION NUMBER: US/09/659,791A
; CURRENT FILING DATE: 2000-09-11
; NUMBER OF SEQ ID NOS: 90
; SEQ ID NO 19
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-659-791A-19

Query Match          1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 122 GGTCTCAGACAATGAGCTCC 141
Db 20 GGTCTCAGACAATGAGCTCC 1

RESULT 23
US-09-659-791A-20/c
; Sequence 20, Application US/09659791A
; Patent No. 6383808
; GENERAL INFORMATION:
; APPLICANT: Susan M. Freier
; TITLE OF INVENTION: ANTISENSE MODULATION OF CLUSTERIN EXPRESSION
; FILE REFERENCE: RTS-0156
; CURRENT APPLICATION NUMBER: US/09/659,791A
; CURRENT FILING DATE: 2000-09-11
; NUMBER OF SEQ ID NOS: 90
; SEQ ID NO 20
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-659-791A-20

Query Match          1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 149 GTCCAATCAGGGAAGTAAGT 168
Db 20 GTCCAATCAGGGAAGTAAGT 1

RESULT 24
US-09-659-791A-21/c
; Sequence 21, Application US/09659791A
; Patent No. 6383808
; GENERAL INFORMATION:
; APPLICANT: Susan M. Freier
; TITLE OF INVENTION: ANTISENSE MODULATION OF CLUSTERIN EXPRESSION
; FILE REFERENCE: RTS-0156
; CURRENT APPLICATION NUMBER: US/09/659,791A
; CURRENT FILING DATE: 2000-09-11
; NUMBER OF SEQ ID NOS: 90
; SEQ ID NO 21
; LENGTH: 20
; TYPE: DNA
```

```
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-659-791A-21

Query Match      1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 166 AGTACGTCATTAAGGAATT 185
|||||
DB 20 AGTACGTCATTAAGGAATT 1

RESULT 25
US-09-659-791A-22/c
; Sequence 22, Application US/09659791A
; Patent No. 6383808
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Susan M. Freier
; TITLE OF INVENTION: ANTISENSE MODULATION OF CLUSTERIN EXPRESSION
; FILE REFERENCE: RTS-0156
; CURRENT APPLICATION NUMBER: US/09/659,791A
; CURRENT FILING DATE: 2000-09-11
; NUMBER OF SEQ ID NOS: 90
; SEQ ID NO 22
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-659-791A-22

Query Match      1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 201 GGGGTGAACAGATAAGAC 220
|||||
DB 20 GGGGTGAACAGATAAGAC 1

RESULT 26
US-09-659-791A-23/c
; Sequence 23, Application US/09659791A
; Patent No. 6383808
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Susan M. Freier
; TITLE OF INVENTION: ANTISENSE MODULATION OF CLUSTERIN EXPRESSION
; FILE REFERENCE: RTS-0156
; CURRENT APPLICATION NUMBER: US/09/659,791A
; CURRENT FILING DATE: 2000-09-11
; NUMBER OF SEQ ID NOS: 90
; SEQ ID NO 23
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-659-791A-23

Query Match      1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 281 GAAGAAGAAAGAGATGCC 300
|||||
DB 20 GAAGAAGAAAGAGATGCC 1

RESULT 27
US-09-659-791A-24/c
; Sequence 24, Application US/09659791A
; Patent No. 6383808
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Susan M. Freier
; TITLE OF INVENTION: ANTISENSE MODULATION OF CLUSTERIN EXPRESSION
; FILE REFERENCE: RTS-0156
; CURRENT APPLICATION NUMBER: US/09/659,791A
; CURRENT FILING DATE: 2000-09-11
; NUMBER OF SEQ ID NOS: 90
; SEQ ID NO 24
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-659-791A-24

Query Match      1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 286 AGAAGAGATGCCCTTAAT 305
|||||
DB 20 AGAAGAGATGCCCTTAAT 1

RESULT 28
US-09-659-791A-25/c
; Sequence 25, Application US/09659791A
; Patent No. 6383808
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Susan M. Freier
; TITLE OF INVENTION: ANTISENSE MODULATION OF CLUSTERIN EXPRESSION
; FILE REFERENCE: RTS-0156
; CURRENT APPLICATION NUMBER: US/09/659,791A
; CURRENT FILING DATE: 2000-09-11
; NUMBER OF SEQ ID NOS: 90
; SEQ ID NO 25
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-659-791A-25

Query Match      1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 298 CCTTAATGAGACAGGGAA 317
|||||
DB 20 CCTTAATGAGACAGGGAA 1

RESULT 29
US-09-659-791A-26/c
; Sequence 26, Application US/09659791A
; Patent No. 6383808
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Susan M. Freier
; TITLE OF INVENTION: ANTISENSE MODULATION OF CLUSTERIN EXPRESSION
; FILE REFERENCE: RTS-0156
; CURRENT APPLICATION NUMBER: US/09/659,791A
; CURRENT FILING DATE: 2000-09-11
; NUMBER OF SEQ ID NOS: 90
; SEQ ID NO 26
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
```

```

; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
; US-09-659-791A-26

Query Match      1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 307 AGACCAGGGAATCAGAGACA 326
Db 20 AGACCAGGGAATCAGAGACA 1

RESULT 30
US-09-659-791A-27/c
; Sequence 27, Application US/09659791A
; Patent No. 6383808
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Susan M. Freier
; TITLE OF INVENTION: ANTISENSE MODULATION OF CLUSTERIN EXPRESSION
; FILE REFERENCE: RTS-0156
; CURRENT APPLICATION NUMBER: US/09/659,791A
; CURRENT FILING DATE: 2000-09-11
; NUMBER OF SEQ ID NOS: 90
; SEQ ID NO 27
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-659-791A-27

Query Match      1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 324 ACAAGCTGAAGGAGCTCCC 343
Db 20 ACAAGCTGAAGGAGCTCCC 1

RESULT 31
US-09-659-791A-28/c
; Sequence 28, Application US/09659791A
; Patent No. 6383808
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Susan M. Freier
; TITLE OF INVENTION: ANTISENSE MODULATION OF CLUSTERIN EXPRESSION
; FILE REFERENCE: RTS-0156
; CURRENT APPLICATION NUMBER: US/09/659,791A
; CURRENT FILING DATE: 2000-09-11
; NUMBER OF SEQ ID NOS: 90
; SEQ ID NO 28
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-659-791A-28

Query Match      1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 359 GACCATGATGGCCCTCTGGG 378
Db 20 GACCATGATGGCCCTCTGGG 1

RESULT 32
US-09-659-791A-29/c
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
; US-09-659-791A-29

Query Match      1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 380 AGAGTGTAAAGCCCTGCCTGA 399
Db 20 AGAGTGTAAAGCCCTGCCTGA 1

RESULT 34
US-09-659-791A-31/c
; Sequence 31, Application US/09659791A
; Patent No. 6383808
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Susan M. Freier
; TITLE OF INVENTION: ANTISENSE MODULATION OF CLUSTERIN EXPRESSION
; FILE REFERENCE: RTS-0156
; CURRENT APPLICATION NUMBER: US/09/659,791A
; CURRENT FILING DATE: 2000-09-11
; NUMBER OF SEQ ID NOS: 90
; SEQ ID NO 31
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-659-791A-30

Query Match      1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 364 TGATGGCCCTCTGGGAAGAG 383
Db 20 TGATGGCCCTCTGGGAAGAG 1

RESULT 33
US-09-659-791A-30/c
; Sequence 30, Application US/09659791A
; Patent No. 6383808
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Susan M. Freier
; TITLE OF INVENTION: ANTISENSE MODULATION OF CLUSTERIN EXPRESSION
; FILE REFERENCE: RTS-0156
; CURRENT APPLICATION NUMBER: US/09/659,791A
; CURRENT FILING DATE: 2000-09-11
; NUMBER OF SEQ ID NOS: 90
; SEQ ID NO 30
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-659-791A-30

Query Match      1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 380 AGAGTGTAAAGCCCTGCCTGA 399
Db 20 AGAGTGTAAAGCCCTGCCTGA 1

RESULT 34
US-09-659-791A-31/c
; Sequence 31, Application US/09659791A
; Patent No. 6383808
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Susan M. Freier
; TITLE OF INVENTION: ANTISENSE MODULATION OF CLUSTERIN EXPRESSION
; FILE REFERENCE: RTS-0156
; CURRENT APPLICATION NUMBER: US/09/659,791A
; CURRENT FILING DATE: 2000-09-11
; NUMBER OF SEQ ID NOS: 90
; SEQ ID NO 31
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-659-791A-30

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; OTHER INFORMATION: Antisense Oligonucleotide
US-09-659-791A-31

Query Match          1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 407 CTCGATGAAGTTCTACGCAC 426
|||||
Db 20 CTCGATGAAGTTCTACGCAC 1

RESULT 35
US-09-659-791A-32/c
; Sequence 32, Application US/09659791A
; Patent No. 6383808
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Susan M. Freier
; TITLE OF INVENTION: ANTISENSE MODULATION OF CLUSTERIN EXPRESSION
; FILE REFERENCE: RTS-0156
; CURRENT APPLICATION NUMBER: US/09/659,791A
; CURRENT FILING DATE: 2000-09-11
; NUMBER OF SEQ ID NOS: 90
; SEQ ID NO 32
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-659-791A-34

Query Match          1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 455 TGGCGCCAGCTTGAGGAGT 474
|||||
Db 20 TGGCGCCAGCTTGAGGAGT 1

RESULT 38
US-09-659-791A-35/c
; Sequence 35, Application US/09659791A
; Patent No. 6383808
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Susan M. Freier
; TITLE OF INVENTION: ANTISENSE MODULATION OF CLUSTERIN EXPRESSION
; FILE REFERENCE: RTS-0156
; CURRENT APPLICATION NUMBER: US/09/659,791A
; CURRENT FILING DATE: 2000-09-11
; NUMBER OF SEQ ID NOS: 90
; SEQ ID NO 35
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-659-791A-35

Query Match          1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 482 CCAGAGCTCGCCCTTCTACT 501
|||||
Db 20 CCAGAGCTCGCCCTTCTACT 1

RESULT 39
US-09-659-791A-36/c
; Sequence 36, Application US/09659791A
; Patent No. 6383808
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Susan M. Freier
; TITLE OF INVENTION: ANTISENSE MODULATION OF CLUSTERIN EXPRESSION
; FILE REFERENCE: RTS-0156
; CURRENT APPLICATION NUMBER: US/09/659,791A
; CURRENT FILING DATE: 2000-09-11
; NUMBER OF SEQ ID NOS: 90
; SEQ ID NO 36
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-659-791A-33/c
; Sequence 33, Application US/09659791A
; Patent No. 6383808
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Susan M. Freier
; TITLE OF INVENTION: ANTISENSE MODULATION OF CLUSTERIN EXPRESSION
; FILE REFERENCE: RTS-0156
; CURRENT APPLICATION NUMBER: US/09/659,791A
; CURRENT FILING DATE: 2000-09-11
; NUMBER OF SEQ ID NOS: 90
; SEQ ID NO 33
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-659-791A-33

Query Match          1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 443 CTCAGGCTGGTTGCCGCC 462
|||||
Db 20 CTCAGGCTGGTTGCCGCC 1

RESULT 36
US-09-659-791A-33/c
; Sequence 33, Application US/09659791A
; Patent No. 6383808
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Susan M. Freier
; TITLE OF INVENTION: ANTISENSE MODULATION OF CLUSTERIN EXPRESSION
; FILE REFERENCE: RTS-0156
; CURRENT APPLICATION NUMBER: US/09/659,791A
; CURRENT FILING DATE: 2000-09-11
; NUMBER OF SEQ ID NOS: 90
; SEQ ID NO 33
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-659-791A-34/c
; Sequence 34, Application US/09659791A
```

```
US-09-659-791A-36
Query Match          1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 492 CCCTTCTACTCTCGATGAA 511
    |||||
Db 20 CCCTTCTACTCTCGATGAA 1

RESULT 40
US-09-659-791A-37/c
; Sequence 37, Application US/09659791A
; Patent No. 6383808
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Susan M. Freier
; TITLE OF INVENTION: ANTISENSE MODULATION OF CLUSTERIN EXPRESSION
; FILE REFERENCE: RTS-0156
; CURRENT APPLICATION NUMBER: US/09/659,791A
; CURRENT FILING DATE: 2000-09-11
; NUMBER OF SEQ ID NOS: 90
; SEQ ID NO 37
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-659-791A-37

Query Match          1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 517 ACCGATCGACTCCCTGCTG 536
    |||||
Db 20 ACCGATCGACTCCCTGCTG 1

RESULT 41
US-09-659-791A-38/c
; Sequence 38, Application US/09659791A
; Patent No. 6383808
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Susan M. Freier
; TITLE OF INVENTION: ANTISENSE MODULATION OF CLUSTERIN EXPRESSION
; FILE REFERENCE: RTS-0156
; CURRENT APPLICATION NUMBER: US/09/659,791A
; CURRENT FILING DATE: 2000-09-11
; NUMBER OF SEQ ID NOS: 90
; SEQ ID NO 38
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-659-791A-38

Query Match          1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 533 GCTGGAGAACGACCGGAGC 552
    |||||
Db 20 GCTGGAGAACGACCGGAGC 1

RESULT 42
US-09-659-791A-39/c
; Sequence 39, Application US/09659791A
; Patent No. 6383808
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Susan M. Freier
; TITLE OF INVENTION: ANTISENSE MODULATION OF CLUSTERIN EXPRESSION
; FILE REFERENCE: RTS-0156
; CURRENT APPLICATION NUMBER: US/09/659,791A
; CURRENT FILING DATE: 2000-09-11
; NUMBER OF SEQ ID NOS: 90
; SEQ ID NO 39
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-659-791A-39

Query Match          1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 553 AGACGCACATGCTGGATGC 572
    |||||
Db 20 AGACGCACATGCTGGATGC 1

RESULT 43
US-09-659-791A-40/c
; Sequence 40, Application US/09659791A
; Patent No. 6383808
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Susan M. Freier
; TITLE OF INVENTION: ANTISENSE MODULATION OF CLUSTERIN EXPRESSION
; FILE REFERENCE: RTS-0156
; CURRENT APPLICATION NUMBER: US/09/659,791A
; CURRENT FILING DATE: 2000-09-11
; NUMBER OF SEQ ID NOS: 90
; SEQ ID NO 40
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-659-791A-40

Query Match          1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 553 AGACGCACATGCTGGATGC 572
    |||||
Db 20 AGACGCACATGCTGGATGC 1

RESULT 44
US-09-659-791A-41/c
; Sequence 41, Application US/09659791A
; Patent No. 6383808
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Susan M. Freier
; TITLE OF INVENTION: ANTISENSE MODULATION OF CLUSTERIN EXPRESSION
; FILE REFERENCE: RTS-0156
; CURRENT APPLICATION NUMBER: US/09/659,791A
; CURRENT FILING DATE: 2000-09-11
; NUMBER OF SEQ ID NOS: 90
; SEQ ID NO 41
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-659-791A-41
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Query Match 1.2%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 12;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 565 TGGATGTCATGACGAGCAC 584  
|||||  
Db 20 TGGATGTCATGACGAGCAC 1

RESULT 45  
US-09-659-791A-42/c  
; Sequence 42, Application US/09659791A  
; Patent No. 6383808  
; GENERAL INFORMATION:  
; APPLICANT: Brett P. Monia  
; TITLE OF INVENTION: ANTISENSE MODULATION OF CLUSTERIN EXPRESSION  
; FILE REFERENCE: RTS-0156  
; CURRENT APPLICATION NUMBER: US/09/659,791A  
; CURRENT FILING DATE: 2000-09-11  
; NUMBER OF SEQ ID NOS: 90  
; SEQ ID NO 42  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Antisense Oligonucleotide  
US-09-659-791A-42

Query Match 1.2%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 12;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 567 GATGTCATGACGAGCACCTT 586  
|||||  
Db 20 GATGTCATGACGAGCACCTT 1

RESULT 46  
US-09-659-791A-43/c  
; Sequence 43, Application US/09659791A  
; Patent No. 6383808  
; GENERAL INFORMATION:  
; APPLICANT: Brett P. Monia  
; TITLE OF INVENTION: ANTISENSE MODULATION OF CLUSTERIN EXPRESSION  
; FILE REFERENCE: RTS-0156  
; CURRENT APPLICATION NUMBER: US/09/659,791A  
; CURRENT FILING DATE: 2000-09-11  
; NUMBER OF SEQ ID NOS: 90  
; SEQ ID NO 43  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Antisense Oligonucleotide  
US-09-659-791A-43

Query Match 1.2%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 12;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 604 TCATAGACGAGCTCTCCAG 623  
|||||  
Db 20 TCATAGACGAGCTCTCCAG 1

RESULT 47  
US-09-659-791A-44/c  
; Sequence 44, Application US/09659791A  
; Patent No. 6383808  
; GENERAL INFORMATION:

; APPLICANT: Brett P. Monia  
; APPLICANT: Susan M. Freier  
; TITLE OF INVENTION: ANTISENSE MODULATION OF CLUSTERIN EXPRESSION  
; FILE REFERENCE: RTS-0156  
; CURRENT APPLICATION NUMBER: US/09/659,791A  
; CURRENT FILING DATE: 2000-09-11  
; NUMBER OF SEQ ID NOS: 90  
; SEQ ID NO 44  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Antisense Oligonucleotide  
US-09-659-791A-44

Query Match 1.2%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 12;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 608 AGACGAGCTCTCCAGGACA 627  
|||||  
Db 20 AGACGAGCTCTCCAGGACA 1

RESULT 48  
US-09-659-791A-45/c  
; Sequence 45, Application US/09659791A  
; Patent No. 6383808  
; GENERAL INFORMATION:  
; APPLICANT: Brett P. Monia  
; APPLICANT: Susan M. Freier  
; TITLE OF INVENTION: ANTISENSE MODULATION OF CLUSTERIN EXPRESSION  
; FILE REFERENCE: RTS-0156  
; CURRENT APPLICATION NUMBER: US/09/659,791A  
; CURRENT FILING DATE: 2000-09-11  
; NUMBER OF SEQ ID NOS: 90  
; SEQ ID NO 45  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Antisense Oligonucleotide  
US-09-659-791A-45

Query Match 1.2%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 12;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 613 AGCTCTCCAGGACAGGTTTC 632  
|||||  
Db 20 AGCTCTCCAGGACAGGTTTC 1

RESULT 49  
US-09-659-791A-46/c  
; Sequence 46, Application US/09659791A  
; Patent No. 6383808  
; GENERAL INFORMATION:  
; APPLICANT: Brett P. Monia  
; APPLICANT: Susan M. Freier  
; TITLE OF INVENTION: ANTISENSE MODULATION OF CLUSTERIN EXPRESSION  
; FILE REFERENCE: RTS-0156  
; CURRENT APPLICATION NUMBER: US/09/659,791A  
; CURRENT FILING DATE: 2000-09-11  
; NUMBER OF SEQ ID NOS: 90  
; SEQ ID NO 46  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Antisense Oligonucleotide  
US-09-659-791A-46

```
Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 690 AGGCTCACTTCTCTTCC 709
| | | | | | | | | | | | | | | | | |
Db 20 AGGCTCACTTCTCTTCC 1

RESULT 50
US-09-659-791A-47/c
; Sequence 47, Application US/09659791A
; Patent No. 6383808
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; TITLE OF INVENTION: ANTISENSE MODULATION OF CLUSTERIN EXPRESSION
; FILE REFERENCE: RTS-0156
; CURRENT APPLICATION NUMBER: US/09/659,791A
; CURRENT FILING DATE: 2000-09-11
; NUMBER OF SEQ ID NOS: 90
; SEQ ID NO 47
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-659-791A-49
Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 776 GTTCCAGCCCTTCCTTGAGA 795
| | | | | | | | | | | | | | | | | |
Db 20 GTTCCAGCCCTTCCTTGAGA 1

RESULT 53
US-09-659-791A-50/c
; Sequence 50, Application US/09659791A
; Patent No. 6383808
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; TITLE OF INVENTION: ANTISENSE MODULATION OF CLUSTERIN EXPRESSION
; FILE REFERENCE: RTS-0156
; CURRENT APPLICATION NUMBER: US/09/659,791A
; CURRENT FILING DATE: 2000-09-11
; NUMBER OF SEQ ID NOS: 90
; SEQ ID NO 50
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-659-791A-50
Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 783 CCCTTCCTTCAGATGATACA 802
| | | | | | | | | | | | | | | | | |
Db 20 CCCTTCCTTCAGATGATACA 1

RESULT 54
US-09-659-791A-51/c
; Sequence 51, Application US/09659791A
; Patent No. 6383808
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; TITLE OF INVENTION: ANTISENSE MODULATION OF CLUSTERIN EXPRESSION
; FILE REFERENCE: RTS-0156
; CURRENT APPLICATION NUMBER: US/09/659,791A
; CURRENT FILING DATE: 2000-09-11
; NUMBER OF SEQ ID NOS: 90
; SEQ ID NO 51
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-659-791A-51
Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 775 TGTTCAGCCCTTCCTTGAG 794
| | | | | | | | | | | | | | | | | |
Db 20 TGTTCAGCCCTTCCTTGAG 1

RESULT 52
US-09-659-791A-49/c
; Sequence 49, Application US/09659791A
; Patent No. 6383808
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
```

Best Local Similarity 100.0%; Pred. No. 12; Mismatches 0; Indels 0; Gaps 0;

Qy 820 TGGACATCCACTTCCACAGC 839  
Db 20 TGGACATCCACTTCCACAGC 1

## RESULT 55

US-09-659-791A-52/c  
; Sequence 52, Application US/09659791A  
; Patent No. 6383808

; GENERAL INFORMATION:

; APPLICANT: Brett P. Monia

; APPLICANT: Susan M. Freier

; TITLE OF INVENTION: ANTISENSE MODULATION OF CLUSTERIN EXPRESSION

; FILE REFERENCE: RTS-0156

; CURRENT APPLICATION NUMBER: US/09/659,791A

; CURRENT FILING DATE: 2000-09-11

; NUMBER OF SEQ ID NOS: 90

; SEQ ID NO 52

; LENGTH: 20

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Antisense Oligonucleotide

US-09-659-791A-52

Query Match 1.2%; Score 20; DB 1; Length 20;

Best Local Similarity 100.0%; Pred. No. 12;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 848 CCAGCACCCGCCAACAAGAT 867  
Db 20 CCAGCACCCGCCAACAAGAT 1

## RESULT 56

US-09-659-791A-53/c  
; Sequence 53, Application US/09659791A  
; Patent No. 6383808

; GENERAL INFORMATION:

; APPLICANT: Brett P. Monia

; APPLICANT: Susan M. Freier

; TITLE OF INVENTION: ANTISENSE MODULATION OF CLUSTERIN EXPRESSION

; FILE REFERENCE: RTS-0156

; CURRENT APPLICATION NUMBER: US/09/659,791A

; CURRENT FILING DATE: 2000-09-11

; NUMBER OF SEQ ID NOS: 90

; SEQ ID NO 53

; LENGTH: 20

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Antisense Oligonucleotide

US-09-659-791A-53

Query Match 1.2%; Score 20; DB 1; Length 20;

Best Local Similarity 100.0%; Pred. No. 12;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 853 ACCCGCCCAACAAGATTCATA 872  
Db 20 ACCCGCCCAACAAGATTCATA 1

## RESULT 57

US-09-659-791A-54/c  
; Sequence 54, Application US/09659791A  
; Patent No. 6383808

; GENERAL INFORMATION:

; APPLICANT: Brett P. Monia

; APPLICANT: Susan M. Freier

; TITLE OF INVENTION: ANTISENSE MODULATION OF CLUSTERIN EXPRESSION

; FILE REFERENCE: RTS-0156

; CURRENT APPLICATION NUMBER: US/09/659,791A

; CURRENT FILING DATE: 2000-09-11

; NUMBER OF SEQ ID NOS: 90

; SEQ ID NO 54

; LENGTH: 20

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Antisense Oligonucleotide

US-09-659-791A-54

Query Match 1.2%; Score 20; DB 1; Length 20;

Best Local Similarity 100.0%; Pred. No. 12;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 893 GACTGTGTGCCGGAGATCC 912  
Db 20 GACTGTGTGCCGGAGATCC 1

## RESULT 58

US-09-659-791A-55/c

; Sequence 55, Application US/09659791A

; Patent No. 6383808

; GENERAL INFORMATION:

; APPLICANT: Brett P. Monia

; APPLICANT: Susan M. Freier

; TITLE OF INVENTION: ANTISENSE MODULATION OF CLUSTERIN EXPRESSION

; FILE REFERENCE: RTS-0156

; CURRENT APPLICATION NUMBER: US/09/659,791A

; CURRENT FILING DATE: 2000-09-11

; NUMBER OF SEQ ID NOS: 90

; SEQ ID NO 55

; LENGTH: 20

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Antisense Oligonucleotide

US-09-659-791A-55

Query Match 1.2%; Score 20; DB 1; Length 20;

Best Local Similarity 100.0%; Pred. No. 12;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 894 ACTGTGTGCCGGAGATCCG 913  
Db 20 ACTGTGTGCCGGAGATCCG 1

## RESULT 59

US-09-659-791A-56/c

; Sequence 56, Application US/09659791A

; Patent No. 6383808

; GENERAL INFORMATION:

; APPLICANT: Brett P. Monia

; APPLICANT: Susan M. Freier

; TITLE OF INVENTION: ANTISENSE MODULATION OF CLUSTERIN EXPRESSION

; FILE REFERENCE: RTS-0156

; CURRENT APPLICATION NUMBER: US/09/659,791A

; CURRENT FILING DATE: 2000-09-11

; NUMBER OF SEQ ID NOS: 90

; SEQ ID NO 56

; LENGTH: 20

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Antisense Oligonucleotide

US-09-659-791A-56

Query Match 1.2%; Score 20; DB 1; Length 20;

Best Local Similarity 100.0%; Pred. No. 12;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 906 GAGATCCGCCACACTCCAC 925  
|||||  
Db 20 GAGATCCGCCACACTCCAC 1

## RESULT 60

US-09-659-791A-57/c  
; Sequence 57, Application US/09659791A  
; Patent No. 6383808  
; GENERAL INFORMATION:  
; APPLICANT: Susan M. Freier  
; TITLE OF INVENTION: ANTISENSE MODULATION OF CLUSTERIN EXPRESSION  
; FILE REFERENCE: RTS-0156  
; CURRENT APPLICATION NUMBER: US/09/659,791A  
; CURRENT FILING DATE: 2000-09-11  
; NUMBER OF SEQ ID NOS: 90  
; SEQ ID NO 57  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Antisense Oligonucleotide  
US-09-659-791A-57

Query Match 1.2%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 12;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 928 GCTGCTCGGATGAAGGAC 947  
|||||  
Db 20 GCTGCTCGGATGAAGGAC 1

## RESULT 61

US-09-659-791A-58/c  
; Sequence 58, Application US/09659791A  
; Patent No. 6383808  
; GENERAL INFORMATION:  
; APPLICANT: Susan M. Freier  
; TITLE OF INVENTION: ANTISENSE MODULATION OF CLUSTERIN EXPRESSION  
; FILE REFERENCE: RTS-0156  
; CURRENT APPLICATION NUMBER: US/09/659,791A  
; CURRENT FILING DATE: 2000-09-11  
; NUMBER OF SEQ ID NOS: 90  
; SEQ ID NO 58  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Antisense Oligonucleotide  
US-09-659-791A-58

Query Match 1.2%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 12;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 967 AGATCTTGCTGGGACTGT 986  
|||||  
Db 20 AGATCTTGCTGGGACTGT 1

## RESULT 62

US-09-659-791A-59/c  
; Sequence 59, Application US/09659791A  
; Patent No. 6383808  
; GENERAL INFORMATION:  
; APPLICANT: Susan M. Freier  
; TITLE OF INVENTION: ANTISENSE MODULATION OF CLUSTERIN EXPRESSION

; FILE REFERENCE: RTS-0156  
; CURRENT APPLICATION NUMBER: US/09/659,791A  
; CURRENT FILING DATE: 2000-09-11  
; NUMBER OF SEQ ID NOS: 90  
; SEQ ID NO 59  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Antisense Oligonucleotide  
US-09-659-791A-59

Query Match 1.2%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 12;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1009 CTAAGCTCGGGGAGCTC 1028  
|||||  
Db 20 CTAAGCTCGGGGAGCTC 1

## RESULT 63

US-09-659-791A-60/c  
; Sequence 60, Application US/09659791A  
; Patent No. 6383808  
; GENERAL INFORMATION:  
; APPLICANT: Brett P. Monia  
; APPLICANT: Susan M. Freier  
; TITLE OF INVENTION: ANTISENSE MODULATION OF CLUSTERIN EXPRESSION  
; FILE REFERENCE: RTS-0156  
; CURRENT APPLICATION NUMBER: US/09/659,791A  
; CURRENT FILING DATE: 2000-09-11  
; NUMBER OF SEQ ID NOS: 90  
; SEQ ID NO 60  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Antisense Oligonucleotide  
US-09-659-791A-60

Query Match 1.2%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 12;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1022 GGAGCTCGACGAATCCCTCC 1041  
|||||  
Db 20 GGAGCTCGACGAATCCCTCC 1

## RESULT 64

US-09-659-791A-61/c  
; Sequence 61, Application US/09659791A  
; Patent No. 6383808  
; GENERAL INFORMATION:  
; APPLICANT: Brett P. Monia  
; APPLICANT: Susan M. Freier  
; TITLE OF INVENTION: ANTISENSE MODULATION OF CLUSTERIN EXPRESSION  
; FILE REFERENCE: RTS-0156  
; CURRENT APPLICATION NUMBER: US/09/659,791A  
; CURRENT FILING DATE: 2000-09-11  
; NUMBER OF SEQ ID NOS: 90  
; SEQ ID NO 61  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Antisense Oligonucleotide  
US-09-659-791A-61

Query Match 1.2%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 12;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1083 AAGTCTACAGTGGAGAT 1102  
|||||  
Db 20 AAGTCTACAGTGGAGAT 1

RESULT 65  
US-09-659-791A-62/c  
; Sequence 62, Application US/09659791A  
; Patent No. 6383808  
; GENERAL INFORMATION:  
; APPLICANT: Brett P. Monia  
; APPLICANT: Susan M. Freier  
; TITLE OF INVENTION: ANTISENSE MODULATION OF CLUSTERIN EXPRESSION  
; FILE REFERENCE: RTS-0156  
; CURRENT APPLICATION NUMBER: US/09/659,791A  
; CURRENT FILING DATE: 2000-09-11  
; NUMBER OF SEQ ID NOS: 90  
; SEQ ID NO 62  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Antisense Oligonucleotide  
US-09-659-791A-62

Query Match 1.2%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 12;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1091 CCAGTGGAGATGCTCAACA 1110  
|||||  
Db 20 CCAGTGGAGATGCTCAACA 1

RESULT 66  
US-09-659-791A-63/c  
; Sequence 63, Application US/09659791A  
; Patent No. 6383808  
; GENERAL INFORMATION:  
; APPLICANT: Brett P. Monia  
; APPLICANT: Susan M. Freier  
; TITLE OF INVENTION: ANTISENSE MODULATION OF CLUSTERIN EXPRESSION  
; FILE REFERENCE: RTS-0156  
; CURRENT APPLICATION NUMBER: US/09/659,791A  
; CURRENT FILING DATE: 2000-09-11  
; NUMBER OF SEQ ID NOS: 90  
; SEQ ID NO 63  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Antisense Oligonucleotide  
US-09-659-791A-63

Query Match 1.2%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 12;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1113 TCCTCTTGTGCTGAGCAGCT 1132  
|||||  
Db 20 TCCTCTTGTGCTGAGCAGCT 1

RESULT 67  
US-09-659-791A-64/c  
; Sequence 64, Application US/09659791A  
; Patent No. 6383808  
; GENERAL INFORMATION:  
; APPLICANT: Brett P. Monia  
; APPLICANT: Susan M. Freier  
; TITLE OF INVENTION: ANTISENSE MODULATION OF CLUSTERIN EXPRESSION  
; FILE REFERENCE: RTS-0156

; CURRENT APPLICATION NUMBER: US/09/659,791A  
; CURRENT FILING DATE: 2000-09-11  
; NUMBER OF SEQ ID NOS: 90  
; SEQ ID NO 64  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Antisense Oligonucleotide  
US-09-659-791A-64

Query Match 1.2%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 12;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1121 GCTGGAGCAGCTGAACGAGC 1140  
|||||  
Db 20 GCTGGAGCAGCTGAACGAGC 1

RESULT 68  
US-09-659-791A-65/c  
; Sequence 65, Application US/09659791A  
; Patent No. 6383808  
; GENERAL INFORMATION:  
; APPLICANT: Brett P. Monia  
; APPLICANT: Susan M. Freier  
; TITLE OF INVENTION: ANTISENSE MODULATION OF CLUSTERIN EXPRESSION  
; FILE REFERENCE: RTS-0156  
; CURRENT APPLICATION NUMBER: US/09/659,791A  
; CURRENT FILING DATE: 2000-09-11  
; NUMBER OF SEQ ID NOS: 90  
; SEQ ID NO 65  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Antisense Oligonucleotide  
US-09-659-791A-65

Query Match 1.2%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 12;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1148 CTGGGTGTCCCGCTGGCAA 1167  
|||||  
Db 20 CTGGGTGTCCCGCTGGCAA 1

RESULT 69  
US-09-659-791A-66/c  
; Sequence 66, Application US/09659791A  
; Patent No. 6383808  
; GENERAL INFORMATION:  
; APPLICANT: Brett P. Monia  
; APPLICANT: Susan M. Freier  
; TITLE OF INVENTION: ANTISENSE MODULATION OF CLUSTERIN EXPRESSION  
; FILE REFERENCE: RTS-0156  
; CURRENT APPLICATION NUMBER: US/09/659,791A  
; CURRENT FILING DATE: 2000-09-11  
; NUMBER OF SEQ ID NOS: 90  
; SEQ ID NO 66  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Antisense Oligonucleotide  
US-09-659-791A-66

Query Match 1.2%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 12;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1182 GAAGACCACTACTATCTGCG 1201  
|||||  
Db 20 GAAGACCACTACTATCTGCG 1

## RESULT 70

US-09-659-791A-67/c  
; Sequence 67, Application US/09659791A  
; Patent No. 6383808  
; GENERAL INFORMATION:  
; APPLICANT: Brett P. Monia  
; TITLE OF INVENTION: ANTISENSE MODULATION OF CLUSTERIN EXPRESSION  
; FILE REFERENCE: RTS-0156  
; CURRENT APPLICATION NUMBER: US/09/659,791A  
; CURRENT FILING DATE: 2000-09-11  
; NUMBER OF SEQ ID NOS: 90  
; SEQ ID NO 67  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Antisense Oligonucleotide  
US-09-659-791A-67

Query Match 1.2%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 12;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1194 TATCTGCGGTCACACCGT 1213  
|||||  
Db 20 TATCTGCGGTCACACCGT 1

## RESULT 71

US-09-659-791A-68/c  
; Sequence 68, Application US/09659791A  
; Patent No. 6383808  
; GENERAL INFORMATION:  
; APPLICANT: Brett P. Monia  
; TITLE OF INVENTION: ANTISENSE MODULATION OF CLUSTERIN EXPRESSION  
; FILE REFERENCE: RTS-0156  
; CURRENT APPLICATION NUMBER: US/09/659,791A  
; CURRENT FILING DATE: 2000-09-11  
; NUMBER OF SEQ ID NOS: 90  
; SEQ ID NO 68  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Antisense Oligonucleotide  
US-09-659-791A-68

Query Match 1.2%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 12;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1216 CTTCACACACTTCTGACTCG 1235  
|||||  
Db 20 CTTCACACACTTCTGACTCG 1

## RESULT 72

US-09-659-791A-69/c  
; Sequence 69, Application US/09659791A  
; Patent No. 6383808  
; GENERAL INFORMATION:  
; APPLICANT: Brett P. Monia  
; TITLE OF INVENTION: ANTISENSE MODULATION OF CLUSTERIN EXPRESSION  
; FILE REFERENCE: RTS-0156  
; CURRENT APPLICATION NUMBER: US/09/659,791A

; CURRENT FILING DATE: 2000-09-11  
; NUMBER OF SEQ ID NOS: 90  
; SEQ ID NO 69  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Antisense Oligonucleotide  
US-09-659-791A-69

Query Match 1.2%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 12;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1275 TTGACTCTGATCCCATCAC 1294  
|||||  
Db 20 TTGACTCTGATCCCATCAC 1

## RESULT 73

US-09-659-791A-70/c  
; Sequence 70, Application US/09659791A  
; Patent No. 6383808  
; GENERAL INFORMATION:  
; APPLICANT: Brett P. Monia  
; APPLICANT: Susan M. Freier  
; TITLE OF INVENTION: ANTISENSE MODULATION OF CLUSTERIN EXPRESSION  
; FILE REFERENCE: RTS-0156  
; CURRENT APPLICATION NUMBER: US/09/659,791A  
; CURRENT FILING DATE: 2000-09-11  
; NUMBER OF SEQ ID NOS: 90  
; SEQ ID NO 70  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Antisense Oligonucleotide  
US-09-659-791A-70

Query Match 1.2%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 12;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1300 CGGTCCCTGTAGAGTCTCC 1319  
|||||  
Db 20 CGGTCCCTGTAGAGTCTCC 1

## RESULT 74

US-09-659-791A-71/c  
; Sequence 71, Application US/09659791A  
; Patent No. 6383808  
; GENERAL INFORMATION:  
; APPLICANT: Brett P. Monia  
; APPLICANT: Susan M. Freier  
; TITLE OF INVENTION: ANTISENSE MODULATION OF CLUSTERIN EXPRESSION  
; FILE REFERENCE: RTS-0156  
; CURRENT APPLICATION NUMBER: US/09/659,791A  
; CURRENT FILING DATE: 2000-09-11  
; NUMBER OF SEQ ID NOS: 90  
; SEQ ID NO 71  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Antisense Oligonucleotide  
US-09-659-791A-71

Query Match 1.2%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 12;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1332 AAATTTATGGAGACCGTGGC 1351

```
Db      20 AATTTATGGAGACCGTGC 1
|||||
RESULT 75
US-09-659-791A-72/c
; Sequence 72, Application US/09659791A
; Patent No. 6383808
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Susan M. Freier
; TITLE OF INVENTION: ANTISENSE MODULATION OF CLUSTERIN EXPRESSION
; FILE REFERENCE: RTS-0156
; CURRENT APPLICATION NUMBER: US/09/659,791A
; CURRENT FILING DATE: 2000-09-11
; NUMBER OF SEQ ID NOS: 90
; SEQ ID NO 72
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-659-791A-72
Query Match      1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1398 GATGTGGATGTCCTTTGC 1417
|||||
Db      20 GATGTGGATGTCCTTTGC 1

RESULT 76
US-09-659-791A-73/c
; Sequence 73, Application US/09659791A
; Patent No. 6383808
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Susan M. Freier
; TITLE OF INVENTION: ANTISENSE MODULATION OF CLUSTERIN EXPRESSION
; FILE REFERENCE: RTS-0156
; CURRENT APPLICATION NUMBER: US/09/659,791A
; CURRENT FILING DATE: 2000-09-11
; NUMBER OF SEQ ID NOS: 90
; SEQ ID NO 73
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-659-791A-73
Query Match      1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1545 GCTCTGGATCCGCACTCTA 1564
|||||
Db      20 GCTCTGGATCCGCACTCTA 1

RESULT 77
US-09-659-791A-74/c
; Sequence 74, Application US/09659791A
; Patent No. 6383808
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Susan M. Freier
; TITLE OF INVENTION: ANTISENSE MODULATION OF CLUSTERIN EXPRESSION
; FILE REFERENCE: RTS-0156
; CURRENT APPLICATION NUMBER: US/09/659,791A
; CURRENT FILING DATE: 2000-09-11
; NUMBER OF SEQ ID NOS: 90
; SEQ ID NO 74
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-659-791A-74
Query Match      1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1600 TGCTCTGCGATGCAACTAAT 1619
|||||
Db      20 TGCTCTGCGATGCAACTAAT 1

RESULT 78
US-09-659-791A-75/c
; Sequence 75, Application US/09659791A
; Patent No. 6383808
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Susan M. Freier
; TITLE OF INVENTION: ANTISENSE MODULATION OF CLUSTERIN EXPRESSION
; FILE REFERENCE: RTS-0156
; CURRENT APPLICATION NUMBER: US/09/659,791A
; CURRENT FILING DATE: 2000-09-11
; NUMBER OF SEQ ID NOS: 90
; SEQ ID NO 75
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-659-791A-75
Query Match      1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1615 CTAATTCATAAAACTGTCT 1634
|||||
Db      20 CTAATTCATAAAACTGTCT 1

RESULT 79
US-09-659-791A-78/c
; Sequence 78, Application US/09659791A
; Patent No. 6383808
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Susan M. Freier
; TITLE OF INVENTION: ANTISENSE MODULATION OF CLUSTERIN EXPRESSION
; FILE REFERENCE: RTS-0156
; CURRENT APPLICATION NUMBER: US/09/659,791A
; CURRENT FILING DATE: 2000-09-11
; NUMBER OF SEQ ID NOS: 90
; SEQ ID NO 78
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-659-791A-78
Query Match      1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      979 TGGACTGTTCCACCAAC 998
|||||
```

Db 20 TGGACTGTTCCACCAAC 1

RESULT 80

US-09-659-791A-80/c

Sequence 80, Application US/09659791A

Patent No. 6383808

GENERAL INFORMATION:

APPLICANT: Brett P. Monia

APPLICANT: Susan M. Preler

TITLE OF INVENTION: ANTISENSE MODULATION OF CLUSTERIN EXPRESSION

FILE REFERENCE: RTS-0156

CURRENT APPLICATION NUMBER: US/09/659,791A

CURRENT FILING DATE: 2000-09-11

NUMBER OF SEQ ID NOS: 90

SEQ ID NO 80

LENGTH: 20

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Antisense Oligonucleotide

US-09-659-791A-80

Query Match 1.2%; Score 20; DB 1; Length 20;

Best Local Similarity 100.0%; Pred. No. 12;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1383 CACCGGAGGAGTGATGT 1402

|||||

Db 20 CACCGGAGGAGTGATGT 1

RESULT 81

US-09-459-749D-13

Sequence 13, Application US/09459749D

Patent No. 6464975

GENERAL INFORMATION:

APPLICANT: Millis, Albert J. T.

TITLE OF INVENTION: Compositions and Methods For Altering Cell Migration

FILE REFERENCE: 0794, 016A

CURRENT APPLICATION NUMBER: US/09/459,749D

CURRENT FILING DATE: 1999-12-10

PRIOR APPLICATION NUMBER: 60/111,856

PRIOR FILING DATE: 1998-12-11

NUMBER OF SEQ ID NOS: 17

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 13

LENGTH: 21

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Description of Artificial Sequence: primer bind

OTHER INFORMATION: synthetic antisense primer based on murine clusterin

US-09-459-749D-13

Query Match 1.2%; Score 19.4; DB 1; Length 21;

Best Local Similarity 95.2%; Pred. No. 17;

Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 271 AAGAGCCAGAGAGAGAG 291

|||||

Db 1 AGGAGCCAGAGAGAGAG 21

RESULT 82

US-08-855-449-10

Sequence 10, Application US/08855449

Patent No. 5910412

GENERAL INFORMATION:

APPLICANT: AKAMATSU, TOYOKAZU

APPLICANT: SUZUKI, TAKAO

TITLE OF INVENTION: METHOD FOR IDENTIFYING THE SEX OF

TITLE OF INVENTION: SPINACH BY DNA MARKERS

US-08-855-449-10

Query Match 1.1%; Score 18.8; DB 1; Length 22;

Best Local Similarity 90.9%; Pred. No. 23;

Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 865 AATTTCATACGAGAGCGACGA 886

|||||

Db 1 AATTTCATACGAGAGCGACGA 22

RESULT 83

US-08-410-540-22/c

Sequence 22, Application US/08410540

Patent No. 5807678

GENERAL INFORMATION:

APPLICANT: Miller, Walter L.

APPLICANT: Lin, Dong

APPLICANT: Strauss III, Jerome F.

TITLE OF INVENTION: IDENTIFICATION OF GENE MUTATIONS

TITLE OF INVENTION: ASSOCIATED WITH CONGENITAL LIPOID ADRENAL HYPERPLASIA

NUMBER OF SEQUENCES: 30

CORRESPONDENCE ADDRESS:

ADDRESSEE: Cooley Godward Castro Huddleson & Tatum

STREET: 5 Palo Alto Square

CITY: Palo Alto

STATE: CA

COUNTRY: US

ZIP: 94306-2155

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/410,540

FILING DATE: 23-MAR-1995



```

; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Neeley, Richard L.
; REGISTRATION NUMBER: 30,092
; REFERENCE/DOCKET NUMBER: UCAL-238/00US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415 853 5070
; TELEFAX: 415 857 0663
; TELEX: 380816COOLEYPA
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (synthetic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; US-08-410-540-22

Query Match 1.1%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1475 GAGAGCTGTGCACGTAC 1492
DB 18 GAGAGCTGTGCACGTAC 1

RESULT 84
US-09-659-791A-4
; Sequence 4, Application US/09659791A
; Patent No. 6383808
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Susan M. Freier
; TITLE OF INVENTION: ANTISENSE MODULATION OF CLUSTERIN EXPRESSION
; FILE REFERENCE: RTS-0156
; CURRENT APPLICATION NUMBER: US/09/659,791A
; CURRENT FILING DATE: 2000-09-11
; NUMBER OF SEQ ID NOS: 90
; SEQ ID NO 4
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: PCR Primer
; US-09-659-791A-4

Query Match 1.1%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 746 TCCGTACGAGCCCTGAA 763
DB 1 TCCGTACGAGCCCTGAA 18

RESULT 85
US-08-397-220B-43/c
; Sequence 43, Application US/08397220B
; Patent No. 6284458
; GENERAL INFORMATION:
; APPLICANT: Anderson et al.
; TITLE OF INVENTION: Compositions And Methods For Treatment Of Hepatitis C Virus-Associated Diseases
; NUMBER OF SEQUENCES: 98
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Jane Massey Licata, Esq.
; STREET: 210 Lake Drive East, Suite 201
; CITY: Cherry Hill
; STATE: NJ
; COUNTRY: USA
```

```

; ZIP: 08002
; COMPUTER READABLE FORM:
; MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
; COMPUTER: IBM 486
; OPERATING SYSTEM: WINDOWS FOR WORKGROUPS
; SOFTWARE: WORDPERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/397,220B
; FILING DATE: 09-Mar-1995
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/JP93/01293
; FILING DATE: 10-Sep-93
; APPLICATION NUMBER: JP 5-87195
; FILING DATE: 14-Apr-93
; APPLICATION NUMBER: 07/945,289
; FILING DATE: 10-Sep-92
; ATTORNEY/AGENT INFORMATION:
; NAME: Jane Massey Licata
; REGISTRATION NUMBER: 32,257
; REFERENCE/DOCKET NUMBER: ISPH-0031
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (609) 779-2400
; TELEFAX: (609) 779-8488
; INFORMATION FOR SEQ ID NO: 43:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20
; TYPE: nucleic acid
; STRANDEDNESS: Single
; TOPOLOGY: Linear
; ANTI-SENSE: Yes
; SEQUENCE DESCRIPTION: SEQ ID NO: 43:
US-08-397-220B-43

Query Match 1.0%; Score 16.8; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 39;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1510 GCCTCCAGGCCCAACTCC 1529
DB 20 GCCTCCAGGCCCAACTCC 1

RESULT 86
US-08-650-093C-43/c
; Sequence 43, Application US/08650093C
; Patent No. 6391542
; GENERAL INFORMATION:
; APPLICANT: Kevin P. Anderson et al.
; TITLE OF INVENTION: Compositions And Methods For Treatment Of Hepatitis C Virus-Associated Diseases
; NUMBER OF SEQUENCES: 118
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LICATA & TYRRELL P.C.
; STREET: 66 E. Main Street
; CITY: Marlton
; STATE: NJ
; COUNTRY: USA
; ZIP: 08053
; COMPUTER READABLE FORM:
; MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: WORDPERFECT 6.1 for Windows
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/650,093C
; FILING DATE: 17-May-1996
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/452,841
; FILING DATE: May 30, 1995
; APPLICATION NUMBER: 08/397,220
; FILING DATE: March 9, 1995
```

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CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
ZIP: 10016
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/256,568B
FILING DATE: 18-JUL-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/EP93/03325
FILING DATE: 26-NOV-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP/93/402,129.6
FILING DATE: 31-AUG-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP/92/403,222.0
FILING DATE: 27-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: CHARLES A. MUSERLIAN
REGISTRATION NUMBER: 19,683
REFERENCE/DOCKET NUMBER: 410.004
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 661-8000
TELEFAX: (212) 661-8002
INFORMATION FOR SEQ ID NO: 97:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: YES
US-08-256-568B-97
Query Match 1.0%; Score 16; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1508 CAGCCTCCAGGCCCCC 1523
DB 16 CAGCCTCCAGGCCCCC 1

RESULT 89
US-09-038-369B-97/c
Sequence 97, Application US/09038369B
Patent No. 6171784
GENERAL INFORMATION:
APPLICANT: MAERTENS, GEERT; STUYVER, LIEVEN;
APPLICANT: ROSSAU, RUDI; VAN HEUVERSWYN, HUGO
TITLE OF INVENTION: PROCESS FOR TYPING OF HCV
TITLE OF INVENTION: ISOLATES
NUMBER OF SEQUENCES: 97
CORRESPONDENCE ADDRESS:
ADDRESSEE: BIERMAN & MUSERLIAN
STREET: 600 THIRD AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
ZIP: 10016
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/038,369B

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;  
; FILING DATE: 31-AUG-1993  
; CLASSIFICATION: 1.0%; Score 16; DB 1; Length 16;  
; PRIOR APPLICATION DATA: Best Local Similarity 100.0%; Pred. No. 32;  
; APPLICATION NUMBER: EP/92/403,222.0 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
; FILING DATE: 27-NOV-1992  
; ATTORNEY/AGENT INFORMATION: 0;  
; NAME: CHARLES A. MUSERLIAN  
; REGISTRATION NUMBER: 19,683  
; REFERENCE/DOCKET NUMBER: 410.004  
; TELECOMMUNICATION INFORMATION: 0;  
; TELEPHONE: (212) 661-8000  
; TELEFAX: (212) 661-8002  
; INFORMATION FOR SEQ ID NO: 97:  
; SEQUENCE CHARACTERISTICS: 0;  
; LENGTH: 16 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cdna  
; HYPOTHETICAL: NO  
; ANTI-SENSE: YES  
US-09-038-369B-97

Query Match 1.0%; Score 16; DB 1; Length 16;  
Best Local Similarity 100.0%; Pred. No. 32;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1508 CAGCCTCCAGGCCCC 1523  
Db 16 CAGCCTCCAGGCCCC 1

RESULT 90  
US-09-378-900A-97/c  
; Sequence 97, Application US/09378900A  
; Patent No. 6495670  
; GENERAL INFORMATION:  
; APPLICANT: MAERTENS, GEERT; STUYVER, LIEVEN;  
; APPLICANT: ROSSAU, RUDI; VAN HEUVERSWYN, HUGO  
; TITLE OF INVENTION: PROCESS FOR TYPING OF HCV  
; NUMBER OF SEQUENCES: 97  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BIERMAN & MUSERLIAN  
; STREET: 600 THIRD AVENUE  
; CITY: NEW YORK  
; STATE: NEW YORK  
; COUNTRY: USA  
; ZIP: 10016  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: ASCII  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/378,900A  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/256,568  
; FILING DATE: 18-JUL-1994  
; APPLICATION NUMBER: PCT/EP93/03325  
; FILING DATE: 26-NOV-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: EP/93/402,129.6

;  
; FILING DATE: 31-AUG-1993  
; CLASSIFICATION: 1.0%; Score 16; DB 1; Length 16;  
; PRIOR APPLICATION DATA: Best Local Similarity 100.0%; Pred. No. 32;  
; APPLICATION NUMBER: EP/92/403,222.0 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
; FILING DATE: 27-NOV-1992  
; ATTORNEY/AGENT INFORMATION: 0;  
; NAME: CHARLES A. MUSERLIAN  
; REGISTRATION NUMBER: 19,683  
; REFERENCE/DOCKET NUMBER: 410.004  
; TELECOMMUNICATION INFORMATION: 0;  
; TELEPHONE: (212) 661-8000  
; TELEFAX: (212) 661-8002  
; INFORMATION FOR SEQ ID NO: 97:  
; SEQUENCE CHARACTERISTICS: 0;  
; LENGTH: 16 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cdna  
; HYPOTHETICAL: NO  
; ANTI-SENSE: YES  
US-09-378-900A-97

Query Match 1.0%; Score 16; DB 1; Length 16;  
Best Local Similarity 100.0%; Pred. No. 32;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1508 CAGCCTCCAGGCCCC 1523  
Db 16 CAGCCTCCAGGCCCC 1

RESULT 91  
US-09-899-044-97/c  
; Sequence 97, Application US/09899044  
; Patent No. 6548244  
; GENERAL INFORMATION:  
; APPLICANT: MAERTENS, GEERT; STUYVER, LIEVEN;  
; APPLICANT: ROSSAU, RUDI; VAN HEUVERSWYN, HUGO  
; TITLE OF INVENTION: PROCESS FOR TYPING OF HCV  
; NUMBER OF SEQUENCES: 97  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BIERMAN & MUSERLIAN  
; STREET: 600 THIRD AVENUE  
; CITY: NEW YORK  
; STATE: NEW YORK  
; COUNTRY: USA  
; ZIP: 10016  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: ASCII  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/899,044  
; FILING DATE: 06-Jul-2001  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 09/378,900  
; FILING DATE: <Unknown>  
; APPLICATION NUMBER: PCT/EP93/03325  
; FILING DATE: 26-NOV-1993  
; APPLICATION NUMBER: EP/93/402,129.6  
; FILING DATE: 31-AUG-1993  
; APPLICATION NUMBER: EP/92/403,222.0  
; FILING DATE: 27-NOV-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: CHARLES A. MUSERLIAN  
; REGISTRATION NUMBER: 19,683  
; REFERENCE/DOCKET NUMBER: 410.004  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 661-8000  
; TELEFAX: (212) 661-8002

```

; INFORMATION FOR SEQ ID NO: 97:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 16 base pairs
;   TYPE: nucleic acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
;   MOLECULE TYPE: cDNA
;   HYPOTHETICAL: NO
;   ANTI-SENSE: YES
;   SEQUENCE DESCRIPTION: SEQ ID NO: 97:
US-09-899-044-97

Query Match          1.0%; Score 16; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1508 CAGCCTCAGGCCCC 1523
Db 16 CAGCCTCAGGCCCC 1

RESULT 92
US-08-173-489C-37
; Sequence 37, Application US/08173489C
; Patent No. 5861244
; GENERAL INFORMATION:
; APPLICANT: WANG, C. -G.
; APPLICANT: HEPBURN, A. G.
; TITLE OF INVENTION: GENETIC SEQUENCE ASSAY USING DNA
; TITLE OF INVENTION: TRIPLE-STRAND FORMATION.
; NUMBER OF SEQUENCES: 365
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PROFILE DIAGNOSTIC SCIENCES, INC.,
; STREET: 510 EAST 73RD STREET,
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: USA
; ZIP: 10021.
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44Mb storage
; COMPUTER: IBM PC/XT/AT
; OPERATING SYSTEM: MS-DOS version 6.2
; SOFTWARE: Wordperfect version 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/173.489C
; FILING DATE: 22 DEC 1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/968,436
; FILING DATE: 29 OCT 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Handelman, Joseph H.
; REGISTRATION NUMBER: 26,179
; REFERENCE/DOCKET NUMBER: U9518-6
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (attorney) (212) 708-1880
; TELEFAX: (attorney) (212) 246-8959
; INFORMATION FOR SEQ ID NO: 37:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 17 base pairs
;   TYPE: Nucleic Acid
;   STRANDEDNESS: double stranded
;   TOPOLOGY: linear
;   MOLECULE TYPE: Genomic DNA
;   DESCRIPTION: dystrophin gene (Accession # M18533,
;   DESCRIPTION: M17154, M18026) nucleotides 5967 to 5983
;   HYPOTHETICAL: NO
;   ANTI-SENSE: NO
;   ORIGINAL SOURCE:
;   ORGANISM: Homo sapiens
;   POSITION IN GENOME:
;   CHROMOSOME/SEGMENT: X-chromosome
;   MAP POSITION: Xp21.3-p21.1

; PUBLICATION INFORMATION:
; AUTHORS: Koenig, M, Hoffman, E P, Bertelson, C J,
; AUTHORS: Monaco, A P, Feener, C, Kunkel, L M.
; TITLE: Complete cloning of the
; TITLE: Duchenne muscular dystrophy (DMD) cDNA and
; TITLE: preliminary genomic organization of the DMD
; TITLE: gene in normal and affected individuals
; JOURNAL: Cell
; VOLUME: 50
; PAGES: 509-517
; DATE: 1987
; AUTHORS: Hoffman, E P, Monaco, A P, Feener, C C,
; AUTHORS: Kunkel, L M.
; TITLE: Conservation of the Duchenne
; TITLE: muscular dystrophy gene in mice and humans
; JOURNAL: Science
; VOLUME: 238
; PAGES: 347-350
; DATE: 1987
; AUTHORS: Koenig, M, Monaco, A P, Kunkel, L M.
; TITLE: The complete sequence of
; TITLE: dystrophin predicts a rod-shaped cytoskeletal
; TITLE: protein
; JOURNAL: Cell
; VOLUME: 53
; PAGES: 219-228
; DATE: 1988
; RELEVANT RESIDUES IN SEQ ID NO: 37 :FROM 1 TO 17
US-08-173-489C-37

Query Match          1.0%; Score 16; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 37;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 280 AGAAGAAGAAAGAGGA 295
Db 1 AGAAGAAGAAAGAGGA 16

RESULT 93
US-08-390-850-535/c
; Sequence 535, Application US/08390850
; Patent No. 5612215
; GENERAL INFORMATION:
; APPLICANT: Draper, Kenneth G.
; APPLICANT: Pavco, Pamela
; APPLICANT: McSwiggen, James
; APPLICANT: Gustofson, John
; APPLICANT: Stinchcomb, Dan T.
; TITLE OF INVENTION: METHOD AND REAGENT FOR TREATMENT
; TITLE OF INVENTION: OF ARTHRITIC CONDITIONS
; NUMBER OF SEQUENCES: 1151
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/390,850
; FILING DATE: February 17, 1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/354,920
; FILING DATE: December 13, 1994
; APPLICATION NUMBER: 08/152,487
```

;; FILING DATE: No. 5612215ember 12, 1993  
;; APPLICATION NUMBER: 07/989,848  
;; FILING DATE: December 7, 1992  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Warburg, Richard  
;; REGISTRATION NUMBER: 32,327  
;; REFERENCE/DOCKET NUMBER: 211/084  
;; TELEPHONE: (213) 489-1600  
;; TELEFAX: (213) 955-0440  
;; TELEX: 67-3510  
;; INFORMATION FOR SEQ ID NO: 535:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 17 base pairs  
;; TYPE: nucleic acid  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
US-08-390-850-535

Query Match 0.9%; Score 15.4; DB 1; Length 17;  
Best Local Similarity 94.1%; Pred. No. 46;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1589 AAGAACAAGAAATTCCTCC 1605  
DB 17 AAGAACAAGAAATTCCTCC 1

RESULT 94  
US-08-435-634-535/c  
; Sequence 535, Application US/08435634  
; Patent No. 5731295  
; GENERAL INFORMATION:  
; APPLICANT: Draper, Kenneth G.  
; APPLICANT: Rayco, Pamela  
; APPLICANT: McSwiggen, James  
; APPLICANT: Gustofson, John  
; APPLICANT: Stinchcomb, Dan T.  
; TITLE OF INVENTION: METHOD AND REAGENT FOR TREATMENT  
; TITLE OF INVENTION: OF ARTHRIITIC CONDITIONS  
; NUMBER OF SEQUENCES: 1151  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Lyon & Lyon  
; STREET: 633 West Fifth Street  
; STREET: Suite 4700  
; CITY: Los Angeles  
; STATE: California  
; COUNTRY: U.S.A.  
; ZIP: 90071  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
; MEDIUM TYPE: storage  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: IBM P.C. DOS 5.0  
; SOFTWARE: FastSeq Version 1.5  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/435,634  
; FILING DATE: 05-MAY-1995  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/390,850  
; FILING DATE: February 17, 1995  
; APPLICATION NUMBER: 08/354,920  
; FILING DATE: December 13, 1994  
; APPLICATION NUMBER: 08/152,487  
; FILING DATE: No. 5731295ember 12, 1993  
; APPLICATION NUMBER: 07/989,848  
; FILING DATE: December 7, 1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Warburg, Richard  
; REGISTRATION NUMBER: 32,327  
; REFERENCE/DOCKET NUMBER: 211/084  
; TELECOMMUNICATION INFORMATION:

;; TELEPHONE: (213) 489-1600  
;; TELEFAX: (213) 955-0440  
;; TELEX: 67-3510  
;; INFORMATION FOR SEQ ID NO: 535:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 17 base pairs  
;; TYPE: nucleic acid  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
US-08-435-634-535

Query Match 0.9%; Score 15.4; DB 1; Length 17;  
Best Local Similarity 94.1%; Pred. No. 46;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1589 AAGAACAAGAAATTCCTCC 1605  
DB 17 AAGAACAAGAAATTCCTCC 1

RESULT 95  
US-09-866-108A-8666  
; Sequence 8666, Application US/09866108A  
; Patent No. 6886188  
; GENERAL INFORMATION:  
; APPLICANT: GU, Yizhong  
; APPLICANT: JI, Yonggang  
; APPLICANT: PENN, Sharron G.  
; APPLICANT: HANZEL, David K.  
; APPLICANT: RANK, David R.  
; APPLICANT: CHEN, Wensheng  
; APPLICANT: SHANNON, Mark  
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE  
; FILE REFERENCE: AEOICA-7  
; CURRENT APPLICATION NUMBER: US/09/866,108A  
; CURRENT FILING DATE: 2001-05-25  
; PRIOR APPLICATION NUMBER: US 60/207,456  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: GB 24263.6  
; PRIOR FILING DATE: 2000-10-04  
; PRIOR APPLICATION NUMBER: US 60/236,359  
; PRIOR FILING DATE: 2000-09-27  
; PRIOR APPLICATION NUMBER: PCT/US01/00666  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00667  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00664  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00669  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00665  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00668  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00663  
; PRIOR FILING DATE: 2001-01-30  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 15755  
; SOFTWARE: Acomica Sequence Listing Engine  
; Patent No. 6886188  
; SEQ ID NO 8666  
; LENGTH: 17  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-866-108A-8666

Query Match 0.9%; Score 15.4; DB 1; Length 17;  
Best Local Similarity 94.1%; Pred. No. 46;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 273 GAAGCCAAGAAAGAGAA 289  
DB 1 GAAGCCAAGAAAGAGAA 17

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/458,101

```
/ FILING DATE: 01-JUN-1995
/ CLASSIFICATION: 424
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Frommer, William S.
/ REGISTRATION NUMBER: 25,506
/ REFERENCE/DOCKET NUMBER: 454310-2740
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (212) 840-3333
/ TELEFAX: (212) 840-0712
/ INFORMATION FOR SEQ ID NO: 280:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 18 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ US-08-458-101-280

Query Match          0.9%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 63;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      222 CTCATAGAAAACCAAC 239
Db      18 CTAATAGAAAACCAAC 1

RESULT 99
US-08-758-306-953/c
; Sequence 953, Application US/08758306
; Patent No. 5807743
; GENERAL INFORMATION:
; APPLICANT: Stinchcomb, Dan T.
; APPLICANT: McSwiggen, James A.
; TITLE OF INVENTION: METHOD AND REAGENT FOR THE
; TITLE OF INVENTION: TREATMENT OF DISEASES
; TITLE OF INVENTION: ASSOCIATED WITH
; TITLE OF INVENTION: INTERLEUKIN-2 RECEPTOR
; TITLE OF INVENTION: GAMMA-CHAIN EXPRESSION
; NUMBER OF SEQUENCES: 1379
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/758,306
; FILING DATE: December 3, 1996
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 212/132
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 953:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
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/ TOPOLOGY: linear
/ US-08-758-306-953

Query Match          0.9%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 63;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1121 GCTGAGCAGCTGAACGA 1138
Db      18 GCAGGAGCAGCTGAAGGA 1

RESULT 100
US-08-390-850-536/c
; Sequence 536, Application US/08390850
; Patent No. 5612215
; GENERAL INFORMATION:
; APPLICANT: Draper, Kenneth G.
; APPLICANT: Pavco, Pamela
; APPLICANT: McSwiggen, James
; APPLICANT: Gustofson, John
; APPLICANT: Stinchcomb, Dan T.
; TITLE OF INVENTION: METHOD AND REAGENT FOR TREATMENT
; TITLE OF INVENTION: OF ARTHRITIC CONDITIONS
; NUMBER OF SEQUENCES: 1151
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Suite 4700
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/390,850
; FILING DATE: February 17, 1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/354,920
; FILING DATE: December 13, 1994
; APPLICATION NUMBER: 08/152,487
; FILING DATE: No 5612215ember 12, 1993
; APPLICATION NUMBER: 07/989,848
; FILING DATE: December 7, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 211/084
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 536:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
/ US-08-390-850-536

Query Match          0.9%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 65;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1589 AAGAACAGAAATGCTC 1604
Db      16 AAGAACAGAAATTCCTC 1
```

RESULT 101  
US-08-435-536/c  
; Sequence 536, Application US/08435634  
; Patent No. 5731295  
; GENERAL INFORMATION:  
; APPLICANT: Draper, Kenneth G.  
; APPLICANT: Pavco, Pamela  
; APPLICANT: McSwiggen, James  
; APPLICANT: Gustofson, John  
; APPLICANT: Stinchcomb, Dan T.  
; TITLE OF INVENTION: METHOD AND REAGENT FOR TREATMENT  
; OF ARTHRITIC CONDITIONS  
; NUMBER OF SEQUENCES: 1151  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Lyon & Lyon  
; STREET: 633 West Fifth Street  
; CITY: Suite 4700  
; STATE: Los Angeles  
; COUNTRY: California  
; ZIP: U.S.A.  
; ZIP: 90071  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
; MEDIUM TYPE: storage  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: IBM P.C. DOS 5.0  
; SOFTWARE: FastSeq Version 1.5  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/435,634  
; FILING DATE: 05-MAY-1995  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/390,850  
; FILING DATE: February 17, 1995  
; APPLICATION NUMBER: 08/354,920  
; FILING DATE: December 13, 1994  
; APPLICATION NUMBER: 08/152,487  
; FILING DATE: No. 5731295 September 12, 1993  
; APPLICATION NUMBER: 07/989,848  
; FILING DATE: December 7, 1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Warburg, Richard  
; REGISTRATION NUMBER: 32,327  
; REFERENCE/DOCKET NUMBER: 211/084  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (213) 489-1600  
; TELEFAX: (213) 955-0440  
; TELEX: 67-3510  
; INFORMATION FOR SEQ ID NO: 536:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 17 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
US-08-435-634-536

Query Match 0.9%; Score 14.4; DB 1; Length 17;  
Best Local Similarity 93.8%; Pred. No. 65;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1589 AAGACAGAAATGCTC 1604  
Db 16 AAGACAGAAATTTCTC 1

RESULT 102  
US-09-282-146-7  
; Sequence 7, Application US/09282146A  
; Patent No. 6303847  
; GENERAL INFORMATION:  
; APPLICANT: KAWAKURA, Akiyoshi  
; APPLICANT: EBINUMA, Hiroyasu

; TITLE OF INVENTION: TRANSCRIPTION FACTOR CONTROLLING PHENYLPROPANOID  
; TITLE OF INVENTION: BIOSYNTHESIS PATHWAY  
; FILE REFERENCE: 4859-0027-0  
; CURRENT APPLICATION NUMBER: US/09/282,146A  
; CURRENT FILING DATE: 1999-03-31  
; EARLIER APPLICATION NUMBER: JP 10-125171  
; EARLIER FILING DATE: 1998-03-31  
; NUMBER OF SEQ ID NOS: 13  
; SOFTWARE: Patent In Ver. 2.1  
; SEQ ID NO 7  
; LENGTH: 17  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic DNA  
US-09-282-146-7

Query Match 0.9%; Score 14.4; DB 1; Length 17;  
Best Local Similarity 93.8%; Pred. No. 65;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1104 CTCAACACCTCTCTCT 1119  
Db 2 CTCAACAACTCTCTCT 17

RESULT 103  
US-09-866-108A-8352/c  
; Sequence 8352, Application US/09866108A  
; Patent No. 6686188  
; GENERAL INFORMATION:  
; APPLICANT: GU, Yizhong  
; APPLICANT: JI, Yonggang  
; APPLICANT: PENN, Sharron G.  
; APPLICANT: HANZEL, David K.  
; APPLICANT: RANK, David R.  
; APPLICANT: CHEN, Wensheng  
; APPLICANT: SHANNON, Mark  
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE  
; FILE REFERENCE: AEOMICA-7  
; CURRENT APPLICATION NUMBER: US/09/866,108A  
; CURRENT FILING DATE: 2001-05-25  
; PRIOR APPLICATION NUMBER: US 60/207,456  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: GB 24263.6  
; PRIOR FILING DATE: 2000-10-04  
; PRIOR APPLICATION NUMBER: US 60/236,359  
; PRIOR FILING DATE: 2000-09-27  
; PRIOR APPLICATION NUMBER: PCT/US01/00666  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00667  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00664  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00669  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00665  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00668  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00663  
; PRIOR FILING DATE: 2001-01-30  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 15755  
; SOFTWARE: Aecomica Sequence Listing Engine  
; Patent No. 6686188  
; SEQ ID NO 8352  
; LENGTH: 17  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-866-108A-8352

Query Match 0.9%; Score 14.4; DB 1; Length 17;



Best Local Similarity 93.8%; Pred. No. 65;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1109 CACCTCCTCTTGCTG 1124  
Db 17 CAGCTCCTCTTGCTG 2

## RESULT 104

US-09-866-108A-8353/c  
; Sequence 8353, Application US/09866108A  
; Patent No. 6686188

; GENERAL INFORMATION:

; APPLICANT: GU, Yizhong

; APPLICANT: JI, Yonggang

; APPLICANT: PENN, Sharron G.

; APPLICANT: HANZEL, David K.

; APPLICANT: RANK, David R.

; APPLICANT: CHEN, Wensheng

; APPLICANT: SHANNON, Mark

; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE

; FILE REFERENCE: AEWICA-7

; CURRENT APPLICATION NUMBER: US/09/866,108A

; CURRENT FILING DATE: 2001-05-25

; PRIOR APPLICATION NUMBER: US 60/207,456

; PRIOR FILING DATE: 2000-05-26

; PRIOR APPLICATION NUMBER: GB 24263.6

; PRIOR FILING DATE: 2000-10-04

; PRIOR APPLICATION NUMBER: US 60/236,359

; PRIOR FILING DATE: 2000-09-27

; PRIOR APPLICATION NUMBER: PCT/US01/00666

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00667

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00664

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00669

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00665

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00668

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00663

; PRIOR FILING DATE: 2001-01-30

; Remaining Prior Application data removed - See File Wrapper or PALM.

; NUMBER OF SEQ ID NOS: 15755

; SOFTWARE: Aemica Sequence Listing Engine

; Patent No. 6686188

; SEQ ID NO 8353

; LENGTH: 17

; TYPE: DNA

; ORGANISM: Homo sapiens

US-09-866-108A-8353

Query Match 0.9%; Score 14.4; DB 1; Length 17;

Best Local Similarity 93.8%; Pred. No. 65;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1109 CACCTCCTCTTGCTG 1124  
Db 16 CAGCTCCTCTTGCTG 1

## RESULT 105

US-09-866-108A-8665

; Sequence 8665, Application US/09866108A

; Patent No. 6686188

; GENERAL INFORMATION:

; APPLICANT: GU, Yizhong

; APPLICANT: JI, Yonggang

; APPLICANT: PENN, Sharron G.

; APPLICANT: HANZEL, David K.

; APPLICANT: RANK, David R.

; APPLICANT: CHEN, Wensheng  
; APPLICANT: SHANNON, Mark  
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE  
; FILE REFERENCE: AEWICA-7

; CURRENT APPLICATION NUMBER: US/09/866,108A

; CURRENT FILING DATE: 2001-05-25

; PRIOR APPLICATION NUMBER: US 60/207,456

; PRIOR FILING DATE: 2000-05-26

; PRIOR APPLICATION NUMBER: GB 24263.6

; PRIOR FILING DATE: 2000-10-04

; PRIOR APPLICATION NUMBER: US 60/236,359

; PRIOR FILING DATE: 2000-09-27

; PRIOR APPLICATION NUMBER: PCT/US01/00666

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00667

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00664

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00669

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00665

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00668

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00663

; PRIOR FILING DATE: 2001-01-30

; Remaining Prior Application data removed - See File Wrapper or PALM.

; NUMBER OF SEQ ID NOS: 15755

; SOFTWARE: Aemica Sequence Listing Engine

; Patent No. 6686188

; SEQ ID NO 8665

; LENGTH: 17

; TYPE: DNA

; ORGANISM: Homo sapiens

US-09-866-108A-8665

Query Match 0.9%; Score 14.4; DB 1; Length 17;

Best Local Similarity 93.8%; Pred. No. 65;

Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 273 GAAGCCAAGAGAAGA 288  
Db 2 GAAGCCAAGAGAAGA 17

## RESULT 106

US-09-866-108A-8667

; Sequence 8667, Application US/09866108A

; Patent No. 6686188

; GENERAL INFORMATION:

; APPLICANT: GU, Yizhong

; APPLICANT: JI, Yonggang

; APPLICANT: PENN, Sharron G.

; APPLICANT: HANZEL, David K.

; APPLICANT: RANK, David R.

; APPLICANT: CHEN, Wensheng

; APPLICANT: SHANNON, Mark

; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE

; FILE REFERENCE: AEWICA-7

; CURRENT APPLICATION NUMBER: US/09/866,108A

; CURRENT FILING DATE: 2001-05-25

; PRIOR APPLICATION NUMBER: US 60/207,456

; PRIOR FILING DATE: 2000-05-26

; PRIOR APPLICATION NUMBER: GB 24263.6

; PRIOR FILING DATE: 2000-10-04

; PRIOR APPLICATION NUMBER: US 60/236,359

; PRIOR FILING DATE: 2000-09-27

; PRIOR APPLICATION NUMBER: PCT/US01/00666

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00667

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00664

; PRIOR FILING DATE: 2001-01-30

```
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Acomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 8667
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-8667

Query Match      0.9%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 65;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      274 AAGCCAGAGAGAGAA 289
Db      1 AAGCCAGAGAGAGAA 16

RESULT 107
US-09-866-108A-10037/c
; Sequence 10037, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: ACOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108A
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Acomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 10037
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-10037
```

```
Query Match      0.9%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 65;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      715 CCGCATCGTCCGACAG 730
Db      17 CCGCATCGTCCACAG 2

RESULT 108
US-09-866-108A-10038/c
; Sequence 10038, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: ACOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108A
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Acomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 10038
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-10038

Query Match      0.9%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 65;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      715 CCGCATCGTCCGACAG 730
Db      16 CCGCATCGTCCACAG 1

RESULT 109
US-08-117-952-797/c
; Sequence 797, Application US/08117952
; Patent No. 5851760
; GENERAL INFORMATION:
; APPLICANT: Evans, Glen A.
; APPLICANT: Smith, Michael W.
; TITLE OF INVENTION: METHOD FOR GENERATION OF SEQUENCE
; TITLE OF INVENTION: SAMPLED MAPS OF COMPLEX GENOMES
```

```
;
; NUMBER OF SEQUENCES: 797
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pretty, Schroeder, Brueggemann & Clark
; STREET: 444 South Flower Street, Suite 2000
; CITY: Los Angeles
; STATE: CA
; COUNTRY: USA
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/117,952
; FILING DATE: 07-SEP-1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/078,471
; FILING DATE: 15-JUN-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Reiter, Stephen E.
; REGISTRATION NUMBER: 31,192
; REFERENCE/DOCKET NUMBER: P41 9423
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-546-4737
; TELEFAX: 619-546-9392
; INFORMATION FOR SEQ ID NO: 797:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Oligonucleotide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; US-08-117-952-797

Query Match 0.9%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 73;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1520 CCCCAACTCGGCCGAG 1535
Db 18 CCCTAACTCGGCCGAG 3

RESULT 110
US-08-758-306-467
; Sequence 467, Application US/08758306
; Patent No. 5807743
; GENERAL INFORMATION:
; APPLICANT: Stinchcomb, Dan T.
; APPLICANT: McSwiggan, James A.
; TITLE OF INVENTION: METHOD AND REAGENT FOR THE
; TITLE OF INVENTION: TREATMENT OF DISEASES
; TITLE OF INVENTION: ASSOCIATED WITH
; TITLE OF INVENTION: INTERLEUKIN-2 RECEPTOR
; TITLE OF INVENTION: GAMMA-CHAIN EXPRESSION
; NUMBER OF SEQUENCES: 1379
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
```

```
;
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/758,306
; FILING DATE: December 3, 1996
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 212/132
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 467:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-758-306-467

Query Match 0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 47.1%; Pred. No. 80;
Matches 8; Conservative 7; Mismatches 2; Indels 0; Gaps 0;

Qy 693 CCTCACTTCTTCTTCC 709
Db 1 CCUCCUCCUCCUCC 17

RESULT 111
US-08-599-455B-25
; Sequence 25, Application US/08599455B
; Patent No. 5972621
; GENERAL INFORMATION:
; APPLICANT: Tartaglia, Louis A.
; APPLICANT: Tepper, Robert I.
; APPLICANT: Culpepper, Janice A.
; TITLE OF INVENTION: METHODS OF IDENTIFYING COMPOUNDS THAT
; TITLE OF INVENTION: MODULATE BODY WEIGHT USING THE OB RECEPTOR
; NUMBER OF SEQUENCES: 44
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/599,455B
; FILING DATE: 22-JAN-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/583,153
; FILING DATE: 28-DEC-1995
; APPLICATION NUMBER: 08/570,142
; FILING DATE: 11-DEC-1995
; APPLICATION NUMBER: 08/569,485
; FILING DATE: 08-DEC-1995
; APPLICATION NUMBER: 08/566,622
; FILING DATE: 04-DEC-1995
; APPLICATION NUMBER: 08/562,663
; FILING DATE: 27-NOV-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Melkijohn, Ph.D., Anita L.
; REGISTRATION NUMBER: 35,283
```

```
; REFERENCE/DOCKET NUMBER: 07334/017001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-542-5070
; TELEFAX: 617-542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 25:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-599-455B-25

Query Match 0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 80;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 660 CACTACCTGCCCTTCAG 676
Db 1 CACTATTGGCCCTTCAG 17

RESULT 112
US-08-599-455B-27
; Sequence 27, Application US/08599455B
; Patent No. 5972621
; GENERAL INFORMATION:
; APPLICANT: Tartaglia, Louis A.
; APPLICANT: Tepper, Robert I.
; APPLICANT: Culpepper, Janice A.
; TITLE OF INVENTION: METHODS OF IDENTIFYING COMPOUNDS THAT
; TITLE OF INVENTION: MODULATE BODY WEIGHT USING THE OB RECEPTOR
; NUMBER OF SEQUENCES: 44
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: Fast-SEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/599,455B
; FILING DATE: 22-JAN-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/583,153
; FILING DATE: 28-DEC-1995
; APPLICATION NUMBER: 08/570,142
; FILING DATE: 11-DEC-1995
; APPLICATION NUMBER: 08/569,485
; FILING DATE: 08-DEC-1995
; APPLICATION NUMBER: 08/566,622
; FILING DATE: 04-DEC-1995
; APPLICATION NUMBER: 08/562,663
; FILING DATE: 27-NOV-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Melklejohn, Ph.D., Anita L.
; REGISTRATION NUMBER: 35,283
; REFERENCE/DOCKET NUMBER: 07334/017001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-542-5070
; TELEFAX: 617-542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 27:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single

; REFERENCE/DOCKET NUMBER: 07334/017001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-542-5070
; TELEFAX: 617-542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-474-700B-21

Query Match 0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 80;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 222 CTCATAGAAAAACAAA 238
Db 17 CTCAAAGAAAAACAAA 1

RESULT 114
US-08-757-024-874/c
; Sequence 874, Application US/08757024
; Patent No. 6025339
; GENERAL INFORMATION:
; APPLICANT: Nyce, Jonathan W.
```

;; TITLE OF INVENTION: METHOD OF TREATMENT FOR ASTHMA  
;; NUMBER OF SEQUENCES: 952  
;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: BELL, SELTZER, PARK & GIBSON  
;; STREET: P.O. Drawer 34009  
;; CITY: Charlotte  
;; STATE: No. 6025339th Carolina  
;; COUNTRY: USA  
;; ZIP: 28234  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Floppy disk  
;; COMPUTER: IBM PC compatible  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: Patent In Release #1.0, Version #1.30  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/757,024  
;; FILING DATE: 26-NOV-1996  
;; CLASSIFICATION: 514  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Sibley, Kenneth D.  
;; REGISTRATION NUMBER: 31,665  
;; REFERENCE/DOCKET NUMBER: 5218-41  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: 919-881-3140  
;; TELEFAX: 919-881-3175  
;; TELEX: 575102  
;; INFORMATION FOR SEQ ID NO: 874:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 17 base pairs  
;; TYPE: nucleic acid  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: DNA (genomic)  
US-08-757-024-874

Query Match 0.8%; Score 13.8; DB 1; Length 17;  
Best Local Similarity 88.2%; Pred. No. 80;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1530 GCCCAGCCTCTCCCGC 1546  
Db 17 GCCCAGCCTGTGCCGC 1

RESULT 115  
US-08-757-024-944/c  
; Sequence 944, Application US/08757024  
; Patent No. 6025339  
; GENERAL INFORMATION:  
; APPLICANT: Nyce, Jonathan W.  
; TITLE OF INVENTION: METHOD OF TREATMENT FOR ASTHMA  
; NUMBER OF SEQUENCES: 952  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BELL, SELTZER, PARK & GIBSON  
; STREET: P.O. Drawer 34009  
; CITY: Charlotte  
; STATE: No. 6025339th Carolina  
; COUNTRY: USA  
; ZIP: 28234  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/757,024  
; FILING DATE: 26-NOV-1996  
; CLASSIFICATION: 514  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Sibley, Kenneth D.  
; REGISTRATION NUMBER: 31,665  
; REFERENCE/DOCKET NUMBER: 5218-41  
; TELECOMMUNICATION INFORMATION:

;; TELEPHONE: 919-881-3140  
;; TELEFAX: 919-881-3175  
;; TELEX: 575102  
;; INFORMATION FOR SEQ ID NO: 944:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 17 base pairs  
;; TYPE: nucleic acid  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: DNA (genomic)  
US-08-757-024-944

Query Match 0.8%; Score 13.8; DB 1; Length 17;  
Best Local Similarity 88.2%; Pred. No. 80;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1530 GCCCAGCCTCTCCCGC 1546  
Db 17 GCCCAGCCTGTGCCGC 1

RESULT 116  
US-09-069-781B-25  
; Sequence 25, Application US/09069781B  
; Patent No. 6287782  
; GENERAL INFORMATION:  
; APPLICANT: Tartaglia, Louis A.  
; APPLICANT: Tepper, Robert I.  
; APPLICANT: Culpepper, Janice A.  
; APPLICANT: White, David W.  
; TITLE OF INVENTION: THE OB RECEPTOR AND METHODS FOR  
; TITLE OF INVENTION: THE DIAGNOSIS AND TREATMENT OF BODY WEIGHT DISORDERS,  
; TITLE OF INVENTION: INCLUDING OBESITY AND CACHEXIA  
; NUMBER OF SEQUENCES: 50  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Fish & Richardson, P.C.  
; STREET: 225 Franklin Street  
; CITY: Boston  
; STATE: MA  
; COUNTRY: US  
; ZIP: 02110-2804  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: Windows95  
; SOFTWARE: FastSEQ for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/069,781B  
; FILING DATE: 29-APRIL-1998  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/864,564  
; FILING DATE: 28-MAY-1997  
; APPLICATION NUMBER: US 08/708,123  
; FILING DATE: 03-SEP-1996  
; APPLICATION NUMBER: US 08/638,524  
; FILING DATE: 26-APR-1996  
; APPLICATION NUMBER: US 08/599,455  
; FILING DATE: 22-JAN-1996  
; APPLICATION NUMBER: US 08/583,153  
; FILING DATE: 28-DEC-1995  
; APPLICATION NUMBER: US 08/570,142  
; FILING DATE: 11-DEC-1995  
; APPLICATION NUMBER: US 08/569,485  
; FILING DATE: 08-DEC-1995  
; APPLICATION NUMBER: US 08/566,622  
; FILING DATE: 04-DEC-1995  
; APPLICATION NUMBER: US 08/562,663  
; FILING DATE: 27-NOV-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Meiklejohn, Ph.D., Anita L.  
; REGISTRATION NUMBER: 35,283  
; REFERENCE/DOCKET NUMBER: 07334/082001  
; TELECOMMUNICATION INFORMATION:

10828394-1\_1-1643.rni.sl

Tue Sep 13 10:53:21 2005

```

; TELEPHONE: (617) 542-5070
; TELEFAX: (617) 542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 25:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-09-069-781B-25

Query Match 0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 80;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 660 CACTACTGCGCCTTCAG 676
Db 1 CACTATTGCGCCTTCAG 17

RESULT 117
US-09-069-781B-27
; Sequence 27, Application US/09069781B
; Patent No. 6287782
; GENERAL INFORMATION:
; APPLICANT: Tartaglia, Louis A.
; APPLICANT: Tepper, Robert I.
; APPLICANT: Culpepper, Janice A.
; APPLICANT: White, David W.
; TITLE OF INVENTION: THE OB RECEPTOR AND METHODS FOR
; TITLE OF INVENTION: THE DIAGNOSIS AND TREATMENT OF BODY WEIGHT DISORDERS,
; TITLE OF INVENTION: INCLUDING OBESITY AND CACHEXIA
; NUMBER OF SEQUENCES: 50
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/069,781B
; FILING DATE: 29-APRIL-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/864,564
; FILING DATE: 28-MAY-1997
; APPLICATION NUMBER: US 08/708,123
; FILING DATE: 03-SEP-1996
; APPLICATION NUMBER: US 08/638,524
; FILING DATE: 28-APR-1996
; APPLICATION NUMBER: US 08/599,455
; FILING DATE: 22-JAN-1996
; APPLICATION NUMBER: US 08/583,153
; FILING DATE: 28-DEC-1995
; APPLICATION NUMBER: US 08/570,142
; FILING DATE: 11-DEC-1995
; APPLICATION NUMBER: US 08/569,485
; FILING DATE: 08-DEC-1995
; APPLICATION NUMBER: US 08/566,622
; FILING DATE: 04-DEC-1995
; APPLICATION NUMBER: US 08/562,663
; FILING DATE: 27-NOV-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Melkielejohn, Ph.D., Anita L.
; REGISTRATION NUMBER: 35,283
; REFERENCE/DOCKET NUMBER: 07334/082001
; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (617) 542-5070
; TELEFAX: (617) 542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 27:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-09-069-781B-27

Query Match 0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 80;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 660 CACTACTGCGCCTTCAG 676
Db 1 CACTATTGCGCCTTCAG 17

RESULT 118
US-08-584-040-7759
; Sequence 7759, Application US/08584040
; Patent No. 6346398
; GENERAL INFORMATION:
; APPLICANT: Pavco, Pamela
; APPLICANT: McSwiggen, James
; APPLICANT: Stinchcomb, Dan T.
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: METHOD AND REAGENT FOR THE
; TITLE OF INVENTION: TREATMENT OF DISEASES OR
; TITLE OF INVENTION: CONDITIONS RELATED TO LEVELS
; TITLE OF INVENTION: OF VASCULAR ENDOTHELIAL
; TITLE OF INVENTION: GROWTH FACTOR
; NUMBER OF SEQUENCES: 8502
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/584,040
; FILING DATE: January 11, 1996
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/005,974
; FILING DATE: October 26, 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 218/064
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 7759:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-584-040-7759

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Query Match 0.8%; Score 13.8; DB 1; Length 17;  
Best Local Similarity 64.7%; Pred. No. 80;  
Matches 11; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1112 CTCCTCTGCTGGAGC 1128  
DB 1 CUCCCCUUGCUGAAGC 17

## RESULT 119

US-08-679-645-687/c  
; Sequence 687, Application US/08679645  
; Patent No. 6350934  
; GENERAL INFORMATION:  
; APPLICANT: Zwick, Michael G.  
; APPLICANT: Edington, Brent E.  
; APPLICANT: McSwiggen, James A.  
; APPLICANT: Merlo, Patricia Ann Owens  
; APPLICANT: Guo, Lining  
; APPLICANT: Skokut, Thomas A.  
; APPLICANT: Young, Scott A.  
; APPLICANT: Folkerts, Otto  
; APPLICANT: Merlo, Donald J.  
; TITLE OF INVENTION: COMPOSITION AND METHODS FOR  
; TITLE OF INVENTION: MODULATION OF GENE EXPRESSION  
; TITLE OF INVENTION: IN PLANTS  
; NUMBER OF SEQUENCES: 1263  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Lyon & Lyon  
; STREET: 633 West Fifth Street  
; SUITE: Suite 4700  
; CITY: Los Angeles  
; STATE: California  
; COUNTRY: U.S.A.  
; ZIP: 90071-2066  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
; MEDIUM TYPE: storage  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: IBM P.C. DOS 5.0  
; SOFTWARE: Word Perfect 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/679,645  
; FILING DATE: July 12, 1996  
; CLASSIFICATION: 800  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 60/001,135  
; FILING DATE: July 13, 1995  
; APPLICATION NUMBER: 08/300,726  
; FILING DATE: September 2, 1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Warburg, Richard J.  
; REGISTRATION NUMBER: 32,327  
; REFERENCE/DOCKET NUMBER: 219/247  
; TELEPHONE: (213) 489-1600  
; TELEFAX: (213) 955-0440  
; TELEX: 67-3510  
; INFORMATION FOR SEQ ID NO: 687:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 17 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
US-08-679-645-687

Query Match 0.8%; Score 13.8; DB 1; Length 17;  
Best Local Similarity 88.2%; Pred. No. 80;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1213 TGGCTTCCCACTTCT 1229  
DB 17 TGGCTTCCCACTTCT 1

## RESULT 120

US-09-137-132-25  
; Sequence 25, Application US/09137132  
; Patent No. 6380363  
; GENERAL INFORMATION:  
; APPLICANT: Tartaglia, Louis A.  
; APPLICANT: Tepper, Robert I.  
; APPLICANT: Culpepper, Janice A.  
; APPLICANT: White, David W.  
; TITLE OF INVENTION: THE OB RECEPTOR AND METHODS FOR  
; TITLE OF INVENTION: THE DIAGNOSIS AND TREATMENT OF BODY WEIGHT DISORDERS,  
; TITLE OF INVENTION: INCLUDING OBESITY AND CACHEXIA  
; NUMBER OF SEQUENCES: 50  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Fish & Richardson, P.C.  
; STREET: 225 Franklin Street  
; CITY: Boston  
; STATE: MA  
; COUNTRY: US  
; ZIP: 02110-2804  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: Windows95  
; SOFTWARE: FastSeq for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/137,132  
; FILING DATE: 18-AUG-1998  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/864,564  
; FILING DATE: 28-MAY-1997  
; APPLICATION NUMBER: 08/708,123  
; FILING DATE: 03-SEP-1996  
; APPLICATION NUMBER: 08/838,524  
; FILING DATE: 26-APR-1996  
; APPLICATION NUMBER: 08/599,455  
; FILING DATE: 22-JAN-1996  
; APPLICATION NUMBER: 08/583,153  
; APPLICATION NUMBER: 08/570,142  
; FILING DATE: 11-DEC-1995  
; APPLICATION NUMBER: 08/569,485  
; FILING DATE: 08-DEC-1995  
; APPLICATION NUMBER: 08/566,622  
; FILING DATE: 04-DEC-1995  
; APPLICATION NUMBER: 08/562,663  
; FILING DATE: 27-NOV-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Meiklejohn, Ph.D., Anita L.  
; REGISTRATION NUMBER: 35,283  
; REFERENCE/DOCKET NUMBER: 07334/019004  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 617-542-5070  
; TELEFAX: 617-542-8906  
; TELEX: 200154  
; INFORMATION FOR SEQ ID NO: 25:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 17 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA  
US-09-137-132-25

Query Match 0.8%; Score 13.8; DB 1; Length 17;  
Best Local Similarity 88.2%; Pred. No. 80;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 660 CACTACCTGCCCTTCAG 676  
DB 1 CACTATTTGCCCTTCAG 17

```
RESULT 121
US-09-137-132-27
; Sequence 27, Application US/09137132
; Patent No. 6380363
; GENERAL INFORMATION:
; APPLICANT: Tartaglia, Louis A.
; APPLICANT: Tepper, Robert I.
; APPLICANT: Culpepper, Janice A.
; APPLICANT: White, David W.
; TITLE OF INVENTION: THE OB RECEPTOR AND METHODS FOR
; TITLE OF INVENTION: THE OB RECEPTOR AND TREATMENT OF BODY WEIGHT DISORDERS,
; TITLE OF INVENTION: INCLUDING OBESITY AND CACHEXIA
; NUMBER OF SEQUENCES: 50
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/137,132
; FILING DATE: 18-AUG-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/864,564
; FILING DATE: 28-MAY-1997
; APPLICATION NUMBER: 08/708,123
; FILING DATE: 03-SEP-1996
; APPLICATION NUMBER: 08/638,524
; FILING DATE: 26-APR-1996
; APPLICATION NUMBER: 08/599,455
; FILING DATE: 22-JAN-1996
; APPLICATION NUMBER: 08/583,153
; FILING DATE: 28-DEC-1995
; APPLICATION NUMBER: 08/570,142
; FILING DATE: 11-DEC-1995
; APPLICATION NUMBER: 08/569,485
; FILING DATE: 08-DEC-1995
; APPLICATION NUMBER: 08/566,622
; FILING DATE: 04-DEC-1995
; APPLICATION NUMBER: 08/562,663
; FILING DATE: 27-NOV-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Meiklejohn, Ph.D., Anita L.
; REGISTRATION NUMBER: 35,283
; REFERENCE/DOCKET NUMBER: 07334/019004
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-542-5070
; TELEFAX: 617-542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 27:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-09-137-132-27
Query Match 0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 80;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 660 CACTACCTGCCCTTCAG 676
Db 1 CACTATTGCCCTTCAG 17

RESULT 122
US-08-864-564A-25
; Sequence 25, Application US/08864564A
; Patent No. 6395498
; GENERAL INFORMATION:
; APPLICANT: Tartaglia, Louis A.
; APPLICANT: Tepper, Robert I.
; APPLICANT: Culpepper, Janice A.
; APPLICANT: White, David W.
; TITLE OF INVENTION: THE OB RECEPTOR AND METHODS FOR
; TITLE OF INVENTION: THE OB RECEPTOR AND TREATMENT OF BODY WEIGHT DISORDERS,
; TITLE OF INVENTION: INCLUDING OBESITY AND CACHEXIA
; NUMBER OF SEQUENCES: 50
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/864,564A
; FILING DATE: 28-MAY-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/708,123
; FILING DATE: 03-SEP-1996
; APPLICATION NUMBER: 08/638,524
; FILING DATE: 26-APR-1996
; APPLICATION NUMBER: 08/599,455
; FILING DATE: 22-JAN-1996
; APPLICATION NUMBER: 08/583,153
; FILING DATE: 28-DEC-1995
; APPLICATION NUMBER: 08/570,142
; FILING DATE: 11-DEC-1995
; APPLICATION NUMBER: 08/569,485
; FILING DATE: 08-DEC-1995
; APPLICATION NUMBER: 08/566,622
; FILING DATE: 04-DEC-1995
; APPLICATION NUMBER: 08/562,663
; FILING DATE: 27-NOV-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Meiklejohn, Ph.D., Anita L.
; REGISTRATION NUMBER: 35,283
; REFERENCE/DOCKET NUMBER: 07334/019002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-542-5070
; TELEFAX: 617-542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 25:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-864-564A-25
Query Match 0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 80;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 660 CACTACCTGCCCTTCAG 676
Db 1 CACTATTGCCCTTCAG 17
```





; Sequence 27, Application US/09094410  
; Patent No. 6403552  
; GENERAL INFORMATION:  
; APPLICANT: Tartaglia, Louis A.  
; APPLICANT: Tepper, Robert I.  
; APPLICANT: Culpepper, Janice A.  
; APPLICANT: White, David W.  
; TITLE OF INVENTION: THE OB RECEPTOR AND METHODS FOR  
; TITLE OF INVENTION: THE DIAGNOSIS AND TREATMENT OF BODY WEIGHT DISORDERS,  
; TITLE OF INVENTION: INCLUDING OBESITY AND CACHEXIA  
; NUMBER OF SEQUENCES: 50  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Fish & Richardson, P.C.  
; STREET: 225 Franklin Street  
; CITY: Boston  
; STATE: MA  
; COUNTRY: US  
; ZIP: 02110-2804  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: Windows95  
; SOFTWARE: FastSEQ for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/094,410  
; FILING DATE: 09-JUN-1998  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/864,564  
; FILING DATE: 28-MAY-1997  
; APPLICATION NUMBER: 08/708,123  
; FILING DATE: 03-SEP-1996  
; APPLICATION NUMBER: 08/638,524  
; FILING DATE: 26-APR-1996  
; APPLICATION NUMBER: 08/599,455  
; FILING DATE: 22-JAN-1996  
; APPLICATION NUMBER: 08/583,153  
; FILING DATE: 28-DEC-1995  
; APPLICATION NUMBER: 08/570,142  
; FILING DATE: 11-DEC-1995  
; APPLICATION NUMBER: 08/569,485  
; FILING DATE: 08-DEC-1995  
; APPLICATION NUMBER: 08/566,622  
; FILING DATE: 04-DEC-1995  
; APPLICATION NUMBER: 08/562,663  
; FILING DATE: 27-NOV-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Meiklejohn, Ph.D., Anita L.  
; REGISTRATION NUMBER: 35,283  
; REFERENCE/DOCKET NUMBER: 07334/019003  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 617-542-5070  
; TELEFAX: 617-542-8906  
; TELEX: 200154  
; INFORMATION FOR SEQ ID NO: 27:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 17 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA  
US-09-094-410-27

Query Match 0.8%; Score 13.8; DB 1; Length 17;  
Best Local Similarity 88.2%; Pred. No. 80;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 660 CACTACCTGCCCTTCAG 676  
|||||  
Db 1 CACTATTGCCCTTCAG 17

RESULT 126  
US-08-708-123D-25

; Sequence 25, Application US/08708123D  
; Patent No. 6482927  
; GENERAL INFORMATION:  
; APPLICANT: Tartaglia, Louis A.  
; APPLICANT: Tepper, Robert I.  
; APPLICANT: Culpepper, Janice A.  
; APPLICANT: White, David W.  
; TITLE OF INVENTION: THE OB RECEPTOR AND METHODS FOR  
; TITLE OF INVENTION: THE DIAGNOSIS AND TREATMENT OF BODY WEIGHT DISORDERS,  
; TITLE OF INVENTION: INCLUDING OBESITY AND CACHEXIA  
; NUMBER OF SEQUENCES: 50  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Fish & Richardson, P.C.  
; STREET: 225 Franklin Street  
; CITY: Boston  
; STATE: MA  
; COUNTRY: US  
; ZIP: 02110-2804  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: Windows95  
; SOFTWARE: FastSEQ for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/708,123D  
; FILING DATE: 03-SEP-1996  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/638,524  
; FILING DATE: 26-APR-1996  
; APPLICATION NUMBER: 08/599,455  
; FILING DATE: 22-JAN-1996  
; APPLICATION NUMBER: 08/583,153  
; FILING DATE: 28-DEC-1995  
; APPLICATION NUMBER: 08/570,142  
; FILING DATE: 11-DEC-1995  
; APPLICATION NUMBER: 08/569,485  
; FILING DATE: 08-DEC-1995  
; APPLICATION NUMBER: 08/566,622  
; FILING DATE: 04-DEC-1995  
; APPLICATION NUMBER: 08/562,663  
; FILING DATE: 27-NOV-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Meiklejohn, Ph.D., Anita L.  
; REGISTRATION NUMBER: 35,283  
; REFERENCE/DOCKET NUMBER: 07334/019001  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 617-542-5070  
; TELEFAX: 617-542-8906  
; TELEX: 200154  
; INFORMATION FOR SEQ ID NO: 25:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 17 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA  
US-08-708-123D-25

Query Match 0.8%; Score 13.8; DB 1; Length 17;  
Best Local Similarity 88.2%; Pred. No. 80;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 660 CACTACCTGCCCTTCAG 676  
|||||  
Db 1 CACTATTGCCCTTCAG 17

RESULT 127  
US-08-708-123D-27  
; Sequence 27, Application US/08708123D  
; Patent No. 6482927  
; GENERAL INFORMATION:  
; APPLICANT: Tartaglia, Louis A.

APPLICANT: Tepper, Robert I.  
APPLICANT: Culpepper, Janice A.  
APPLICANT: White, David W.  
TITLE OF INVENTION: THE OB RECEPTOR AND METHODS FOR  
TITLE OF INVENTION: THE OB RECEPTOR AND TREATMENT OF BODY WEIGHT DISORDERS,  
TITLE OF INVENTION: INCLUDING OBESITY AND CACHEXIA  
NUMBER OF SEQUENCES: 50  
CORRESPONDENCE ADDRESS:  
STREET: 225 Franklin Street  
CITY: Boston  
STATE: MA  
COUNTRY: US  
ZIP: 02110-2804  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: Windows95  
SOFTWARE: FastSEQ for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/708,123D  
FILING DATE: 03-SEP-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/538,524  
FILING DATE: 26-APR-1996  
APPLICATION NUMBER: 08/599,455  
FILING DATE: 22-JAN-1996  
APPLICATION NUMBER: 08/583,153  
FILING DATE: 28-DEC-1995  
APPLICATION NUMBER: 08/570,142  
FILING DATE: 11-DEC-1995  
APPLICATION NUMBER: 08/569,485  
FILING DATE: 08-DEC-1995  
APPLICATION NUMBER: 08/566,622  
FILING DATE: 04-DEC-1995  
APPLICATION NUMBER: 08/562,663  
FILING DATE: 27-NOV-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Meiklejohn, Ph.D., Anita L.  
REGISTRATION NUMBER: 35,283  
REFERENCE/DOCKET NUMBER: 07334/019001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617-542-5070  
TELEFAX: 617-542-8906  
TELEX: 200154  
INFORMATION FOR SEQ ID NO: 27:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 17 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
US-08-708-123D-27

Query Match 0.8%; Score 13.8; DB 1; Length 17;  
Best Local Similarity 88.2%; Pred. No. 80;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 660 CACTACCTGCCCTTCAG 676  
||||| |||||||  
DB 1 CACTATTGCGCCTTCAG 17

RESULT 128  
US-08-583-153A-25  
Sequence 25, Application US/08583153A  
Patent No. 6506877  
GENERAL INFORMATION:  
APPLICANT: Tartaglia, Louis A.  
APPLICANT: Tepper, Robert I.  
APPLICANT: Culpepper, Janice A.  
TITLE OF INVENTION: THE OB RECEPTOR AND METHODS FOR THE  
TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF BODY WEIGHT DISORDERS, INCLUDING  
NUMBER OF SEQUENCES: 41  
CORRESPONDENCE ADDRESS:  
STREET: 225 Franklin Street  
CITY: Boston  
STATE: MA  
COUNTRY: US  
ZIP: 02110-2804  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette

TITLE OF INVENTION: OBESITY AND CACHEXIA  
NUMBER OF SEQUENCES: 41  
CORRESPONDENCE ADDRESS:  
STREET: 225 Franklin Street  
CITY: Boston  
STATE: MA  
COUNTRY: US  
ZIP: 02110-2804  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSEQ Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/583,153A  
FILING DATE: 28-DEC-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/570,142  
FILING DATE: 11-DEC-1995  
APPLICATION NUMBER: 08/569,485  
FILING DATE: 08-DEC-1995  
APPLICATION NUMBER: 08/566,622  
FILING DATE: 04-DEC-1995  
APPLICATION NUMBER: 08/562,663  
FILING DATE: 27-NOV-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Meiklejohn, Anita L.  
REGISTRATION NUMBER: 35,283  
REFERENCE/DOCKET NUMBER: 07334/016001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617-542-5070  
TELEFAX: 617-542-8906  
TELEX: 200154  
INFORMATION FOR SEQ ID NO: 25:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 17 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
US-08-583-153A-25

Query Match 0.8%; Score 13.8; DB 1; Length 17;  
Best Local Similarity 88.2%; Pred. No. 80;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 660 CACTACCTGCCCTTCAG 676  
||||| |||||||  
DB 1 CACTATTGCGCCTTCAG 17

RESULT 129  
US-08-583-153A-27  
Sequence 27, Application US/08583153A  
Patent No. 6506877  
GENERAL INFORMATION:  
APPLICANT: Tartaglia, Louis A.  
APPLICANT: Tepper, Robert I.  
APPLICANT: Culpepper, Janice A.  
TITLE OF INVENTION: THE OB RECEPTOR AND METHODS FOR THE  
TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF BODY WEIGHT DISORDERS, INCLUDING  
NUMBER OF SEQUENCES: 41  
CORRESPONDENCE ADDRESS:  
STREET: 225 Franklin Street  
CITY: Boston  
STATE: MA  
COUNTRY: US  
ZIP: 02110-2804  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSEQ Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/583,153A  
FILING DATE: 28-DEC-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/570,142  
FILING DATE: 11-DEC-1995  
APPLICATION NUMBER: 08/569,485  
FILING DATE: 08-DEC-1995  
APPLICATION NUMBER: 08/566,622  
FILING DATE: 04-DEC-1995  
APPLICATION NUMBER: 08/562,663  
FILING DATE: 27-NOV-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Meiklejohn, Anita L.  
REGISTRATION NUMBER: 35,283  
REFERENCE/DOCKET NUMBER: 07334/016001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617-542-5070  
TELEFAX: 617-542-8906  
TELEX: 200154  
INFORMATION FOR SEQ ID NO: 27:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 17 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
US-08-583-153A-27

Query Match 0.8%; Score 13.8; DB 1; Length 17;  
Best Local Similarity 88.2%; Pred. No. 80;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 660 CACTACTGCGCCTTCAG 676  
||||| |||||||  
Db 1 CACTATTGCGCCTTCAG 17

RESULT 130  
US-08-638-524B-25  
Sequence 25, Application US/08638524B  
Patent No. 6548269  
GENERAL INFORMATION:  
APPLICANT: Tartaglia, Louis A.  
APPLICANT: Tepper, Robert I.  
APPLICANT: Culpepper, Janice A.  
APPLICANT: White, David W.  
TITLE OF INVENTION: THE OB RECEPTOR AND METHODS FOR THE  
TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF BODY WEIGHT DISORDERS, INCLUDING OB  
TITLE OF INVENTION: CACHEXIA  
NUMBER OF SEQUENCES: 50  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fish & Richardson, P.C.  
STREET: 225 Franklin Street  
CITY: Boston  
STATE: MA  
COUNTRY: US  
ZIP: 02110-2804  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: Windows95  
SOFTWARE: FastSEQ for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/638,524B  
FILING DATE: 26-APR-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/599,455  
FILING DATE: 22-JAN-1996  
APPLICATION NUMBER: 08/583,153  
FILING DATE: 28-DEC-1995  
APPLICATION NUMBER: 08/570,142  
FILING DATE: 11-DEC-1995  
APPLICATION NUMBER: 08/569,485  
FILING DATE: 08-DEC-1995  
APPLICATION NUMBER: 08/566,622

FILING DATE: 28-DEC-1995  
APPLICATION NUMBER: 08/570,142  
FILING DATE: 11-DEC-1995  
APPLICATION NUMBER: 08/569,485  
FILING DATE: 08-DEC-1995  
APPLICATION NUMBER: 08/566,622  
FILING DATE: 04-DEC-1995  
APPLICATION NUMBER: 08/562,663  
FILING DATE: 27-NOV-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Meiklejohn, Ph.D., Anita L.  
REGISTRATION NUMBER: 35,283  
REFERENCE/DOCKET NUMBER: 07334/018001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617-542-5070  
TELEFAX: 617-542-8906  
TELEX: 200154  
INFORMATION FOR SEQ ID NO: 25:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 17 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
US-08-638-524B-25

Query Match 0.8%; Score 13.8; DB 1; Length 17;  
Best Local Similarity 88.2%; Pred. No. 80;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 660 CACTACTGCGCCTTCAG 676  
||||| |||||||  
Db 1 CACTATTGCGCCTTCAG 17

RESULT 131

US-08-638-524B-27  
Sequence 27, Application US/08638524B  
Patent No. 6548269  
GENERAL INFORMATION:  
APPLICANT: Tartaglia, Louis A.  
APPLICANT: Tepper, Robert I.  
APPLICANT: Culpepper, Janice A.  
APPLICANT: White, David W.  
TITLE OF INVENTION: THE OB RECEPTOR AND METHODS FOR THE  
TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF BODY WEIGHT DISORDERS, INCLUDING OB  
TITLE OF INVENTION: CACHEXIA  
NUMBER OF SEQUENCES: 50  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fish & Richardson, P.C.  
STREET: 225 Franklin Street  
CITY: Boston  
STATE: MA  
COUNTRY: US  
ZIP: 02110-2804  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: Windows95  
SOFTWARE: FastSEQ for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/638,524B  
FILING DATE: 26-APR-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/599,455  
FILING DATE: 22-JAN-1996  
APPLICATION NUMBER: 08/583,153  
FILING DATE: 28-DEC-1995  
APPLICATION NUMBER: 08/570,142  
FILING DATE: 11-DEC-1995  
APPLICATION NUMBER: 08/569,485  
FILING DATE: 08-DEC-1995  
APPLICATION NUMBER: 08/566,622

;  
; FILING DATE: 04-DEC-1995  
; APPLICATION NUMBER: 08/562,663  
; FILING DATE: 27-NOV-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Meiklejohn, Ph.D.; Anita L.  
; REGISTRATION NUMBER: 35,283  
; REFERENCE/DOCKET NUMBER: 07334/018001  
; TELEPHONE: 617-542-5070  
; TELEFAX: 617-542-8906  
; TELEX: 200154  
; INFORMATION FOR SEQ ID NO: 27:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 17 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA  
US-08-638-524B-27

Query Match 0.8%; Score 13.8; DB 1; Length 17;  
Best Local Similarity 88.2%; Pred. No. 80;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 660 CACTACCTGCCCTTCAG 676  
| | | | | | | | | | | | | | | | |  
Db 1 CACTATTGGCCCTTCAG 17

RESULT 132  
US-09-371-772B-3543  
; Sequence 3543, Application US/09371772B  
; Patent No. 6566127  
; GENERAL INFORMATION:  
; APPLICANT: Ribozyme Pharmaceuticals, Inc.  
; APPLICANT: Pavco, Pam  
; APPLICANT: McSwiggen, Jim  
; APPLICANT: Stinchcomb, Dan  
; APPLICANT: Escobedo, Jaime  
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re  
; FILE REFERENCE: MBH00,876-J (237/198)  
; CURRENT APPLICATION NUMBER: US/09/371,772B  
; CURRENT FILING DATE: 1999-08-10  
; PRIOR APPLICATION NUMBER: US 60/005,974  
; PRIOR FILING DATE: 1995-10-26  
; PRIOR APPLICATION NUMBER: US 08/584,040  
; PRIOR FILING DATE: 1996-01-08  
; NUMBER OF SEQ ID NOS: 14225  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 3543  
; LENGTH: 17  
; TYPE: RNA  
; ORGANISM: Mus sp.  
US-09-371-772B-3543

Query Match 0.8%; Score 13.8; DB 1; Length 17;  
Best Local Similarity 64.7%; Pred. No. 80;  
Matches 11; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy 1112 CTCCTCCTTGCTGGAGC 1128  
| | | | | | | | | | | | | | | | |  
Db 1 CUCCCCUUGCUGAAGC 17

RESULT 133  
US-09-371-772B-4182  
; Sequence 4182, Application US/09371772B  
; Patent No. 6566127  
; GENERAL INFORMATION:  
; APPLICANT: Ribozyme Pharmaceuticals, Inc.  
; APPLICANT: Pavco, Pam  
; APPLICANT: McSwiggen, Jim

; APPLICANT: Stinchcomb, Dan  
; APPLICANT: Escobedo, Jaime  
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re  
; FILE REFERENCE: MBH00,876-J (237/198)  
; CURRENT APPLICATION NUMBER: US/09/371,772B  
; CURRENT FILING DATE: 1999-08-10  
; PRIOR APPLICATION NUMBER: US 60/005,974  
; PRIOR FILING DATE: 1995-10-26  
; PRIOR APPLICATION NUMBER: US 08/584,040  
; PRIOR FILING DATE: 1996-01-08  
; NUMBER OF SEQ ID NOS: 14225  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 4182  
; LENGTH: 17  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-09-371-772B-4182

Query Match 0.8%; Score 13.8; DB 1; Length 17;  
Best Local Similarity 70.6%; Pred. No. 80;  
Matches 12; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 1115 CTCCTTGCTGGAGCAGC 1131  
| | | | | | | | | | | | | | | | |  
Db 1 CUCCUGGCGGAGCGC 17

RESULT 134  
US-09-866-108A-1895/c  
; Sequence 1895, Application US/09866108A  
; Patent No. 6686188  
; GENERAL INFORMATION:  
; APPLICANT: GU, Yizhong  
; APPLICANT: Ji, Yonggang  
; APPLICANT: PENN, Sharron G.  
; APPLICANT: HANZEL, David K.  
; APPLICANT: RANK, David R.  
; APPLICANT: CHEN, Wensheng  
; APPLICANT: SHANNON, Mark  
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE  
; FILE REFERENCE: AEOMICA-7  
; CURRENT APPLICATION NUMBER: US/09/866,108A  
; CURRENT FILING DATE: 2001-05-25  
; PRIOR APPLICATION NUMBER: US 60/207,456  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: GB 24263.6  
; PRIOR FILING DATE: 2000-10-04  
; PRIOR APPLICATION NUMBER: US 60/236,359  
; PRIOR FILING DATE: 2000-09-27  
; PRIOR APPLICATION NUMBER: PCT/US01/00666  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00667  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00664  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00669  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00665  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00668  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00663  
; PRIOR FILING DATE: 2001-01-30  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 15755  
; SOFTWARE: Aeomica Sequence Listing Engine  
; Patent No. 6686188  
; SEQ ID NO 1895  
; LENGTH: 17  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-866-108A-1895

Query Match 0.8%; Score 13.8; DB 1; Length 17;  
 Best Local Similarity 88.2%; Pred. No. 80;  
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 93 GAGAGTGGGCGAGTCT 109  
 ||||| || ||||| |||||  
 Db 17 GAGAGAGCCAGGTCT 1

RESULT 135  
 US-09-866-108A-2643/c  
 ; Sequence 2643, Application US/09866108A  
 ; Patent No. 6686188  
 ; GENERAL INFORMATION:  
 ; APPLICANT: GU, Yizhong  
 ; APPLICANT: JI, Yonggang  
 ; APPLICANT: PENN, Sharron G.  
 ; APPLICANT: HANZEL, David K.  
 ; APPLICANT: RANK, David R.  
 ; APPLICANT: CHEN, Wensheng  
 ; APPLICANT: SHANNON, Mark  
 ; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE  
 ; FILE REFERENCE: AEOMICA-7  
 ; CURRENT APPLICATION NUMBER: US/09/866,108A  
 ; CURRENT FILING DATE: 2001-05-25  
 ; PRIOR APPLICATION NUMBER: US 60/207,456  
 ; PRIOR FILING DATE: 2000-05-26  
 ; PRIOR APPLICATION NUMBER: GB 24263.6  
 ; PRIOR FILING DATE: 2000-10-04  
 ; PRIOR APPLICATION NUMBER: US 60/236,359  
 ; PRIOR FILING DATE: 2000-09-27  
 ; PRIOR APPLICATION NUMBER: PCT/US01/00666  
 ; PRIOR FILING DATE: 2001-01-30  
 ; PRIOR APPLICATION NUMBER: PCT/US01/00667  
 ; PRIOR FILING DATE: 2001-01-30  
 ; PRIOR APPLICATION NUMBER: PCT/US01/00664  
 ; PRIOR FILING DATE: 2001-01-30  
 ; PRIOR APPLICATION NUMBER: PCT/US01/00669  
 ; PRIOR FILING DATE: 2001-01-30  
 ; PRIOR APPLICATION NUMBER: PCT/US01/00665  
 ; PRIOR FILING DATE: 2001-01-30  
 ; PRIOR APPLICATION NUMBER: PCT/US01/00668  
 ; PRIOR FILING DATE: 2001-01-30  
 ; PRIOR APPLICATION NUMBER: PCT/US01/00663  
 ; PRIOR FILING DATE: 2001-01-30  
 ; Remaining Prior Application data removed - See File Wrapper or PALM.  
 ; NUMBER OF SEQ ID NOS: 15755  
 ; SOFTWARE: Aecomica Sequence Listing Engine  
 ; Patent No. 6686188  
 ; SEQ ID NO 7355  
 ; LENGTH: 17  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 ; US-09-866-108A-7355

Query Match 0.8%; Score 13.8; DB 1; Length 17;  
 Best Local Similarity 88.2%; Pred. No. 80;  
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 845 CTTCAGCAGCCGCCAA 861  
 ||||| ||||| ||||| |||||  
 Db 17 CTGCCAGGACCGCCAA 1

RESULT 136  
 US-09-866-108A-7355  
 ; Sequence 7355, Application US/09866108A  
 ; Patent No. 6686188  
 ; GENERAL INFORMATION:  
 ; APPLICANT: GU, Yizhong  
 ; APPLICANT: JI, Yonggang

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; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Acomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 7485
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-866-108A-7485

Query Match      0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 80;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1530 GCCACGCTCTCCCGC 1546
DB 17 GTCCAGCTCTCCTCGC 1

RESULT 138
US-09-866-108A-8568
; Sequence 8568, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: ACOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108A
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Acomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 8568
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
```

```
US-09-866-108A-8568

Query Match      0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 80;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 292 AGGATGCCCTAAATGAG 308
DB 1 AGGATGACCTGAATGAG 17

RESULT 139
US-09-866-108A-8660
; Sequence 8660, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: ACOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108A
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Acomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 8660
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-866-108A-8660

Query Match      0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 80;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 267 CTAGAAGAAGCCAGAA 283
DB 1 CTGGAGGAAGCCAGAA 17

RESULT 140
US-09-866-108A-8661
; Sequence 8661, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
```

```
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108A
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aeomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 8663
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-8663

Query Match 0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 80;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 270 GAGGAGCCCAAGAGAA 286
Db 1 GAGGAGCCCAAGAGAA 17

RESULT 142
US-09-866-108A-8664
; Sequence 8664, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108A
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aeomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 8664
; LENGTH: 17
; TYPE: DNA

Qy 268 TAGAGAGCCCAAGAG 284
Db 1 TGAGGAGCCCAAGAG 17

RESULT 141
US-09-866-108A-8663
; Sequence 8663, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108A
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
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; ORGANISM: Homo sapiens  
US-09-866-108A-9686

Query Match 0.8%; Score 13.8; DB 1; Length 17;  
Best Local Similarity 88.2%; Pred. No. 80;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 271 AAGAAGCCCAAGAAG 287  
| | | | | | | | | | | | | | | | | | |  
Db 1 AGGAAGCCCAAGAAG 17

## RESULT 143

US-09-866-108A-9687/c  
; Sequence 9687, Application US/09866108A

; Patent No. 6686188

; GENERAL INFORMATION:

; APPLICANT: GU, Yizhong

; APPLICANT: JI, Yonggang

; APPLICANT: PENN, Sharron G.

; APPLICANT: HANZEL, David K.

; APPLICANT: RANK, David R.

; APPLICANT: CHEN, Wensheng

; APPLICANT: SHANNON, Mark

; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE

; FILE REFERENCE: AEOICA-7

; CURRENT APPLICATION NUMBER: US/09/866,108A

; CURRENT FILING DATE: 2001-05-25

; PRIOR APPLICATION NUMBER: US 60/207,456

; PRIOR FILING DATE: 2000-05-26

; PRIOR APPLICATION NUMBER: GB 24263.6

; PRIOR FILING DATE: 2000-10-04

; PRIOR APPLICATION NUMBER: US 60/236,359

; PRIOR FILING DATE: 2000-09-27

; PRIOR APPLICATION NUMBER: PCT/US01/00666

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00667

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00664

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00669

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00665

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00668

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00663

; PRIOR FILING DATE: 2001-01-30

; Remaining Prior Application data removed - See File Wrapper or PALM.

; SOFTWARE: Aecomica Sequence Listing Engine

; Patent No. 6686188

; SEQ ID NO 9687

; LENGTH: 17

; TYPE: DNA

; ORGANISM: Homo sapiens

US-09-866-108A-9687

Query Match 0.8%; Score 13.8; DB 1; Length 17;  
Best Local Similarity 88.2%; Pred. No. 80;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 93 GAGAGTGGCGAGTCTCT 109  
| | | | | | | | | | | | | | | | | | |  
Db 17 GAGAGTGGCGAGTCTCT 1

## RESULT 144

US-09-866-108A-9688/c

; Sequence 9688, Application US/09866108A

; Patent No. 6686188

; GENERAL INFORMATION:

; APPLICANT: GU, Yizhong

; APPLICANT: JI, Yonggang  
; APPLICANT: PENN, Sharron G.  
; APPLICANT: HANZEL, David K.  
; APPLICANT: RANK, David R.  
; APPLICANT: CHEN, Wensheng  
; APPLICANT: SHANNON, Mark

; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE

; FILE REFERENCE: AEOICA-7

; CURRENT APPLICATION NUMBER: US/09/866,108A

; CURRENT FILING DATE: 2001-05-25

; PRIOR APPLICATION NUMBER: US 60/207,456

; PRIOR FILING DATE: 2000-05-26

; PRIOR APPLICATION NUMBER: GB 24263.6

; PRIOR FILING DATE: 2000-10-04

; PRIOR APPLICATION NUMBER: US 60/236,359

; PRIOR FILING DATE: 2000-09-27

; PRIOR APPLICATION NUMBER: PCT/US01/00666

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00667

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00664

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00669

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00665

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00668

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00663

; PRIOR FILING DATE: 2001-01-30

; Remaining Prior Application data removed - See File Wrapper or PALM.  
; SOFTWARE: Aecomica Sequence Listing Engine  
; Patent No. 6686188  
; SEQ ID NO 9688

; LENGTH: 17

; TYPE: DNA

; ORGANISM: Homo sapiens

US-09-866-108A-9688

Query Match 0.8%; Score 13.8; DB 1; Length 17;  
Best Local Similarity 88.2%; Pred. No. 80;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 92 GGAGAGTGGCGAGTCC 108  
| | | | | | | | | | | | | | | | | | |  
Db 17 GGAGAGTGGCGAGTCC 1

## RESULT 145

US-09-866-108A-9689/c

; Sequence 9689, Application US/09866108A

; Patent No. 6686188

; GENERAL INFORMATION:

; APPLICANT: GU, Yizhong

; APPLICANT: JI, Yonggang

; APPLICANT: PENN, Sharron G.

; APPLICANT: HANZEL, David K.

; APPLICANT: RANK, David R.

; APPLICANT: CHEN, Wensheng

; APPLICANT: SHANNON, Mark

; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE

; FILE REFERENCE: AEOICA-7

; CURRENT APPLICATION NUMBER: US/09/866,108A

; CURRENT FILING DATE: 2001-05-25

; PRIOR APPLICATION NUMBER: US 60/207,456

; PRIOR FILING DATE: 2000-05-26

; PRIOR APPLICATION NUMBER: GB 24263.6

; PRIOR FILING DATE: 2000-10-04

; PRIOR APPLICATION NUMBER: US 60/236,359

; PRIOR FILING DATE: 2000-09-27

; PRIOR APPLICATION NUMBER: PCT/US01/00666

; PRIOR FILING DATE: 2001-01-30

```
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Acomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 9689
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-9689

Query Match          0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 80;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 91 GGGAGAGTGGCAGGTC 107
   |||||
Db 17 GGGAGAGTGGCAGGTC 1

RESULT 146
US-09-685-664B-3543
; Sequence 3543, Application US/09685664B
; Patent No. 6818447
; GENERAL INFORMATION:
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggan, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for Treatment of Diseases or Conditions Related to Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MBH00-876-K (400/021)
; CURRENT APPLICATION NUMBER: US/09/685,664B
; CURRENT FILING DATE: 2000-10-10
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; PRIOR APPLICATION NUMBER: US 09/371,772
; PRIOR FILING DATE: 1999-08-10
; NUMBER OF SEQ ID NOS: 8231
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3543
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Mus musculus
US-09-685-664B-3543

Query Match          0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 64.7%; Pred. No. 80;
Matches 11; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1112 CTCCTCCTTGCTGGAGC 1128
   |||||
Db 1 CUCCCCCUUGCUGAAGC 17

RESULT 147
US-09-093-972C-874/c
; Sequence 874, Application US/09093972C
; Patent No. 6825174
```

```
; GENERAL INFORMATION:
; APPLICANT: Nyce, Jonathan W.
; TITLE OF INVENTION: COMPOSITION, FORMULATIONS & METHOD FOR PREVENTION
; & TREATMENT OF DISEASES & CONDITIONS ASSOCIATED WITH
; BRONCHOCONSTRICTION, ALLERGY(IES) & INFLAMMATION
; NUMBER OF SEQUENCES: 996
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: EPIGENESIS PHARMACEUTICALS, INC.
; STREET: 7 Clarke Drive
; CITY: Cranbury
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 08512
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/093,972C
; FILING DATE: 09-Jun-1998
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/472,527
; FILING DATE: 7-June-1995
; APPLICATION NUMBER: US 08/757,024
; FILING DATE: 26-11-1996
; APPLICATION NUMBER: US 08/472,527
; FILING DATE: 7-June-1995
; APPLICATION NUMBER: US 09/016,464
; FILING DATE: 30-January-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Anzel, Viviana
; REGISTRATION NUMBER: 30,930
; REFERENCE/DOCKET NUMBER: EPI-00672
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 609-409-3035
; TELEFAX: 413-254-9245
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 874:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; SEQUENCE DESCRIPTION: SEQ ID NO: 874:
US-09-093-972C-874

Query Match          0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 80;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1530 GCCCAGCCTCTCCCGC 1546
   |||||
Db 17 GCCCAGCCTGTGCCCGC 1

RESULT 148
US-09-093-972C-944/c
; Sequence 944, Application US/09093972C
; Patent No. 6825174
; GENERAL INFORMATION:
; APPLICANT: Nyce, Jonathan W.
; TITLE OF INVENTION: COMPOSITION, FORMULATIONS & METHOD FOR PREVENTION
; & TREATMENT OF DISEASES & CONDITIONS ASSOCIATED WITH
; BRONCHOCONSTRICTION, ALLERGY(IES) & INFLAMMATION
; NUMBER OF SEQUENCES: 996
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: EPIGENESIS PHARMACEUTICALS, INC.
; STREET: 7 Clarke Drive
; CITY: Cranbury
; STATE: New Jersey
```

; COUNTRY: USA  
; ZIP: 08512  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/093,972C  
; FILING DATE: 09-Jun-1998  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/472,527  
; FILING DATE: 7-June-1995  
; APPLICATION NUMBER: US 08/757,024  
; FILING DATE: 26-11-1996  
; APPLICATION NUMBER: US 08/472,527  
; FILING DATE: 7-June-1995  
; APPLICATION NUMBER: US 09/016,464  
; FILING DATE: 30-January-1998  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Amzel, Viviana  
; REGISTRATION NUMBER: 30,930  
; REFERENCE/DOCKET NUMBER: EPI-00672  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 609-409-3035  
; TELEFAX: 413-254-9245  
; TELEX: <Unknown>  
; INFORMATION FOR SEQ ID NO: 944:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 17 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
; SEQUENCE DESCRIPTION: SEQ ID NO: 944:  
US-09-093-972C-944

Query Match 0.8%; Score 13.8; DB 1; Length 17;  
Best Local Similarity 88.2%; Pred. No. 80;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1530 GCCCAGCCTCTCCCGC 1546  
Db 17 GCCCAGCCTGTCCCGC 1

RESULT 149  
PCT-US95-05812-21/c  
; Sequence 21, Application PC/TUS9505812  
; GENERAL INFORMATION:  
; APPLICANT: Wakisaka, Jack  
; TITLE OF INVENTION: ANTISENSE INHIBITION OF  
; TITLE OF INVENTION: HEPATITIS C VIRUS  
; NUMBER OF SEQUENCES: 38  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Fish & Richardson  
; STREET: 225 Franklin Street  
; CITY: Boston  
; STATE: Massachusetts  
; COUNTRY: U.S.A.  
; ZIP: 02110-2804  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
; COMPUTER: IBM PS/2 Model 502 or 55SX  
; OPERATING SYSTEM: MS-DOS (Version 5.0)  
; SOFTWARE: WordPerfect (Version 5.1)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US95/05812  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/240,382  
; FILING DATE: 10 May 1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Clark, Paul T.  
; REGISTRATION NUMBER: 30,162  
; REFERENCE/DOCKET NUMBER: 00786/221001  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617) 542-5070  
; TELEFAX: (617) 542-8906  
; TELEX: 200154  
; INFORMATION FOR SEQ ID NO: 21:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 17  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; PCT-US95-05812-21

Query Match 0.8%; Score 13.8; DB 1; Length 17;  
Best Local Similarity 88.2%; Pred. No. 80;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 222 CTCATAGAAAAACAAA 238  
Db 17 CTCATAGAAAAACAAA 1

RESULT 150  
US-08-291-932A-160  
; Sequence 160, Application US/08291932A  
; Patent No. 5658780  
; GENERAL INFORMATION:  
; APPLICANT: Stinchcomb, Dan T.  
; APPLICANT: Draper, Kenneth G.  
; APPLICANT: McSwiggen, James  
; TITLE OF INVENTION: RIBOZYME TREATMENT OF  
; TITLE OF INVENTION: DISEASES OR CONDITIONS  
; TITLE OF INVENTION: RELATED TO LEVELS OF  
; TITLE OF INVENTION: NF-KB  
; NUMBER OF SEQUENCES: 830  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Lyon & Lyon  
; STREET: 633 West Fifth Street  
; STREET: Suite 4700  
; CITY: Los Angeles  
; STATE: California  
; COUNTRY: U.S.A.  
; ZIP: 90071-2066  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
; MEDIUM TYPE: storage  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: IBM P.C. DOS 5.0  
; SOFTWARE: Word Perfect 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/291,932A  
; FILING DATE: August 15, 1994  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; PRIOR APPLICATION DATA: including application  
; PRIOR APPLICATION DATA: described below:  
; APPLICATION NUMBER: 08/245,466  
; FILING DATE: May 18, 1994  
; APPLICATION NUMBER: 07/987,132  
; FILING DATE: December 7, 1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Warburg, Richard J.  
; REGISTRATION NUMBER: 32,327  
; REFERENCE/DOCKET NUMBER: 208/157  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (213) 489-1600  
; TELEFAX: (213) 955-0440  
; TELEX: 67-3510

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; INFORMATION FOR SEQ ID NO: 160:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 15 base pairs
;   TYPE: nucleic acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
US-08-291-932A-160

Query Match          0.8%; Score 13.4; DB 1; Length 15;
Best Local Similarity 86.7%; Pred. No. 71;
Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      1507 CCAGCCTCCAGGCC 1521
DB      1 CCAGCCUCCAGGCUC 15

RESULT 151
US-09-180-437-151/c
; Sequence 151, Application US/09180437
; Patent No. 6251873
; GENERAL INFORMATION:
; APPLICANT: FUKUSAKO, Shioji
; APPLICANT: MORISAWA, Yoshifumi
; APPLICANT: KUSUYAMA, Takeshi
; TITLE OF INVENTION: Antisense Compounds to CD14
; FILE REFERENCE: 1110-209P
; CURRENT APPLICATION NUMBER: US/09/180,437
; CURRENT FILING DATE: 1998-11-06
; EARLIER APPLICATION NUMBER: PCT/JP98/00953
; EARLIER FILING DATE: 1998-03-09
; EARLIER APPLICATION NUMBER: 09-053518 JAPAN
; EARLIER FILING DATE: 1997-03-07
; NUMBER OF SEQ ID NOS: 289
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 151
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:other nucleic
US-09-180-437-151

Query Match          0.8%; Score 13.4; DB 1; Length 15;
Best Local Similarity 93.3%; Pred. No. 71;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      432 TGCAGAGTGGGTCA 446
DB      15 TGCAGCAGTGGGTCA 1

RESULT 152
US-09-081-646-174/c
; Sequence 174, Application US/09081646
; Patent No. 6333152
; GENERAL INFORMATION:
; APPLICANT: Kinzler, Kenneth
; APPLICANT: Vogelstein, Bert
; APPLICANT: Zhang, Lin
; APPLICANT: Zhou, Wei
; TITLE OF INVENTION: Gene Expression Profiles in No. 6333152mal and
; FILE REFERENCE: 01107.74664
; CURRENT APPLICATION NUMBER: US/09/081,646
; CURRENT FILING DATE: 1998-05-20
; EARLIER APPLICATION NUMBER: 60/047,352
; EARLIER FILING DATE: 1997-05-21
; NUMBER OF SEQ ID NOS: 871
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 174
; LENGTH: 15

; INFORMATION FOR SEQ ID NO: 160:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 15 base pairs
;   TYPE: nucleic acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
US-08-291-932A-160

Query Match          0.8%; Score 13.4; DB 1; Length 15;
Best Local Similarity 86.7%; Pred. No. 71;
Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      1507 CCAGCCTCCAGGCC 1521
DB      1 CCAGCCUCCAGGCUC 15

RESULT 151
US-09-180-437-151/c
; Sequence 151, Application US/09180437
; Patent No. 6251873
; GENERAL INFORMATION:
; APPLICANT: FUKUSAKO, Shioji
; APPLICANT: MORISAWA, Yoshifumi
; APPLICANT: KUSUYAMA, Takeshi
; TITLE OF INVENTION: Antisense Compounds to CD14
; FILE REFERENCE: 1110-209P
; CURRENT APPLICATION NUMBER: US/09/180,437
; CURRENT FILING DATE: 1998-11-06
; EARLIER APPLICATION NUMBER: PCT/JP98/00953
; EARLIER FILING DATE: 1998-03-09
; EARLIER APPLICATION NUMBER: 09-053518 JAPAN
; EARLIER FILING DATE: 1997-03-07
; NUMBER OF SEQ ID NOS: 289
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 151
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:other nucleic
US-09-180-437-151

Query Match          0.8%; Score 13.4; DB 1; Length 15;
Best Local Similarity 93.3%; Pred. No. 71;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      432 TGCAGAGTGGGTCA 446
DB      15 TGCAGCAGTGGGTCA 1

RESULT 152
US-09-081-646-174/c
; Sequence 174, Application US/09081646
; Patent No. 6333152
; GENERAL INFORMATION:
; APPLICANT: Kinzler, Kenneth
; APPLICANT: Vogelstein, Bert
; APPLICANT: Zhang, Lin
; APPLICANT: Zhou, Wei
; TITLE OF INVENTION: Gene Expression Profiles in No. 6333152mal and
; FILE REFERENCE: 01107.74664
; CURRENT APPLICATION NUMBER: US/09/081,646
; CURRENT FILING DATE: 1998-05-20
; EARLIER APPLICATION NUMBER: 60/047,352
; EARLIER FILING DATE: 1997-05-21
; NUMBER OF SEQ ID NOS: 871
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 174
; LENGTH: 15

; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-081-646-174

Query Match          0.8%; Score 13.4; DB 1; Length 15;
Best Local Similarity 93.3%; Pred. No. 71;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      807 GCTCAGCAGGCCATG 821
DB      15 GCCCAGCAGGCCATG 1

RESULT 153
US-09-081-646-783/c
; Sequence 783, Application US/09081646
; Patent No. 6333152
; GENERAL INFORMATION:
; APPLICANT: Kinzler, Kenneth
; APPLICANT: Vogelstein, Bert
; APPLICANT: Zhang, Lin
; APPLICANT: Zhou, Wei
; TITLE OF INVENTION: Gene Expression Profiles in No. 6333152mal and
; FILE REFERENCE: 01107.74664
; CURRENT APPLICATION NUMBER: US/09/081,646
; CURRENT FILING DATE: 1998-05-20
; EARLIER APPLICATION NUMBER: 60/047,352
; EARLIER FILING DATE: 1997-05-21
; NUMBER OF SEQ ID NOS: 871
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 783
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-081-646-783

Query Match          0.8%; Score 13.4; DB 1; Length 15;
Best Local Similarity 93.3%; Pred. No. 71;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      807 GCTCAGCAGGCCATG 821
DB      15 GCCCAGCAGGCCATG 1

RESULT 154
US-09-736-116-75/c
; Sequence 75, Application US/09736116
; Patent No. 6727085
; GENERAL INFORMATION:
; APPLICANT: Sejersgard, Tina
; APPLICANT: Mikkelsen, Frank
; TITLE OF INVENTION: Subtilase variants having an improved wash performance on egg stain
; FILE REFERENCE: 6108.410
; CURRENT APPLICATION NUMBER: US/09/736,116
; CURRENT FILING DATE: 2001-05-24
; NUMBER OF SEQ ID NOS: 105
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 75
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Primer
US-09-736-116-75

Query Match          0.8%; Score 13.4; DB 1; Length 15;
Best Local Similarity 93.3%; Pred. No. 71;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1076 GCTGCTAAGTCCTA 1090
DB      15 GCTGCTAAGTCCTA 1090
```

Db 15 GCTGTTAAAGTCCTA 1

RESULT 155  
US-08-173-489C-32/c  
; Sequence 32, Application US/08173489C  
; Patent No. 5861244  
; GENERAL INFORMATION:  
; APPLICANT: WANG, C. -G.  
; APPLICANT: HEPBURN, A. G.  
; TITLE OF INVENTION: GENETIC SEQUENCE ASSAY USING DNA  
; TITLE OF INVENTION: TRIPLE-STRAND FORMATION.  
; NUMBER OF SEQUENCES: 365  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: PROFILE DIAGNOSTIC SCIENCES, INC.,  
; STREET: 510 EAST 73RD STREET,  
; CITY: NEW YORK  
; STATE: NEW YORK  
; COUNTRY: USA  
; ZIP: 10021.  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5 inch, 1.44MB storage  
; COMPUTER: IBM PC/XT/AT  
; OPERATING SYSTEM: MS-DOS version 6.2  
; SOFTWARE: Wordperfect version 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/173,489C  
; FILING DATE: 22 DEC 1993  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/968,436  
; FILING DATE: 29 OCT 1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Handelman, Joseph H.  
; REGISTRATION NUMBER: 26,179  
; REFERENCE/DOCKET NUMBER: U9518-6  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (attorney) (212) 708-1880  
; TELEPHONE: (attorney) (212) 246-8959  
; INFORMATION FOR SEQ ID NO: 32:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 16 bases  
; TYPE: Nucleic Acid  
; STRANDEDNESS: single stranded  
; TOPOLOGY: linear  
; MOLECULE TYPE: other nucleic acid  
; DESCRIPTION: third strand derived from dystrophin  
; DESCRIPTION: sequence region in Seq ID No. 586124431  
; HYPOTHETICAL: Yes  
; ANTI-SENSE: NO  
; PUBLICATION INFORMATION:  
; RELEVANT RESIDUES IN SEQ ID NO: 32 :FROM 1 TO 16  
US-08-173-489C-32

Query Match 0.8%; Score 13.4; DB 1; Length 16;  
Best Local Similarity 93.3%; Pred. No. 81;  
Matches 14; Conservative 0; Mismatches 1; Indels 0;  
Gaps 0;

QY 271 AGAAGCCAAAGA 285  
Db 15 AAGAAGCAAAGA 1

RESULT 156  
US-09-034-205-67  
; Sequence 67, Application US/09034205  
; Patent No. 6194149  
; GENERAL INFORMATION:  
; APPLICANT: Lyamichev, Victor I.  
; APPLICANT: Brow, Mary Ann D.  
; APPLICANT: Fors, Lance  
; APPLICANT: Neri, Bruce P.  
; TITLE OF INVENTION: TARGET-DEPENDENT REACTIONS USING  
; TITLE OF INVENTION: STRUCTURE-BRIDGING OLIGONUCLEOTIDES  
; NUMBER OF SEQUENCES: 68  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: MEDLEN & CARROLL, LLP  
; STREET: 220 Montgomery Street, Suite 2200  
; CITY: San Francisco  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94104  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/034,205  
; FILING DATE:  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: MacKnight, Kamrin T.  
; REGISTRATION NUMBER: 38,230  
; REFERENCE/DOCKET NUMBER: FORS-03268  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 705-8410  
; TELEFAX: (415) 397-8338  
; INFORMATION FOR SEQ ID NO: 67:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 16 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: other nucleic acid  
; DESCRIPTION: /desc = "DNA"  
US-09-034-205-67

Query Match 0.8%; Score 13.4; DB 1; Length 16;  
Best Local Similarity 93.3%; Pred. No. 81;  
Matches 14; Conservative 0; Mismatches 1; Indels 1;  
QY 1508 CAGCCTCCAGGCC 1522  
Db 2 CAGCCTCCAGGCC 16

RESULT 157  
US-09-034-205-68  
; Sequence 68, Application US/09034205  
; Patent No. 6194149  
; GENERAL INFORMATION:  
; APPLICANT: Lyamichev, Victor I.  
; APPLICANT: Brow, Mary Ann D.  
; APPLICANT: Fors, Lance  
; APPLICANT: Neri, Bruce P.  
; TITLE OF INVENTION: TARGET-DEPENDENT REACTIONS USING  
; TITLE OF INVENTION: STRUCTURE-BRIDGING OLIGONUCLEOTIDES  
; NUMBER OF SEQUENCES: 68  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: MEDLEN & CARROLL, LLP  
; STREET: 220 Montgomery Street, Suite 2200  
; CITY: San Francisco  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94104  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/034,205  
; FILING DATE:  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: MacKnight, Kamrin T.  
; REGISTRATION NUMBER: 38,230  
; REFERENCE/DOCKET NUMBER: FORS-03268  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 705-8410  
; TELEFAX: (415) 397-8338  
; INFORMATION FOR SEQ ID NO: 67:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 16 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: other nucleic acid  
; DESCRIPTION: /desc = "DNA"  
US-09-034-205-67

Db 15 GCTGTTAAAGTCCTA 1

RESULT 155  
US-08-173-489C-32/c  
Sequence 32, Application US/08173489C  
Patent No. 5861244  
GENERAL INFORMATION:  
APPLICANT: WANG, C. -G.  
APPLICANT: HEPBURN, A. G.  
TITLE OF INVENTION: GENETIC SEQUENCE ASSAY USING DNA  
TITLE OF INVENTION: TRIPLE-STRAND FORMATION.  
NUMBER OF SEQUENCES: 365  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: PROFILE DIAGNOSTIC SCIENCES, INC.,  
STREET: 510 EAST 73RD STREET,  
CITY: NEW YORK  
STATE: NEW YORK  
COUNTRY: USA  
ZIP: 10021.  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch, 1.44MB storage  
COMPUTER: IBM PC/XT/AT  
OPERATING SYSTEM: MS-DOS version 6.2  
SOFTWARE: Wordperfect version 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/173,489C  
FILING DATE: 22 DEC 1993  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/968,436  
FILING DATE: 29 OCT 1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Handelman, Joseph H.  
REGISTRATION NUMBER: 26,179  
REFERENCE/DOCKET NUMBER: U9518-6  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (attorney) (212) 708-1880  
TELEPHONE: (attorney) (212) 246-8959  
INFORMATION FOR SEQ ID NO: 32:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 16 bases  
TYPE: Nucleic Acid  
STRANDEDNESS: single stranded  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid  
DESCRIPTION: third strand derived from dystrophin  
DESCRIPTION: sequence region in Seq ID No. 586124431  
HYPOTHETICAL: Yes  
ANTI-SENSE: NO  
PUBLICATION INFORMATION:  
RELEVANT RESIDUES IN SEQ ID NO: 32 :FROM 1 TO 16  
US-08-173-489C-32

Query Match 0.8%; Score 13.4; DB 1; Length 16;  
Best Local Similarity 93.3%; Pred. No. 81;  
Matches 14; Conservative 0; Mismatches 1; Indels 0;  
QY 271 AGAAGCCAAAGA 285  
Db 15 AAGAAGCAAAGA 1

RESULT 156  
US-09-034-205-67  
Sequence 67, Application US/09034205  
Patent No. 6194149  
GENERAL INFORMATION:  
APPLICANT: Lyamichev, Victor I.  
APPLICANT: Brow, Mary Ann D.  
APPLICANT: Fors, Lance  
TITLE OF INVENTION: TARGET-DEPENDENT REACTIONS USING  
TITLE OF INVENTION: TARGET-DEPENDENT REACTIONS USING  
NUMBER OF SEQUENCES: 68  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MEDLEN & CARROLL, LLP  
STREET: 220 Montgomery Street, Suite 2200  
CITY: San Francisco  
STATE: CA  
COUNTRY: USA  
ZIP: 94104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/034,205  
FILING DATE:  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: MacKnight, Kamrin T.  
REGISTRATION NUMBER: 38,230  
REFERENCE/DOCKET NUMBER: FORS-03268  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 705-8410  
TELEFAX: (415) 397-8338  
INFORMATION FOR SEQ ID NO: 67:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 16 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid  
DESCRIPTION: /desc = "DNA"  
US-09-034-205-67

Query Match 0.8%; Score 13.4; DB 1; Length 16;  
Best Local Similarity 93.3%; Pred. No. 81;  
Matches 14; Conservative 0; Mismatches 1; Indels 1;  
QY 1508 CAGCCTCCAGGCC 1522  
Db 2 CAGCCTCCAGGCC 16

RESULT 157  
US-09-034-205-68  
Sequence 68, Application US/09034205  
Patent No. 6194149  
GENERAL INFORMATION:  
APPLICANT: Lyamichev, Victor I.  
APPLICANT: Brow, Mary Ann D.  
APPLICANT: Fors, Lance  
APPLICANT: Neri, Bruce P.  
TITLE OF INVENTION: TARGET-DEPENDENT REACTIONS USING  
TITLE OF INVENTION: STRUCTURE-BRIDGING OLIGONUCLEOTIDES  
NUMBER OF SEQUENCES: 68  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MEDLEN & CARROLL, LLP  
STREET: 220 Montgomery Street, Suite 2200  
CITY: San Francisco  
STATE: CA  
COUNTRY: USA  
ZIP: 94104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/034,205  
FILING DATE:  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: MacKnight, Kamrin T.  
REGISTRATION NUMBER: 38,230  
REFERENCE/DOCKET NUMBER: FORS-03268  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 705-8410  
TELEFAX: (415) 397-8338  
INFORMATION FOR SEQ ID NO: 67:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 16 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid  
DESCRIPTION: /desc = "DNA"  
US-09-034-205-67

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Query Match          0.8%; Score 13.4; DB 1; Length 16;
Best Local Similarity 93.3%; Pred. No. 81;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1508 CAGCCTCCAGGCCCC 1522
      |||||
DB       2 CAGCCTCCAGGACCC 16

RESULT 159
US-09-677-218B-68
; Sequence 68, Application US/09677218B
; Patent No. 6355437
; GENERAL INFORMATION:
; APPLICANT: Lyamichev, Victor I.
;           Brow, Mary Ann D.
;           Fors, Lance P.
;           Neri, Bruce P.
; TITLE OF INVENTION: TARGET-DEPENDENT REACTIONS USING
;                   STRUCTURE-BRIDGING OLIGONUCLEOTIDES
; NUMBER OF SEQUENCES: 68
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MEDLEN & CARROLL, LLP
; STREET: 220 Montgomery Street, Suite 2200
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/677,218B
; FILING DATE: 02-Oct-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/034,205
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: MacKnight, Kamrin T.
; REGISTRATION NUMBER: 38,210
; REFERENCE/DOCKET NUMBER: FORS-03268
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 705-8410
; TELEFAX: (415) 397-8338
; INFORMATION FOR SEQ ID NO: 68:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "DNA"
; SEQUENCE DESCRIPTION: SEQ ID NO: 68:
;
US-09-677-218B-68

Query Match          0.8%; Score 13.4; DB 1; Length 16;
Best Local Similarity 93.3%; Pred. No. 81;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1508 CAGCCTCCAGGCCCC 1522
      |||||
DB       2 CAGCCTCCAGGACCC 16

RESULT 160
US-09-677-192-67
; Sequence 67, Application US/09677192
; Patent No. 6358691
; GENERAL INFORMATION:

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; APPLICANT: Lyamichev, Victor I.
; APPLICANT: Brow, Mary Ann D.
; APPLICANT: Fors, Lance
; APPLICANT: Neri, Bruce P.
; TITLE OF INVENTION: TARGET-DEPENDENT REACTIONS USING STRUCTURE-BRIDGING
; FILE REFERENCE: OLIGONUCLEOTIDES
; FILE REFERENCE: FORS-04708
; CURRENT APPLICATION NUMBER: US/09/677,192
; CURRENT FILING DATE: 2000-10-02
; PRIOR APPLICATION NUMBER: 09/034,205
; PRIOR FILING DATE: 1998-03-03
; NUMBER OF SEQ ID NOS: 68
; SOFTWARE: PatentIn ver. 2.0
; SEQ ID NO 67
; LENGTH: 16
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-677-192-67

Query Match          0.8%; Score 13.4; DB 1; Length 16;
Best Local Similarity 93.3%; Pred. No. 81;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1508 CAGCCTCCAGGCCCC 1522
Db 2 CAGCCTCCAGGACCC 16
|||||

RESULT 161
US-09-677-192-68
; Sequence 68, Application US/09677192
; Patent No. 6358691
; GENERAL INFORMATION:
; APPLICANT: Lyamichev, Victor I.
; APPLICANT: Brow, Mary Ann D.
; APPLICANT: Fors, Lance
; APPLICANT: Neri, Bruce P.
; TITLE OF INVENTION: TARGET-DEPENDENT REACTIONS USING STRUCTURE-BRIDGING
; FILE REFERENCE: OLIGONUCLEOTIDES
; FILE REFERENCE: FORS-04708
; CURRENT APPLICATION NUMBER: US/09/677,192
; CURRENT FILING DATE: 2000-10-02
; PRIOR APPLICATION NUMBER: 09/034,205
; PRIOR FILING DATE: 1998-03-03
; NUMBER OF SEQ ID NOS: 68
; SOFTWARE: PatentIn ver. 2.0
; SEQ ID NO 68
; LENGTH: 16
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-677-192-68

Query Match          0.8%; Score 13.4; DB 1; Length 16;
Best Local Similarity 93.3%; Pred. No. 81;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1508 CAGCCTCCAGGCCCC 1522
Db 2 CAGCCTCCAGGACCC 16
|||||

RESULT 162
US-09-402-618B-67
; Sequence 67, Application US/09402618B
; Patent No. 6709815
; GENERAL INFORMATION:
; APPLICANT: Dong, Fang
; APPLICANT: Lyamichev, Victor
; APPLICANT: Prudent, James
```

```
; APPLICANT: Fors, Lance
; APPLICANT: Neri, Bruce
; APPLICANT: Brow, Mary Ann
; APPLICANT: Anderson, Todd
; APPLICANT: Dahlberg, James
; TITLE OF INVENTION: Target-Dependent Reactions Using Structure-Bridging Oligonucleotides
; FILE REFERENCE: FORS-04012
; CURRENT APPLICATION NUMBER: US/09/402,618B
; CURRENT FILING DATE: 2000-07-18
; PRIOR APPLICATION NUMBER: PCT/US98/03194
; PRIOR FILING DATE: 1998-05-05
; NUMBER OF SEQ ID NOS: 128
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 67
; LENGTH: 16
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-09-402-618B-67

Query Match          0.8%; Score 13.4; DB 1; Length 16;
Best Local Similarity 93.3%; Pred. No. 81;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1508 CAGCCTCCAGGCCCC 1522
Db 2 CAGCCTCCAGGACCC 16
|||||

RESULT 163
US-09-402-618B-68
; Sequence 68, Application US/09402618B
; Patent No. 6709815
; GENERAL INFORMATION:
; APPLICANT: Dong, Fang
; APPLICANT: Lyamichev, Victor
; APPLICANT: Prudent, James
; APPLICANT: Fors, Lance
; APPLICANT: Neri, Bruce
; APPLICANT: Brow, Mary Ann
; APPLICANT: Anderson, Todd
; APPLICANT: Dahlberg, James
; TITLE OF INVENTION: Target-Dependent Reactions Using Structure-Bridging Oligonucleotides
; FILE REFERENCE: FORS-04012
; CURRENT APPLICATION NUMBER: US/09/402,618B
; CURRENT FILING DATE: 2000-07-18
; PRIOR APPLICATION NUMBER: PCT/US98/03194
; PRIOR FILING DATE: 1998-05-05
; NUMBER OF SEQ ID NOS: 128
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 68
; LENGTH: 16
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-09-402-618B-68

Query Match          0.8%; Score 13.4; DB 1; Length 16;
Best Local Similarity 93.3%; Pred. No. 81;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1508 CAGCCTCCAGGCCCC 1522
Db 2 CAGCCTCCAGGACCC 16
|||||

RESULT 164
US-08-796-031-1/c
; Sequence 1, Application US/08796031
; Patent No. 5849903
; GENERAL INFORMATION:
```

```

; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/561,302
; FILING DATE: 1 January 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Fish, Robert D.
; REGISTRATION NUMBER: 33,880
; REFERENCE/DOCKET NUMBER: 213/015-CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 714-525-3433
; TELEFAX: 714-525-3303
; TELEX:
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: DNA (genomic)
;
US-09-055-913-1
;
Query Match 0.8%; Score 13; DB 1; Length 14;
Best Local Similarity 100.0%; Pred.No. 71;
Matches 13; Conservative 0; Mismatches 0; Indels

Qy 1239 GTTCCTCCGGTG 1251
Db 13 GTTCCTCCGGTG 1

RESULT 166
US-08-985-090-23/c
; Sequence 23 Application US/08985090
; Patent No. 5885893
; GENERAL INFORMATION:
; APPLICANT: Andrew D.J. Goodearl
; TITLE OF INVENTION: MUSCARINIC RECEPTORS AND USES THEREFOR
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/985,090
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Jean M. Silveri
; REGISTRATION NUMBER: 39,030
; REFERENCE/DOCKET NUMBER: MNI-032
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)742-4214
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
;
US-08-985-090-23
;
Query Match 0.8%; Score 12.8; DB 1; Length 16;

```



```
Best Local Similarity 87.5%; Pred. No. 99;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 72 GTGGGCTGCTGCTGA 87
    |||||
Db 16 GTGGGCTGCTGCTCA 1

RESULT 167
US-08-757-024-875/c
; Sequence 875, Application US/08757024
; Patent No. 6025339
; GENERAL INFORMATION:
; APPLICANT: Nyce, Jonathan W.
; TITLE OF INVENTION: METHOD OF TREATMENT FOR ASTHMA
; NUMBER OF SEQUENCES: 952
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BELL, SELTZER, PARK & GIBSON
; STREET: P.O. Drawer 34009
; CITY: Charlotte
; STATE: No. 6025339th Carolina
; COUNTRY: USA
; ZIP: 28234
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/757,024
; FILING DATE: 26-NOV-1996
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Sibley, Kenneth D.
; REGISTRATION NUMBER: 31,665
; REFERENCE/DOCKET NUMBER: 5218-41
; TELEPHONE: 919-881-3140
; TELEFAX: 919-881-3175
; TELEX: 575102
; INFORMATION FOR SEQ ID NO: 875:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-757-024-882
Query Match 0.8%; Score 12.8; DB 1; Length 16;
Best Local Similarity 87.5%; Pred. No. 99;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1530 GCCAGCCTCTCCCGC 1545
    |||||
Db 16 GCCAGCCTGTGCCG 1

RESULT 169
US-08-757-024-945/c
; Sequence 945, Application US/08757024
; Patent No. 6025339
; GENERAL INFORMATION:
; APPLICANT: Nyce, Jonathan W.
; TITLE OF INVENTION: METHOD OF TREATMENT FOR ASTHMA
; NUMBER OF SEQUENCES: 952
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BELL, SELTZER, PARK & GIBSON
; STREET: P.O. Drawer 34009
; CITY: Charlotte
; STATE: No. 6025339th Carolina
; COUNTRY: USA
; ZIP: 28234
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/757,024
; FILING DATE: 26-NOV-1996
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Sibley, Kenneth D.
; REGISTRATION NUMBER: 31,665
; REFERENCE/DOCKET NUMBER: 5218-41
; TELEPHONE: 919-881-3140
; TELEFAX: 919-881-3175
; TELEX: 575102
; INFORMATION FOR SEQ ID NO: 945:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-757-024-875
Query Match 0.8%; Score 12.8; DB 1; Length 16;
Best Local Similarity 87.5%; Pred. No. 99;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1531 CCCAGCCTCTCCCGC 1546
    |||||
Db 16 CCCAGCCTGTGCCG 1

RESULT 168
US-08-757-024-882/c
; Sequence 882, Application US/08757024
; Patent No. 6025339
; GENERAL INFORMATION:
; APPLICANT: Nyce, Jonathan W.
; TITLE OF INVENTION: METHOD OF TREATMENT FOR ASTHMA
; NUMBER OF SEQUENCES: 952
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BELL, SELTZER, PARK & GIBSON
; STREET: P.O. Drawer 34009
; CITY: Charlotte
; STATE: No. 6025339th Carolina
; COUNTRY: USA
; ZIP: 28234
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ZIP: 08512  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/093,972C  
FILING DATE: 09-Jun-1998  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/472,527  
FILING DATE: 7-June-1995  
APPLICATION NUMBER: US 08/757,024  
FILING DATE: 26-11-1996  
APPLICATION NUMBER: US 08/472,527  
FILING DATE: 7-June-1995  
APPLICATION NUMBER: US 09/016,464  
FILING DATE: 30-January-1998  
ATTORNEY/AGENT INFORMATION:  
NAME: Amzel, Viviana  
REGISTRATION NUMBER: 30,930  
REFERENCE/DOCKET NUMBER: EPI-00672  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 609-409-3035  
TELEFAX: 413-254-9245  
TELEX: <Unknown>  
INFORMATION FOR SEQ ID NO: 875:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 16 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
SEQUENCE DESCRIPTION: SEQ ID NO: 875:  
US-09-093-972C-875  
Query Match 0.8%; Score 12.8; DB 1; Length 16;  
Best Local Similarity 87.5%; Pred. No. 99;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 1531 CCACGCTCTCCCGC 1546  
|||||  
Db 16 CCACGCTGTGCCGC 1  
RESULT 173  
US-09-093-972C-882/c  
; Sequence 882, Application US/09093972C  
; Patent No. 6825174  
; GENERAL INFORMATION:  
; APPLICANT: Nyce, Jonathan W.  
; TITLE OF INVENTION: COMPOSITION, FORMULATIONS & METHOD FOR PREVENTION  
; & TREATMENT OF DISEASES & CONDITIONS ASSOCIATED WITH  
; BRONCHOCONSTRICTION, ALLERGY(IES) & INFLAMMATION  
; NUMBER OF SEQUENCES: 996  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: EPIGENESIS PHARMACEUTICALS, INC.  
; STREET: 7 Clarke Drive  
; CITY: Cranbury  
; STATE: New Jersey  
; COUNTRY: USA  
; ZIP: 08512  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/093,972C  
; FILING DATE: 09-Jun-1998  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/472,527  
FILING DATE: 7-June-1995  
APPLICATION NUMBER: US 08/757,024  
FILING DATE: 26-11-1996  
APPLICATION NUMBER: US 08/472,527  
FILING DATE: 7-June-1995  
APPLICATION NUMBER: US 09/016,464  
FILING DATE: 30-January-1998  
ATTORNEY/AGENT INFORMATION:  
NAME: Amzel, Viviana  
REGISTRATION NUMBER: 30,930  
REFERENCE/DOCKET NUMBER: EPI-00672  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 609-409-3035  
TELEFAX: 413-254-9245  
TELEX: <Unknown>  
INFORMATION FOR SEQ ID NO: 882:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 16 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
SEQUENCE DESCRIPTION: SEQ ID NO: 882:  
US-09-093-972C-882  
Query Match 0.8%; Score 12.8; DB 1; Length 16;  
Best Local Similarity 87.5%; Pred. No. 99;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 1530 GCCACGCTCTCCCGC 1545  
|||||  
Db 16 GCCACGCTGTGCCGC 1  
RESULT 174  
US-09-093-972C-945/c  
; Sequence 945, Application US/09093972C  
; Patent No. 6825174  
; GENERAL INFORMATION:  
; APPLICANT: Nyce, Jonathan W.  
; TITLE OF INVENTION: COMPOSITION, FORMULATIONS & METHOD FOR PREVENTION  
; & TREATMENT OF DISEASES & CONDITIONS ASSOCIATED WITH  
; BRONCHOCONSTRICTION, ALLERGY(IES) & INFLAMMATION  
; NUMBER OF SEQUENCES: 996  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: EPIGENESIS PHARMACEUTICALS, INC.  
; STREET: 7 Clarke Drive  
; CITY: Cranbury  
; STATE: New Jersey  
; COUNTRY: USA  
; ZIP: 08512  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/093,972C  
; FILING DATE: 09-Jun-1998  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/472,527  
; FILING DATE: 7-June-1995  
; APPLICATION NUMBER: US 08/757,024  
; FILING DATE: 26-11-1996  
; APPLICATION NUMBER: US 08/472,527  
; FILING DATE: 7-June-1995  
; APPLICATION NUMBER: US 09/016,464  
; FILING DATE: 30-January-1998  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Amzel, Viviana  
; REGISTRATION NUMBER: 30,930

REFERENCE/DOCKET NUMBER: EPI-00672  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 609-409-3035  
TELEFAX: 413-254-9245  
TELEX: <Unknown>  
INFORMATION FOR SEQ ID NO: 945:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 16 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
SEQUENCE DESCRIPTION: SEQ ID NO: 945:  
US-09-093-972C-945

Query Match 0.8%; Score 12.8; DB 1; Length 16;  
Best Local Similarity 87.5%; Pred. No. 99;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1530 GCCACGCTCTCCCG 1545  
Db 16 GCCACGCTGTGCCG 1

## RESULT 175

US-08-650-093C-97  
Sequence 97, Application US/08650093C  
Patent No. 6391542

## GENERAL INFORMATION:

APPLICANT: Kevin P. Anderson et al.  
TITLE OF INVENTION: Compositions And Methods For Treatment Of  
Hepatitis C Virus-Associated Diseases

NUMBER OF SEQUENCES: 118

CORRESPONDENCE ADDRESS:

ADDRESSEE: LICATA & TYRRELL P.C.

STREET: 66 E. Main Street

CITY: Marlton

STATE: NJ

COUNTRY: USA

ZIP: 08053

## COMPUTER READABLE FORM:

MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE

COMPUTER: IBM Compatible

OPERATING SYSTEM: Windows 95

SOFTWARE: WORDPERFECT 6.1 for Windows

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/650,093C

FILING DATE: 17-MAY-1996

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/452,841

FILING DATE: May 30, 1995

APPLICATION NUMBER: 08/397,220

FILING DATE: March 9, 1995

APPLICATION NUMBER: 07/945,289

FILING DATE: September 10, 1992

ATTORNEY/AGENT INFORMATION:

NAME: Jane Massey Licata

REGISTRATION NUMBER: 32,257

REFERENCE/DOCKET NUMBER: ISPH-

TELECOMMUNICATION INFORMATION:

TELEPHONE: (609) 779-2400

TELEFAX: (609) 779-8488

INFORMATION FOR SEQ ID NO: 97:

SEQUENCE CHARACTERISTICS:

LENGTH: 14

TYPE: Nucleic Acid

STRANDEDNESS: Single

TOPOLOGY: Linear

ANTI-SENSE: No

SEQUENCE DESCRIPTION: SEQ ID NO: 97:

US-08-650-093C-97

Query Match 0.8%; Score 12.4; DB 1; Length 14;  
Best Local Similarity 85.7%; Pred. No. 88;  
Matches 12; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1510 GCCTCCAGGCCCC 1523  
Db 1 GCCUCCAGGACCC 14

## RESULT 176

US-09-720-435A-172

Sequence 172, Application US/09720435A

Patent No. 6803187

GENERAL INFORMATION:

APPLICANT: Stuyver, Lieven

TITLE OF INVENTION: Method for detection of drug-selected mutations in the protease

TITLE OF INVENTION: Gene

FILE REFERENCE: 11362.0030.PCUS00 INNS:030

CURRENT APPLICATION NUMBER: US/09/720,435A

CURRENT FILING DATE: 2001-06-25

PRIOR APPLICATION NUMBER: PCT/EP99/04317

PRIOR FILING DATE: 1999-06-22

PRIOR APPLICATION NUMBER: 98870143.9

PRIOR FILING DATE: 1998-06-24

NUMBER OF SEQ ID NOS: 529

SOFTWARE: Patentin version 3.2

SEQ ID NO 172

LENGTH: 14

TYPE: DNA

ORGANISM: Aids-associated retrovirus

US-09-720-435A-172

Query Match 0.8%; Score 12.4; DB 1; Length 14;  
Best Local Similarity 92.9%; Pred. No. 88;  
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 37 GAATTGGAGGCATG 50  
Db 1 GAATTGGAGGCTTG 14

## RESULT 177

US-08-050-073-65

Sequence 65, Application US/08050073

Patent No. 5567809

GENERAL INFORMATION:

APPLICANT: Apple, Raymond J.

APPLICANT: Begovich, Ann B.

APPLICANT: Bugawan, Teodorica L.

APPLICANT: Erlich, Henry A.

APPLICANT: Griffith, Robert L.

APPLICANT: Scharf, Stephen J.

TITLE OF INVENTION: Methods and Reagents for HLA DRbeta DNA

TITLE OF INVENTION: Typing

NUMBER OF SEQUENCES: 315

CORRESPONDENCE ADDRESS:

ADDRESSEE: Hoffmann-La Roche Inc.

STREET: 340 Kingsland Street

CITY: Nutley

STATE: New Jersey

COUNTRY: U.S.A.

ZIP: 07110

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/050,073

FILING DATE:

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Petry, Douglas A.

REGISTRATION NUMBER: 35,321  
REFERENCE/DOCKET NUMBER: 8769  
TELEPHONE: (510) 814-2974  
TELEFAX: (510) 814-2977  
INFORMATION FOR SEQ ID NO: 65:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 15 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: genomic DNA  
US-08-050-073-65

Query Match 0.8%; Score 12.4; DB 1; Length 15;  
Best Local Similarity 92.9%; Pred. No. 1e+02;  
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1074 GAGCTGCTTAAGTC 1087  
|||||  
DB 1 GAGCTGCTTAAGTC 14

RESULT 178  
US-08-182-968A-2  
Sequence 2, Application US/08182968A  
Patent No. 5610054  
GENERAL INFORMATION:  
APPLICANT: Draper, Kenneth G.  
TITLE OF INVENTION: METHOD AND REAGENT FOR  
TITLE OF INVENTION: INHIBITING HEPATITIS C  
TITLE OF INVENTION: VIRUS REPLICATION  
NUMBER OF SEQUENCES: 497  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lyon & Lyon  
STREET: 633 West Fifth Street  
CITY: Suite 4700  
STATE: Los Angeles  
CITY: California  
COUNTRY: U.S.A.  
ZIP: 90071-2066

COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
MEDIUM TYPE: storage  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: IBM P.C. DOS 5.0  
SOFTWARE: Word Perfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/182,968A  
FILING DATE: 13-JANUARY-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/882,888  
FILING DATE: 14-MAY-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Warburg, Richard J.  
REGISTRATION NUMBER: 32,327  
REFERENCE/DOCKET NUMBER: 205/277  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 15  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-182-968A-2

Query Match 0.8%; Score 12.4; DB 1; Length 15;  
Best Local Similarity 85.7%; Pred. No. 1e+02;  
Matches 12; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1508 CAGCCTCCAGGCC 1521  
|||||  
DB 2 CAGCCUCCAGGACC 15  
RESULT 179  
US-08-182-968A-422/c  
Sequence 422, Application US/08182968A  
Patent No. 5610054  
GENERAL INFORMATION:  
APPLICANT: Draper, Kenneth G.  
TITLE OF INVENTION: METHOD AND REAGENT FOR  
TITLE OF INVENTION: INHIBITING HEPATITIS C  
TITLE OF INVENTION: VIRUS REPLICATION  
NUMBER OF SEQUENCES: 497  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lyon & Lyon  
STREET: 633 West Fifth Street  
CITY: Suite 4700  
STATE: Los Angeles  
CITY: California  
COUNTRY: U.S.A.  
ZIP: 90071-2066  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
MEDIUM TYPE: storage  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: IBM P.C. DOS 5.0  
SOFTWARE: Word Perfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/182,968A  
FILING DATE: 13-JANUARY-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/882,888  
FILING DATE: 14-MAY-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Warburg, Richard J.  
REGISTRATION NUMBER: 32,327  
REFERENCE/DOCKET NUMBER: 205/277  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
INFORMATION FOR SEQ ID NO: 422:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 15  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-182-968A-422

Query Match 0.8%; Score 12.4; DB 1; Length 15;  
Best Local Similarity 92.9%; Pred. No. 1e+02;  
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 870 ATACGAGAAGCGCA 883  
|||||  
DB 15 ATACGATAAGCGCA 2

RESULT 180  
US-08-182-968A-423/c  
Sequence 423, Application US/08182968A  
Patent No. 5610054  
GENERAL INFORMATION:  
APPLICANT: Draper, Kenneth G.  
TITLE OF INVENTION: METHOD AND REAGENT FOR  
TITLE OF INVENTION: INHIBITING HEPATITIS C  
TITLE OF INVENTION: VIRUS REPLICATION  
NUMBER OF SEQUENCES: 497  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lyon & Lyon  
STREET: 633 West Fifth Street

```
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/182,968A
; FILING DATE: 13-JANUARY-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/882,888
; FILING DATE: 14-MAY-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 205/277
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 423:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-182-968A-423

Query Match 0.8%; Score 12.4; DB 1; Length 15;
Best Local Similarity 92.9%; Pred. No. 1e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 870 ATACGAGAAGCGCA 883
Db 14 ATACGATAGGCGA 1

RESULT 181
US-08-363-240A-237
; Sequence 237, Application US/08363240A
; Patent No. 5705388
; GENERAL INFORMATION:
; APPLICANT: Couture, Larry
; APPLICANT: McSwiggen, James
; APPLICANT: Bisgaier, Charles
; APPLICANT: Pape, Michael
; TITLE OF INVENTION: METHOD AND REAGENT FOR
; TITLE OF INVENTION: PREVENTION, INHIBITION OF
; TITLE OF INVENTION: PROGRESSION AND REGRESSION
; NUMBER OF SEQUENCES: 1243
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/363,240A
; FILING DATE: December 23, 1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 210/096
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 528:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 base pairs
```

```
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 210/096
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 237:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-363-240A-237

Query Match 0.8%; Score 12.4; DB 1; Length 15;
Best Local Similarity 71.4%; Pred. No. 1e+02;
Matches 10; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1309 TAGAGTCTCCAGG 1322
Db 1 UAGAAGUCUCCAG 14

RESULT 182
US-08-363-240A-528
; Sequence 528, Application US/08363240A
; Patent No. 5705388
; GENERAL INFORMATION:
; APPLICANT: Couture, Larry
; APPLICANT: McSwiggen, James
; APPLICANT: Bisgaier, Charles
; APPLICANT: Pape, Michael
; TITLE OF INVENTION: METHOD AND REAGENT FOR
; TITLE OF INVENTION: PREVENTION, INHIBITION OF
; TITLE OF INVENTION: PROGRESSION AND REGRESSION
; NUMBER OF SEQUENCES: 1243
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/363,240A
; FILING DATE: December 23, 1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 210/096
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 528:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 base pairs
```

TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-363-240A-528

Query Match 0.8%; Score 12.4; DB 1; Length 15;  
Best Local Similarity 78.6%; Pred. No. 1e+02;  
Matches 11; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 841 CGGCCTTCCAGCAC 854  
Db 2 CGGCCUCCAGCGC 15

## RESULT 183

US-08-363-240A-529  
Sequence 529, Application US/08363240A  
Patent No. 5705388

GENERAL INFORMATION:  
APPLICANT: Couture, Larry  
APPLICANT: McSwiggen, James  
APPLICANT: Bisgaier, Charles  
APPLICANT: Pape, Michael  
TITLE OF INVENTION: METHOD AND REAGENT FOR  
PREVENTION, INHIBITION OF  
TITLE OF INVENTION: PROGRESSION AND REGRESSION  
TITLE OF INVENTION: OF VASCULAR DISEASES  
NUMBER OF SEQUENCES: 1243  
CORRESPONDENCE ADDRESS:

ADDRESSEE: Lyon & Lyon  
STREET: 633 West Fifth Street  
CITY: Los Angeles  
STATE: California  
COUNTRY: U.S.A.  
ZIP: 90071

COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
MEDIUM TYPE: storage  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: IBM P.C. DOS 5.0  
SOFTWARE: Word Perfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/363,240A  
FILING DATE: December 23, 1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:

FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Warburg, Richard  
REGISTRATION NUMBER: 32,327  
REFERENCE/DOCKET NUMBER: 210/096  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
TELEX: 67-3510  
INFORMATION FOR SEQ ID NO: 529:

SEQUENCE CHARACTERISTICS:  
LENGTH: 15 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-363-240A-529

Query Match 0.8%; Score 12.4; DB 1; Length 15;  
Best Local Similarity 78.6%; Pred. No. 1e+02;  
Matches 11; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 841 CGGCCTTCCAGCAC 854  
Db 1 CGGCCUCCAGCGC 14

## RESULT 184

US-08-363-240A-724/c  
Sequence 724, Application US/08363240A  
Patent No. 5705388

GENERAL INFORMATION:  
APPLICANT: Couture, Larry  
APPLICANT: McSwiggen, James  
APPLICANT: Bisgaier, Charles  
APPLICANT: Pape, Michael  
TITLE OF INVENTION: METHOD AND REAGENT FOR  
PREVENTION, INHIBITION OF  
TITLE OF INVENTION: PROGRESSION AND REGRESSION  
TITLE OF INVENTION: OF VASCULAR DISEASES  
NUMBER OF SEQUENCES: 1243  
CORRESPONDENCE ADDRESS:

ADDRESSEE: Lyon & Lyon  
STREET: 633 West Fifth Street  
CITY: Los Angeles  
STATE: California  
COUNTRY: U.S.A.  
ZIP: 90071

COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
MEDIUM TYPE: storage  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: IBM P.C. DOS 5.0  
SOFTWARE: Word Perfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/363,240A  
FILING DATE: December 23, 1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:

FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Warburg, Richard  
REGISTRATION NUMBER: 32,327  
REFERENCE/DOCKET NUMBER: 210/096  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
TELEX: 67-3510

INFORMATION FOR SEQ ID NO: 724:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 15 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-363-240A-724

Query Match 0.8%; Score 12.4; DB 1; Length 15;  
Best Local Similarity 92.9%; Pred. No. 1e+02;  
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1471 CAGAGAGAGCTCTG 1484  
Db 14 CGGAGAGAGCTCTG 1

## RESULT 185

US-08-311-486C-533/c  
Sequence 533, Application US/08311486C  
Patent No. 5811300

GENERAL INFORMATION:  
APPLICANT: Sean Sullivan  
APPLICANT: Kenneth Draper  
APPLICANT: Kevin Kisich  
APPLICANT: Dan T. Stinchcomb  
APPLICANT: James McSwiggen  
TITLE OF INVENTION: RIBOZYME TREATMENT OF  
DISEASES OR CONDITIONS  
TITLE OF INVENTION: RELATED TO LEVELS OF  
TNF-





PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/505,314  
FILING DATE: 05-APR-1990  
ATTORNEY/AGENT INFORMATION:  
NAME: Brook Esq., David E.  
REGISTRATION NUMBER: 22,592  
REFERENCE/DOCKET NUMBER: RC90-01AZ  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 861-6240  
TELEFAX: (617) 861-9540  
INFORMATION FOR SEQ ID NO: 30:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 15 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: unknown  
US-08-452-724A-30

Query Match 0.8%; Score 12.4; DB 1; Length 15;  
Best Local Similarity 92.9%; Pred. No. 1e+02;  
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1303 TCCTGTAGATC 1316  
DB 14 TCCATGTAGATC 1

RESULT 188  
US-08-774-306A-2  
; Sequence 2, Application US/08774306A  
; Patent No. 5869253  
; GENERAL INFORMATION:  
; APPLICANT: Draper, Kenneth G.  
; TITLE OF INVENTION: METHOD AND REAGENT FOR  
; TITLE OF INVENTION: INHIBITING HEPATITIS C  
; TITLE OF INVENTION: VIRUS REPLICATION  
; NUMBER OF SEQUENCES: 497  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Lyon & Lyon  
; STREET: 633 West Fifth Street  
; STREET: Suite 4700  
; CITY: Los Angeles  
; STATE: California  
; COUNTRY: U.S.A.  
; ZIP: 90071-2066  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
; MEDIUM TYPE: storage  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: IBM P.C. DOS 5.0  
; SOFTWARE: Word Perfect 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/774,306A  
; FILING DATE: December 26, 1996  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/182,968  
; FILING DATE: January 13, 1994  
; APPLICATION NUMBER: 07/882,888  
; FILING DATE: May 14, 1992  
; NAME: Warburg, Richard J.  
; ATTORNEY/AGENT INFORMATION:  
; REGISTRATION NUMBER: 32,327  
; REFERENCE/DOCKET NUMBER: 223/227  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (213) 489-1600  
; TELEFAX: (213) 955-0440  
; TELEX: 67-3510  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 15  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear

US-08-774-306A-2

Query Match 0.8%; Score 12.4; DB 1; Length 15;  
Best Local Similarity 85.7%; Pred. No. 1e+02;  
Matches 12; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
QY 1508 CAGCCTCAGGCC 1521  
DB 2 CAGCCUCCAGGACC 15

RESULT 189  
US-08-774-306A-422/c  
; Sequence 422, Application US/08774306A  
; Patent No. 5869253  
; GENERAL INFORMATION:  
; APPLICANT: Draper, Kenneth G.  
; TITLE OF INVENTION: METHOD AND REAGENT FOR  
; TITLE OF INVENTION: INHIBITING HEPATITIS C  
; TITLE OF INVENTION: VIRUS REPLICATION  
; NUMBER OF SEQUENCES: 497  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Lyon & Lyon  
; STREET: 633 West Fifth Street  
; STREET: Suite 4700  
; CITY: Los Angeles  
; STATE: California  
; COUNTRY: U.S.A.  
; ZIP: 90071-2066  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
; MEDIUM TYPE: storage  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: IBM P.C. DOS 5.0  
; SOFTWARE: Word Perfect 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/774,306A  
; FILING DATE: December 26, 1996  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/182,968  
; FILING DATE: January 13, 1994  
; APPLICATION NUMBER: 07/882,888  
; FILING DATE: May 14, 1992  
; NAME: Warburg, Richard J.  
; ATTORNEY/AGENT INFORMATION:  
; REGISTRATION NUMBER: 32,327  
; REFERENCE/DOCKET NUMBER: 223/227  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (213) 489-1600  
; TELEFAX: (213) 955-0440  
; TELEX: 67-3510  
; INFORMATION FOR SEQ ID NO: 422:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 15  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
US-08-774-306A-422

Query Match 0.8%; Score 12.4; DB 1; Length 15;  
Best Local Similarity 92.9%; Pred. No. 1e+02;  
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 870 ATACGAGAGCGCA 883  
DB 15 ATACGATAGGCGA 2

RESULT 190  
US-08-774-306A-423/c  
; Sequence 423, Application US/08774306A  
; Patent No. 5869253  
; GENERAL INFORMATION:

```
; APPLICANT: Draper, Kenneth G.
; TITLE OF INVENTION: METHOD AND REAGENT FOR
; TITLE OF INVENTION: INHIBITING HEPATITIS C
; TITLE OF INVENTION: VIRUS REPLICATION
; NUMBER OF SEQUENCES: 497
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/774,306A
; FILING DATE: December 26, 1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/182,968
; FILING DATE: January 13, 1994
; APPLICATION NUMBER: 07/882,888
; FILING DATE: May 14, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 223/227
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 423:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-774-306A-423

Query Match 0.8%; Score 12.4; DB 1; Length 15;
Best Local Similarity 92.9%; Pred. No. 1e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 870 ATACGAGAAGCGGA 883
Db 14 ATACGATAAGCGGA 1
|||||:|||||

RESULT 191
US-09-064-156A-2
; Sequence 2, Application US/09064156A
; Patent No. 6132966
; GENERAL INFORMATION:
; APPLICANT: Draper, Kenneth G.
; TITLE OF INVENTION: METHOD AND REAGENT FOR
; TITLE OF INVENTION: INHIBITING HEPATITIS C
; TITLE OF INVENTION: VIRUS REPLICATION
; NUMBER OF SEQUENCES: 498
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/064,156A
; FILING DATE: April 21, 1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/774,306
; FILING DATE: December 26, 1996
; APPLICATION NUMBER: 08/182,968
; FILING DATE: January 13, 1994
; APPLICATION NUMBER: 07/882,888
; FILING DATE: May 14, 1992
; ATTORNEY/AGENT INFORMATION:
```

```
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/064,156A
; FILING DATE: April 21, 1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/774,306
; FILING DATE: December 26, 1996
; APPLICATION NUMBER: 08/182,968
; FILING DATE: January 13, 1994
; APPLICATION NUMBER: 07/882,888
; FILING DATE: May 14, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 234/083
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-09-064-156A-2

Query Match 0.8%; Score 12.4; DB 1; Length 15;
Best Local Similarity 85.7%; Pred. No. 1e+02;
Matches 12; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1508 CAGCCTCCAGGCC 1521
Db 2 CAGCCUCCAGGACC 15
|||||:|||||

RESULT 192
US-09-064-156A-422/c
; Sequence 422, Application US/09064156A
; Patent No. 6132966
; GENERAL INFORMATION:
; APPLICANT: Draper, Kenneth G.
; TITLE OF INVENTION: METHOD AND REAGENT FOR
; TITLE OF INVENTION: INHIBITING HEPATITIS C
; TITLE OF INVENTION: VIRUS REPLICATION
; NUMBER OF SEQUENCES: 498
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/064,156A
; FILING DATE: April 21, 1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/774,306
; FILING DATE: December 26, 1996
; APPLICATION NUMBER: 08/182,968
; FILING DATE: January 13, 1994
; APPLICATION NUMBER: 07/882,888
; FILING DATE: May 14, 1992
; ATTORNEY/AGENT INFORMATION:
```

```
/ NAME: Warburg, Richard J.
/ REGISTRATION NUMBER: 32,327
/ REFERENCE/DOCKET NUMBER: 234/083
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (213) 489-1600
/ TELEFAX: (213) 955-0440
/ TELEX: 67-3510
/ INFORMATION FOR SEQ ID NO: 422:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 15
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ US-09-064-156A-422

Query Match 0.8%; Score 12.4; DB 1; Length 15;
Best Local Similarity 92.9%; Pred. No. 1e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 870 ATACGAGNAGGCGA 883
Db 15 ATACGATAGGCGA 2

RESULT 193
US-09-064-156A-423/c
; Sequence 423, Application US/09064156A
; Patent No. 6132966
; GENERAL INFORMATION:
; APPLICANT: Draper, Kenneth G.
; TITLE OF INVENTION: METHOD AND REAGENT FOR
; TITLE OF INVENTION: INHIBITING HEPATITIS C
; TITLE OF INVENTION: VIRUS REPLICATION
; NUMBER OF SEQUENCES: 498
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: Storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/064,156A
; FILING DATE: April 21, 1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/774,306
; FILING DATE: December 26, 1996
; APPLICATION NUMBER: 08/192,968
; FILING DATE: January 13, 1994
; APPLICATION NUMBER: 07/882,888
; FILING DATE: May 14, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 234/083
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 423:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
/ US-09-064-156A-423
```

```
Query Match 0.8%; Score 12.4; DB 1; Length 15;
Best Local Similarity 92.9%; Pred. No. 1e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 870 ATACGAGNAGGCGA 883
Db 14 ATACGATAGGCGA 1

RESULT 194
US-09-081-646-126
; Sequence 126, Application US/09081646
; Patent No. 6333152
; GENERAL INFORMATION:
; APPLICANT: Kinzler, Kenneth
; APPLICANT: Vogelstein, Bert
; APPLICANT: Zhang, Lin
; APPLICANT: Zhou, Wei
; TITLE OF INVENTION: Gene Expression Profiles in No. 6333152mal and
; FILE REFERENCE: 01107.74664
; CURRENT APPLICATION NUMBER: US/09/081,646
; CURRENT FILING DATE: 1998-05-20
; EARLIER APPLICATION NUMBER: 60/047,352
; EARLIER FILING DATE: 1997-05-21
; NUMBER OF SEQ ID NOS: 871
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 126
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-081-646-126

Query Match 0.8%; Score 12.4; DB 1; Length 15;
Best Local Similarity 92.9%; Pred. No. 1e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1101 ATGCTCAACACCTC 1114
Db 2 ATGCTCAACATCTC 15

RESULT 195
US-09-081-646-326
; Sequence 326, Application US/09081646
; Patent No. 6333152
; GENERAL INFORMATION:
; APPLICANT: Kinzler, Kenneth
; APPLICANT: Vogelstein, Bert
; APPLICANT: Zhang, Lin
; APPLICANT: Zhou, Wei
; TITLE OF INVENTION: Gene Expression Profiles in No. 6333152mal and
; TITLE OF INVENTION: Cancer Cells
; FILE REFERENCE: 01107.74664
; CURRENT APPLICATION NUMBER: US/09/081,646
; CURRENT FILING DATE: 1998-05-20
; EARLIER APPLICATION NUMBER: 60/047,352
; EARLIER FILING DATE: 1997-05-21
; NUMBER OF SEQ ID NOS: 871
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 326
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-081-646-326

Query Match 0.8%; Score 12.4; DB 1; Length 15;
Best Local Similarity 92.9%; Pred. No. 1e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 923 CACGGGCTGCCTGC 936
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Search completed: September 13, 2005, 10:44:50  
Job time : 5 secs

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: September 13, 2005, 10:46:55 ; Search time 10 Seconds  
(without alignments)  
3.440 Million cell updates/sec

Title: us-10-828-394-1  
Perfect score: 1643  
Sequence: 1 gaattccgcgtgaccgag.....taaaactgtctgtgagctg 1643

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 0.5

Searched: 497 seqs, 10470 residues

Total number of hits satisfying chosen parameters: 994

Minimum DB seq length: 8  
Maximum DB seq length: 50

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 497 summaries

Database : rnpdb.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	ID	Description
1	25	1.5	25	1 US-10-717-597-1314 Sequence 1314, Ap
2	25	1.5	25	1 US-10-717-597-1315 Sequence 1315, Ap
3	25	1.5	25	1 US-10-717-597-1316 Sequence 1316, Ap
4	25	1.5	25	1 US-10-717-597-1317 Sequence 1317, Ap
5	25	1.5	25	1 US-10-717-597-1318 Sequence 1318, Ap
6	25	1.5	25	1 US-10-717-597-1319 Sequence 1319, Ap
7	25	1.5	25	1 US-10-717-597-1320 Sequence 1320, Ap
8	25	1.5	25	1 US-10-717-597-1321 Sequence 1321, Ap
9	25	1.5	25	1 US-10-717-597-1322 Sequence 1322, Ap
10	25	1.5	25	1 US-10-717-597-1323 Sequence 1323, Ap
11	25	1.5	25	1 US-10-717-597-1324 Sequence 1324, Ap
12	25	1.5	25	1 US-10-717-597-1325 Sequence 1325, Ap
13	25	1.5	25	1 US-10-717-597-1326 Sequence 1326, Ap
14	25	1.5	25	1 US-10-717-597-1327 Sequence 1327, Ap
15	25	1.5	25	1 US-10-717-597-1328 Sequence 1328, Ap
16	25	1.5	25	1 US-10-717-597-1329 Sequence 1329, Ap
17	25	1.5	25	1 US-10-717-597-1330 Sequence 1330, A
18	25	1.5	25	1 US-10-717-597-1331 Sequence 1331, A
19	25	1.5	25	1 US-10-717-597-1332 Sequence 1332, A
20	25	1.5	25	1 US-10-717-597-1333 Sequence 1333, A
21	25	1.5	25	1 US-10-717-597-1334 Sequence 1334, A
22	25	1.5	25	1 US-10-717-597-1335 Sequence 1335, A
23	25	1.5	25	1 US-10-717-597-1336 Sequence 1336, A
24	25	1.5	25	1 US-10-717-597-1337 Sequence 1337, A
25	25	1.5	25	1 US-10-717-597-1338 Sequence 1338, A
26	25	1.5	25	1 US-10-717-597-1339 Sequence 1339, A
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123	25	1.5	25	1	US-10-956-157-281215	Sequence 281215,	c 196	21	1.3	21	1	US-10-646-391A-3	Sequence 3, Appl
124	25	1.5	25	1	US-10-956-157-285427	Sequence 285427,	c 197	21	1.3	21	1	US-10-646-391A-4	Sequence 4, Appl
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130	25	1.5	25	1	US-10-956-157-292272	Sequence 292272,	c 203	21	1.3	21	1	US-10-646-391A-10	Sequence 10, Appl
131	25	1.5	25	1	US-10-956-157-292272	Sequence 292272,	c 204	21	1.3	21	1	US-10-646-391A-11	Sequence 11, Appl
132	25	1.5	25	1	US-10-956-157-302171	Sequence 302171,	c 205	21	1.3	21	1	US-10-646-391A-12	Sequence 12, Appl
133	25	1.5	25	1	US-10-956-157-316681	Sequence 316681,	c 206	21	1.3	21	1	US-10-646-391A-20	Sequence 20, Appl
134	25	1.5	25	1	US-10-956-157-317598	Sequence 317598,	c 207	21	1.3	21	1	US-10-646-391A-21	Sequence 21, Appl
135	25	1.5	25	1	US-10-956-157-317598	Sequence 317598,	c 208	21	1.3	21	1	US-10-646-391A-22	Sequence 22, Appl
136	25	1.5	25	1	US-10-956-157-287991	Sequence 287991,	c 209	21	1.3	21	1	US-10-646-391A-23	Sequence 23, Appl
137	25	1.5	25	1	US-10-956-157-287991	Sequence 287991,	c 210	21	1.3	21	1	US-10-646-391A-25	Sequence 25, Appl
138	25	1.5	25	1	US-10-956-157-287991	Sequence 287991,	c 211	21	1.3	21	1	US-10-646-391A-36	Sequence 36, Appl
139	25	1.5	25	1	US-10-956-157-287991	Sequence 287991,	c 212	21	1.3	21	1	US-10-646-391A-37	Sequence 37, Appl
140	25	1.5	25	1	US-10-956-157-287991	Sequence 287991,	c 213	21	1.3	21	1	US-10-646-391A-38	Sequence 38, Appl
141	25	1.5	25	1	US-10-956-157-287991	Sequence 287991,	c 214	21	1.3	21	1	US-10-646-391A-39	Sequence 39, Appl
142	25	1.5	25	1	US-10-956-157-287991	Sequence 287991,	c 215	21	1.3	21	1	US-10-646-391A-40	Sequence 40, Appl
143	25	1.5	25	1	US-10-956-157-287991	Sequence 287991,	c 216	21	1.3	21	1	US-10-646-391A-41	Sequence 41, Appl
144	25	1.5	25	1	US-10-956-157-287991	Sequence 287991,	c 217	21	1.3	21	1	US-10-646-436-1	Sequence 1, Appl
145	25	1.5	25	1	US-10-956-157-287991	Sequence 287991,	c 218	21	1.3	21	1	US-10-646-436-2	Sequence 2, Appl
146	25	1.5	25	1	US-10-956-157-287991	Sequence 287991,	c 219	21	1.3	21	1	US-10-646-436-3	Sequence 3, Appl
147	25	1.5	25	1	US-10-956-157-287991	Sequence 287991,	c 220	21	1.3	21	1	US-10-646-436-4	Sequence 4, Appl
148	25	1.5	25	1	US-10-956-157-287991	Sequence 287991,	c 221	21	1.3	21	1	US-10-646-436-5	Sequence 5, Appl
149	25	1.5	25	1	US-10-956-157-287991	Sequence 287991,	c 222	21	1.3	21	1	US-10-646-436-6	Sequence 6, Appl
150	25	1.5	25	1	US-10-956-157-287991	Sequence 287991,	c 223	21	1.3	21	1	US-10-646-436-58	Sequence 58, Appl
151	25	1.5	25	1	US-10-956-157-287991	Sequence 287991,	c 224	21	1.3	21	1	US-10-646-436-59	Sequence 59, Appl
152	25	1.5	25	1	US-10-956-157-287991	Sequence 287991,	c 225	21	1.3	21	1	US-10-646-436-61	Sequence 61, Appl
153	25	1.5	25	1	US-10-956-157-287991	Sequence 287991,	c 226	21	1.3	21	1	US-10-646-436-62	Sequence 62, Appl
154	25	1.5	25	1	US-10-956-157-287991	Sequence 287991,	c 227	21	1.3	21	1	US-10-646-436-65	Sequence 65, Appl
155	25	1.5	25	1	US-10-956-157-287991	Sequence 287991,	c 228	21	1.3	21	1	US-10-828-394-4	Sequence 4, Appl
156	25	1.5	25	1	US-10-956-157-287991	Sequence 287991,	c 229	21	1.3	21	1	US-10-828-394-5	Sequence 5, Appl
157	25	1.5	25	1	US-10-956-157-287991	Sequence 287991,	c 230	21	1.3	21	1	US-10-828-394-6	Sequence 6, Appl
158	25	1.5	25	1	US-10-956-157-287991	Sequence 287991,	c 231	21	1.3	21	1	US-10-828-394-7	Sequence 7, Appl
159	25	1.5	25	1	US-10-956-157-287991	Sequence 287991,	c 232	21	1.3	21	1	US-10-828-394-8	Sequence 8, Appl
160	25	1.5	25	1	US-10-956-157-287991	Sequence 287991,	c 233	21	1.3	21	1	US-10-828-394-9	Sequence 9, Appl
161	25	1.5	25	1	US-10-956-157-287991	Sequence 287991,	c 234	21	1.3	21	1	US-10-828-394-10	Sequence 10, Appl
162	25	1.5	25	1	US-10-956-157-287991	Sequence 287991,	c 235	21	1.3	21	1	US-10-828-394-11	Sequence 11, Appl
163	25	1.5	25	1	US-10-956-157-287991	Sequence 287991,	c 236	21	1.3	21	1	US-10-828-394-12	Sequence 12, Appl
164	25	1.5	25	1	US-10-956-157-287991	Sequence 287991,	c 237	21	1.3	21	1	US-10-828-394-13	Sequence 13, Appl
165	25	1.5	25	1	US-10-956-157-287991	Sequence 287991,	c 238	21	1.3	21	1	US-10-828-395-4	Sequence 4, Appl
166	25	1.5	25	1	US-10-956-157-287991	Sequence 287991,	c 239	21	1.3	21	1	US-10-828-395-5	Sequence 5, Appl
167	25	1.5	25	1	US-10-956-157-287991	Sequence 287991,	c 240	21	1.3	21	1	US-10-828-395-6	Sequence 6, Appl
168	25	1.5	25	1	US-10-956-157-287991	Sequence 287991,	c 241	21	1.3	21	1	US-10-828-395-7	Sequence 7, Appl
169	25	1.5	25	1	US-10-956-157-287991	Sequence 287991,	c 242	21	1.3	21	1	US-10-828-395-8	Sequence 8, Appl
170	25	1.5	25	1	US-10-956-157-287991	Sequence 287991,	c 243	21	1.3	21	1	US-10-828-395-9	Sequence 9, Appl
171	25	1.5	25	1	US-10-956-157-287991	Sequence 287991,	c 244	21	1.3	21	1	US-10-828-395-10	Sequence 10, Appl
172	25	1.5	25	1	US-10-956-157-287991	Sequence 287991,	c 245	21	1.3	21	1	US-10-828-395-11	Sequence 11, Appl
173	25	1.5	25	1	US-10-956-157-287991	Sequence 287991,	c 246	21	1.3	21	1	US-10-828-395-12	Sequence 12, Appl
174	25	1.5	25	1	US-10-956-157-287991	Sequence 287991,	c 247	21	1.3	21	1	US-10-828-395-13	Sequence 13, Appl
175	25	1.5	25	1	US-10-956-157-287991	Sequence 287991,	c 248	20.8	1.3	25	1	US-10-719-900-695781	Sequence 695781,
176	25	1.5	25	1	US-10-956-157-287991	Sequence 287991,	c 249	20.2	1.2	25	1	US-10-719-900-65803	Sequence 56803, A
177	25	1.5	25	1	US-10-956-157-287991	Sequence 287991,	c 250	20.2	1.2	25	1	US-10-719-900-452919	Sequence 452919,
178	25	1.5	25	1	US-10-956-157-287991	Sequence 287991,	c 251	20.2	1.2	25	1	US-10-719-900-815717	Sequence 815717,
179	25	1.5	25	1	US-10-956-157-287991	Sequence 287991,	c 252	20.2	1.2	25	1	US-10-719-900-892166	Sequence 892166,

253	20.2	1.2	25	1	US-10-809-189-31758	Sequence 31758, A	c 326	20	1.2	20	1	US-10-380-124-80	Sequence 80, Appl
254	20.2	1.2	25	1	US-10-956-157-271151	Sequence 271151, A	327	20	1.2	20	1	US-10-980-850-17	Sequence 17, Appl
255	20.2	1.2	25	1	US-10-719-956-30750	Sequence 30750, A	328	20	1.2	20	1	US-10-980-850-18	Sequence 18, Appl
256	20.2	1.2	25	1	US-10-719-956-70566	Sequence 70566, A	c 329	20	1.2	20	1	US-10-980-850-33	Sequence 33, Appl
257	20.2	1.2	25	1	US-10-719-956-335802	Sequence 335802, A	330	20	1.2	21	1	US-10-646-331A-28	Sequence 28, Appl
258	20.2	1.2	25	1	US-10-719-956-374027	Sequence 374027, A	331	20	1.2	21	1	US-10-646-436-9	Sequence 9, Appl
259	20.2	1.2	25	1	US-10-719-956-501380	Sequence 501380, A	332	19.4	1.2	21	1	US-09-459-749D-13	Sequence 13, Appl
260	20.2	1.2	25	1	US-10-719-956-517912	Sequence 517912, A	333	19.4	1.2	21	1	US-10-270-871-13	Sequence 13, Appl
261	20.2	1.2	25	1	US-10-719-956-604881	Sequence 604881, A	334	19	1.2	19	1	US-10-646-391A-42	Sequence 42, Appl
262	20.2	1.2	25	1	US-10-719-956-612441	Sequence 612441, A	c 335	19	1.2	19	1	US-10-646-391A-43	Sequence 43, Appl
263	20	1.2	25	1	US-10-380-124-14	Sequence 14, Appl	336	19	1.2	19	1	US-10-646-436-67	Sequence 67, Appl
264	20	1.2	20	1	US-10-380-124-15	Sequence 15, Appl	c 337	19	1.2	19	1	US-10-646-436-68	Sequence 68, Appl
265	20	1.2	20	1	US-10-380-124-16	Sequence 16, Appl	338	19	1.2	19	1	US-10-828-394-16	Sequence 16, Appl
266	20	1.2	20	1	US-10-380-124-17	Sequence 17, Appl	339	19	1.2	19	1	US-10-828-394-17	Sequence 17, Appl
267	20	1.2	20	1	US-10-380-124-18	Sequence 18, Appl	340	19	1.2	19	1	US-10-828-394-18	Sequence 18, Appl
268	20	1.2	20	1	US-10-380-124-19	Sequence 19, Appl	341	19	1.2	19	1	US-10-828-395-16	Sequence 16, Appl
269	20	1.2	20	1	US-10-380-124-20	Sequence 20, Appl	342	19	1.2	19	1	US-10-828-395-17	Sequence 17, Appl
270	20	1.2	20	1	US-10-380-124-21	Sequence 21, Appl	343	19	1.2	19	1	US-10-828-395-18	Sequence 18, Appl
271	20	1.2	20	1	US-10-380-124-22	Sequence 22, Appl	c 344	19	1.2	21	1	US-10-646-436-10	Sequence 29, Appl
272	20	1.2	20	1	US-10-380-124-23	Sequence 23, Appl	c 345	19	1.2	21	1	US-10-646-436-10	Sequence 10, Appl
273	20	1.2	20	1	US-10-380-124-24	Sequence 24, Appl	346	18	1.1	18	1	US-10-380-124-4	Sequence 4, Appl
274	20	1.2	20	1	US-10-380-124-25	Sequence 25, Appl	c 347	17.8	1.1	21	1	US-09-967-726A-15	Sequence 15, Appl
275	20	1.2	20	1	US-10-380-124-26	Sequence 26, Appl	c 348	17.8	1.1	21	1	US-10-080-794-15	Sequence 15, Appl
276	20	1.2	20	1	US-10-380-124-27	Sequence 27, Appl	349	17.8	1.1	21	1	US-10-751-736-11047	Sequence 11047, A
277	20	1.2	20	1	US-10-380-124-28	Sequence 28, Appl	c 350	16.8	1.0	20	1	US-10-921-868A-37	Sequence 37, Appl
278	20	1.2	20	1	US-10-380-124-29	Sequence 29, Appl	c 351	16.8	1.0	21	1	US-10-786-720-3371	Sequence 3371, Ap
279	20	1.2	20	1	US-10-380-124-30	Sequence 30, Appl	c 352	16.8	1.0	21	1	US-10-786-720-4073	Sequence 4073, Ap
280	20	1.2	20	1	US-10-380-124-31	Sequence 31, Appl	c 353	16.8	1.0	21	1	US-10-786-720-4811	Sequence 4811, Ap
281	20	1.2	20	1	US-10-380-124-32	Sequence 32, Appl	c 354	16.8	1.0	21	1	US-10-751-736-24026	Sequence 24026, A
282	20	1.2	20	1	US-10-380-124-33	Sequence 33, Appl	c 355	16.8	1.0	21	1	US-10-911-318-81	Sequence 81, Appl
283	20	1.2	20	1	US-10-380-124-34	Sequence 34, Appl	c 356	16	1.0	16	1	US-09-294-121A-97	Sequence 97, Appl
284	20	1.2	20	1	US-10-380-124-35	Sequence 35, Appl	c 357	16	1.0	16	1	US-09-899-082A-97	Sequence 97, Appl
285	20	1.2	20	1	US-10-380-124-36	Sequence 36, Appl	c 358	16	1.0	16	1	US-09-899-302-97	Sequence 97, Appl
286	20	1.2	20	1	US-10-380-124-37	Sequence 37, Appl	c 359	16	1.0	16	1	US-09-899-044-97	Sequence 97, Appl
287	20	1.2	20	1	US-10-380-124-38	Sequence 38, Appl	c 360	16	1.0	16	1	US-10-822-711-97	Sequence 97, Appl
288	20	1.2	20	1	US-10-380-124-39	Sequence 39, Appl	c 361	16	1.0	20	1	US-10-160-787-84	Sequence 84, Appl
289	20	1.2	20	1	US-10-380-124-40	Sequence 40, Appl	362	16	1.0	20	1	US-10-160-787-137	Sequence 137, App
290	20	1.2	20	1	US-10-380-124-41	Sequence 41, Appl	363	15.8	1.0	19	1	US-10-646-391A-24	Sequence 24, Appl
291	20	1.2	20	1	US-10-380-124-42	Sequence 42, Appl	364	15.8	1.0	19	1	US-10-646-391A-26	Sequence 26, Appl
292	20	1.2	20	1	US-10-380-124-43	Sequence 43, Appl	c 365	15.8	1.0	19	1	US-10-646-391A-27	Sequence 27, Appl
293	20	1.2	20	1	US-10-380-124-44	Sequence 44, Appl	c 366	15.8	1.0	19	1	US-10-646-436-7	Sequence 7, Appl
294	20	1.2	20	1	US-10-380-124-45	Sequence 45, Appl	c 367	15.8	1.0	19	1	US-10-646-436-8	Sequence 8, Appl
295	20	1.2	20	1	US-10-380-124-46	Sequence 46, Appl	c 368	15.8	1.0	19	1	US-10-667-271-305	Sequence 305, App
296	20	1.2	20	1	US-10-380-124-47	Sequence 47, Appl	c 369	15.8	1.0	19	1	US-10-667-271-1001	Sequence 1001, Ap
297	20	1.2	20	1	US-10-380-124-48	Sequence 48, Appl	370	15.4	0.9	17	1	US-09-866-108-8666	Sequence 8666, Ap
298	20	1.2	20	1	US-10-380-124-49	Sequence 49, Appl	c 371	15.4	0.9	17	1	US-09-780-533A-170	Sequence 170, App
299	20	1.2	20	1	US-10-380-124-50	Sequence 50, Appl	372	15.4	0.9	17	1	US-09-740-332-1542	Sequence 1542, Ap
300	20	1.2	20	1	US-10-380-124-51	Sequence 51, Appl	c 373	15.4	0.9	17	1	US-09-740-332-3013	Sequence 3013, Ap
301	20	1.2	20	1	US-10-380-124-52	Sequence 52, Appl	374	15.4	0.9	17	1	US-09-817-879-1542	Sequence 1542, Ap
302	20	1.2	20	1	US-10-380-124-53	Sequence 53, Appl	c 375	15.4	0.9	17	1	US-09-817-879-3013	Sequence 3013, Ap
303	20	1.2	20	1	US-10-380-124-54	Sequence 54, Appl	376	15.4	0.9	17	1	US-10-669-841-4135	Sequence 4135, Ap
304	20	1.2	20	1	US-10-380-124-55	Sequence 55, Appl	c 377	15.4	0.9	17	1	US-10-669-841-5606	Sequence 5606, Ap
305	20	1.2	20	1	US-10-380-124-56	Sequence 56, Appl	378	15.4	0.9	17	1	US-10-723-361-8666	Sequence 8666, Ap
306	20	1.2	20	1	US-10-380-124-57	Sequence 57, Appl	c 379	15.4	0.9	17	1	US-10-828-394-19	Sequence 19, Appl
307	20	1.2	20	1	US-10-380-124-58	Sequence 58, Appl	c 380	15.4	0.9	17	1	US-10-828-395-19	Sequence 19, Appl
308	20	1.2	20	1	US-10-380-124-59	Sequence 59, Appl	c 381	15	0.9	15	1	US-10-758-451-883	Sequence 883, App
309	20	1.2	20	1	US-10-380-124-60	Sequence 60, Appl	c 382	15	0.9	17	1	US-09-740-332-3014	Sequence 3014, Ap
310	20	1.2	20	1	US-10-380-124-61	Sequence 61, Appl	c 383	15	0.9	17	1	US-09-817-879-3014	Sequence 3014, Ap
311	20	1.2	20	1	US-10-380-124-62	Sequence 62, Appl	c 384	15	0.9	17	1	US-10-669-841-5607	Sequence 5607, Ap
312	20	1.2	20	1	US-10-380-124-63	Sequence 63, Appl	c 385	14.8	0.9	18	1	US-10-497-692-11	Sequence 11, Appl
313	20	1.2	20	1	US-10-380-124-64	Sequence 64, Appl	c 386	14.4	0.9	17	1	US-09-866-108-8352	Sequence 8352, Ap
314	20	1.2	20	1	US-10-380-124-65	Sequence 65, Appl	c 387	14.4	0.9	17	1	US-09-866-108-8353	Sequence 8353, Ap
315	20	1.2	20	1	US-10-380-124-66	Sequence 66, Appl	c 388	14.4	0.9	17	1	US-09-866-108-8665	Sequence 8665, Ap
316	20	1.2	20	1	US-10-380-124-67	Sequence 67, Appl	389	14.4	0.9	17	1	US-09-866-108-8667	Sequence 8667, Ap
317	20	1.2	20	1	US-10-380-124-68	Sequence 68, Appl	c 390	14.4	0.9	17	1	US-09-866-108-10037	Sequence 10037, A
318	20	1.2	20	1	US-10-380-124-69	Sequence 69, Appl	c 391	14.4	0.9	17	1	US-09-866-108-10038	Sequence 10038, A
319	20	1.2	20	1	US-10-380-124-70	Sequence 70, Appl	392	14.4	0.9	17	1	US-09-928-412-7	Sequence 7, Appl
320	20	1.2	20	1	US-10-380-124-71	Sequence 71, Appl	c 393	14.4	0.9	17	1	US-09-780-533A-171	Sequence 171, App
321	20	1.2	20	1	US-10-380-124-72	Sequence 72, Appl	c 394	14.4	0.9	17	1	US-09-877-478-1745	Sequence 1745, Ap
322	20	1.2	20	1	US-10-380-124-73	Sequence 73, Appl	c 395	14.4	0.9	17	1	US-09-740-332-1543	Sequence 1543, Ap
323	20	1.2	20	1	US-10-380-124-74	Sequence 74, Appl	396	14.4	0.9	17	1	US-09-817-879-1543	Sequence 1543, Ap
324	20	1.2	20	1	US-10-380-124-75	Sequence 75, Appl	397	14.4	0.9	17	1	US-10-298-255-4	Sequence 4, Appl
325	20	1.2	20	1	US-10-380-124-78	Sequence 78, Appl	c 398	14.4	0.9	17	1	US-10-238-700-2912	Sequence 2912, Ap

399	14.4	0.9	17	1	US-10-339-793-366	Sequence 366, App	472	13.8	0.8	17	1	US-10-430-882-880	Sequence 880, App
C 400	14.4	0.9	17	1	US-10-342-902-1745	Sequence 1745, App	473	13.8	0.8	17	1	US-10-138-674-3543	Sequence 3543, App
C 401	14.4	0.9	17	1	US-10-138-674-8431	Sequence 8431, App	474	13.8	0.8	17	1	US-10-138-674-4182	Sequence 4182, App
C 402	14.4	0.9	17	1	US-10-287-949A-8431	Sequence 8431, App	475	13.8	0.8	17	1	US-10-287-949A-3543	Sequence 3543, App
C 403	14.4	0.9	17	1	US-10-669-841-1745	Sequence 1745, App	476	13.8	0.8	17	1	US-10-287-949A-4182	Sequence 4182, App
C 404	14.4	0.9	17	1	US-10-669-841-4136	Sequence 4136, App	C 477	13.8	0.8	17	1	US-10-712-672-564	Sequence 564, App
C 405	14.4	0.9	17	1	US-10-723-361-8352	Sequence 8352, App	C 478	13.8	0.8	17	1	US-10-712-672-1193	Sequence 1193, App
C 406	14.4	0.9	17	1	US-10-723-361-8353	Sequence 8353, App	479	13.8	0.8	17	1	US-10-669-841-3225	Sequence 3225, App
C 407	14.4	0.9	17	1	US-10-723-361-8665	Sequence 8665, App	480	13.8	0.8	17	1	US-10-669-841-4754	Sequence 4754, App
C 408	14.4	0.9	17	1	US-10-723-361-8667	Sequence 8667, App	C 481	13.8	0.8	17	1	US-10-669-841-5605	Sequence 5605, App
C 409	14.4	0.9	17	1	US-10-723-361-10037	Sequence 10037, A	C 482	13.8	0.8	17	1	US-10-723-361-1895	Sequence 1895, App
C 410	14.4	0.9	17	1	US-10-723-361-10038	Sequence 10038, A	C 483	13.8	0.8	17	1	US-10-723-361-2643	Sequence 2643, App
C 411	14.4	0.9	17	1	US-10-723-361-10038	Sequence 10038, A	C 484	13.8	0.8	17	1	US-10-723-361-7355	Sequence 7355, App
C 412	14.4	0.9	17	1	US-10-712-633-3472	Sequence 3472, App	C 485	13.8	0.8	17	1	US-10-723-361-7485	Sequence 7485, App
C 413	14.4	0.9	17	1	US-10-724-270-1591	Sequence 1591, App	C 486	13.8	0.8	17	1	US-10-723-361-8568	Sequence 8568, App
C 414	14.4	0.9	17	1	US-11-016-291-4	Sequence 4, Appli	487	13.8	0.8	17	1	US-10-723-361-8568	Sequence 8568, App
C 415	14.4	0.9	18	1	US-09-263-959-1251	Sequence 1251, App	488	13.8	0.8	17	1	US-10-723-361-8661	Sequence 8661, App
C 416	14.4	0.9	18	1	US-10-108-260A-5102	Sequence 5102, App	489	13.8	0.8	17	1	US-10-723-361-8663	Sequence 8663, App
C 417	14	0.9	14	1	US-09-758-451-884	Sequence 884, App	490	13.8	0.8	17	1	US-10-723-361-8664	Sequence 8664, App
C 418	14	0.9	17	1	US-09-930-423-9	Sequence 9, Appli	C 491	13.8	0.8	17	1	US-10-723-361-9687	Sequence 9687, App
C 419	14	0.9	17	1	US-09-930-423-359	Sequence 359, App	C 492	13.8	0.8	17	1	US-10-723-361-9688	Sequence 9688, App
C 420	14	0.9	17	1	US-09-930-423-360	Sequence 360, App	C 493	13.8	0.8	17	1	US-10-723-361-9689	Sequence 9689, App
C 421	14	0.9	17	1	US-09-740-332-1541	Sequence 1541, App	C 494	13.8	0.8	17	1	US-10-758-451-944	Sequence 944, App
C 422	14	0.9	17	1	US-09-745-237A-9	Sequence 9, Appli	C 495	13.8	0.8	17	1	US-10-890-776A-748	Sequence 748, App
C 423	14	0.9	17	1	US-09-745-237A-359	Sequence 359, App	496	13.8	0.8	17	1	US-10-890-776A-749	Sequence 749, App
C 424	14	0.9	17	1	US-09-817-879-1541	Sequence 1541, App	497	13.8	0.8	17	1	US-10-890-776A-1238	Sequence 1238, App
C 425	14	0.9	17	1	US-10-307-005-955	Sequence 955, App							
C 426	14	0.9	17	1	US-10-307-005-956	Sequence 956, App							
C 427	14	0.9	17	1	US-10-669-841-4134	Sequence 4134, App							
C 428	13.8	0.8	17	1	US-09-866-108-1895	Sequence 1895, App							
C 429	13.8	0.8	17	1	US-09-866-108-2643	Sequence 2643, App							
C 430	13.8	0.8	17	1	US-09-866-108-7355	Sequence 7355, App							
C 431	13.8	0.8	17	1	US-09-866-108-7485	Sequence 7485, App							
C 432	13.8	0.8	17	1	US-09-866-108-8568	Sequence 8568, App							
C 433	13.8	0.8	17	1	US-09-866-108-8661	Sequence 8661, App							
C 434	13.8	0.8	17	1	US-09-866-108-8663	Sequence 8663, App							
C 435	13.8	0.8	17	1	US-09-866-108-8664	Sequence 8664, App							
C 436	13.8	0.8	17	1	US-09-866-108-9687	Sequence 9687, App							
C 437	13.8	0.8	17	1	US-09-866-108-9688	Sequence 9688, App							
C 438	13.8	0.8	17	1	US-09-866-108-9689	Sequence 9689, App							
C 439	13.8	0.8	17	1	US-09-776-291A-4	Sequence 4, Appli							
C 440	13.8	0.8	17	1	US-09-864-785-115	Sequence 115, App							
C 441	13.8	0.8	17	1	US-09-864-785-117	Sequence 117, App							
C 442	13.8	0.8	17	1	US-09-864-785-213	Sequence 213, App							
C 443	13.8	0.8	17	1	US-09-864-785-215	Sequence 215, App							
C 444	13.8	0.8	17	1	US-09-864-785-336	Sequence 336, App							
C 445	13.8	0.8	17	1	US-09-864-785-1519	Sequence 1519, App							
C 446	13.8	0.8	17	1	US-09-864-785-1520	Sequence 1520, App							
C 447	13.8	0.8	17	1	US-09-864-785-2036	Sequence 2036, App							
C 448	13.8	0.8	17	1	US-09-961-077-687	Sequence 687, App							
C 449	13.8	0.8	17	1	US-09-533A-1053	Sequence 1053, App							
C 450	13.8	0.8	17	1	US-09-780-533A-1885	Sequence 1885, App							
C 451	13.8	0.8	17	1	US-09-933-972C-874	Sequence 874, App							
C 452	13.8	0.8	17	1	US-09-933-972C-874	Sequence 874, App							
C 453	13.8	0.8	17	1	US-09-933-972C-944	Sequence 944, App							
C 454	13.8	0.8	17	1	US-09-930-423-57	Sequence 57, Appli							
C 455	13.8	0.8	17	1	US-09-827-395A-880	Sequence 880, App							
C 456	13.8	0.8	17	1	US-09-740-332-632	Sequence 632, App							
C 457	13.8	0.8	17	1	US-09-740-332-2161	Sequence 2161, App							
C 458	13.8	0.8	17	1	US-09-740-332-3012	Sequence 3012, App							
C 459	13.8	0.8	17	1	US-09-792-818-440	Sequence 440, App							
C 460	13.8	0.8	17	1	US-09-745-237A-57	Sequence 57, Appli							
C 461	13.8	0.8	17	1	US-09-817-879-632	Sequence 632, App							
C 462	13.8	0.8	17	1	US-09-817-879-2161	Sequence 2161, App							
C 463	13.8	0.8	17	1	US-09-817-879-3012	Sequence 3012, App							
C 464	13.8	0.8	17	1	US-10-079-625-25	Sequence 25, Appli							
C 465	13.8	0.8	17	1	US-10-079-625-27	Sequence 27, Appli							
C 466	13.8	0.8	17	1	US-10-060-756A-748	Sequence 748, App							
C 467	13.8	0.8	17	1	US-10-060-756A-749	Sequence 749, App							
C 468	13.8	0.8	17	1	US-10-060-756A-1238	Sequence 1238, App							
C 469	13.8	0.8	17	1	US-10-156-306-2719	Sequence 2719, App							
C 470	13.8	0.8	17	1	US-10-156-306-5069	Sequence 5069, App							
C 471	13.8	0.8	17	1	US-10-156-306-5948	Sequence 5948, App							

ALIGNMENTS

RESULT 1

US-10-717-597-1314

Sequence 1314, Application US/10717597

Publication No. US20040110221A1

GENERAL INFORMATION:

APPLICANT: Wyeth

APPLICANT: Burczynski, Michael E.

APPLICANT: Twine, Natalie C.

APPLICANT: Dorner, Andrew J.

APPLICANT: Trepicchio, William L.

APPLICANT: Slonim, Donna K.

APPLICANT: Stover, Jennifer A.

TITLE OF INVENTION: METHODS FOR DIAGNOSING RCC AND OTHER SOLID TUMORS

FILE REFERENCE: AM101080L

CURRENT APPLICATION NUMBER: US/10/717,597

PRIOR FILING DATE: 2003-11-21

PRIOR APPLICATION NUMBER: US 60/459,782

PRIOR FILING DATE: 2003-04-03

PRIOR APPLICATION NUMBER: US 60/427,982

PRIOR FILING DATE: 2002-11-21

NUMBER OF SEQ ID NOS: 4904

SOFTWARE: PatentIn version 3.2

SEQ ID NO 1314

LENGTH: 25

TYPE: DNA

ORGANISM: Homo sapiens

US-10-717-597-1314

Query Match 1.5%; Score 25; DB 1; Length 25;

Best Local Similarity 100.0%; Pred. No. 72;

Mismatches 0; Indels 0; Gaps 0;

Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1088 CTACAGTGGAGATGCTCAACACC 1112

Db 1 CTACAGTGGAGATGCTCAACACC 25

RESULT 2

US-10-717-597-1315

Sequence 1315, Application US/10717597

Publication No. US20040110221A1

GENERAL INFORMATION:



; APPLICANT: Wyeth  
; APPLICANT: Burczynski, Michael E.  
; APPLICANT: Twine, Natalie C.  
; APPLICANT: Dörner, Andrew J.  
; APPLICANT: Trepicchio, William L.  
; APPLICANT: Slonim, Donna K.  
; APPLICANT: Stover, Jennifer A.  
; TITLE OF INVENTION: METHODS FOR DIAGNOSING RCC AND OTHER SOLID TUMORS  
; FILE REFERENCE: AM101080L  
; CURRENT APPLICATION NUMBER: US/10/717,597  
; CURRENT FILING DATE: 2003-11-21  
; PRIOR APPLICATION NUMBER: US 60/459,782  
; PRIOR FILING DATE: 2003-04-03  
; PRIOR APPLICATION NUMBER: US 60/427,982  
; PRIOR FILING DATE: 2002-11-21  
; NUMBER OF SEQ ID NOS: 4904  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 1315  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-717-597-1315

Query Match 1.5%; Score 25; DB 1; Length 25;  
Best Local Similarity 100.0%; Pred. No. 72;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1177 AAGCGGAGACCACTACTATCTGCG 1201  
|||||  
DB 1 AAGCGGAGACCACTACTATCTGCG 25

RESULT 3  
US-10-717-597-1316  
; Sequence 1316, Application US/10717597  
; Publication No. US20040110221A1  
; GENERAL INFORMATION:  
; APPLICANT: Wyeth  
; APPLICANT: Burczynski, Michael E.  
; APPLICANT: Twine, Natalie C.  
; APPLICANT: Dörner, Andrew J.  
; APPLICANT: Trepicchio, William L.  
; APPLICANT: Slonim, Donna K.  
; APPLICANT: Stover, Jennifer A.  
; TITLE OF INVENTION: METHODS FOR DIAGNOSING RCC AND OTHER SOLID TUMORS  
; FILE REFERENCE: AM101080L  
; CURRENT APPLICATION NUMBER: US/10/717,597  
; CURRENT FILING DATE: 2003-11-21  
; PRIOR APPLICATION NUMBER: US 60/459,782  
; PRIOR FILING DATE: 2003-04-03  
; PRIOR APPLICATION NUMBER: US 60/427,982  
; PRIOR FILING DATE: 2002-11-21  
; NUMBER OF SEQ ID NOS: 4904  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 1316  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-717-597-1316

Query Match 1.5%; Score 25; DB 1; Length 25;  
Best Local Similarity 100.0%; Pred. No. 72;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1196 TCTGCGGGTCACCGGTGGCTTCC 1220  
|||||  
DB 1 TCTGCGGGTCACCGGTGGCTTCC 25

RESULT 4  
US-10-717-597-1317  
; Sequence 1317, Application US/10717597  
; Publication No. US20040110221A1

; GENERAL INFORMATION:  
; APPLICANT: Wyeth  
; APPLICANT: Burczynski, Michael E.  
; APPLICANT: Twine, Natalie C.  
; APPLICANT: Dörner, Andrew J.  
; APPLICANT: Trepicchio, William L.  
; APPLICANT: Slonim, Donna K.  
; APPLICANT: Stover, Jennifer A.  
; TITLE OF INVENTION: METHODS FOR DIAGNOSING RCC AND OTHER SOLID TUMORS  
; FILE REFERENCE: AM101080L  
; CURRENT APPLICATION NUMBER: US/10/717,597  
; CURRENT FILING DATE: 2003-11-21  
; PRIOR APPLICATION NUMBER: US 60/459,782  
; PRIOR FILING DATE: 2003-04-03  
; PRIOR APPLICATION NUMBER: US 60/427,982  
; PRIOR FILING DATE: 2002-11-21  
; NUMBER OF SEQ ID NOS: 4904  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 1317  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-717-597-1317

Query Match 1.5%; Score 25; DB 1; Length 25;  
Best Local Similarity 100.0%; Pred. No. 72;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1256 TGAGTGGTGGTGAAGCTCTTTGAC 1280  
|||||  
DB 1 TGAGTGGTGGTGAAGCTCTTTGAC 25

RESULT 5  
US-10-717-597-1318  
; Sequence 1318, Application US/10717597  
; Publication No. US20040110221A1  
; GENERAL INFORMATION:  
; APPLICANT: Wyeth  
; APPLICANT: Burczynski, Michael E.  
; APPLICANT: Twine, Natalie C.  
; APPLICANT: Dörner, Andrew J.  
; APPLICANT: Trepicchio, William L.  
; APPLICANT: Slonim, Donna K.  
; APPLICANT: Stover, Jennifer A.  
; TITLE OF INVENTION: METHODS FOR DIAGNOSING RCC AND OTHER SOLID TUMORS  
; FILE REFERENCE: AM101080L  
; CURRENT APPLICATION NUMBER: US/10/717,597  
; CURRENT FILING DATE: 2003-11-21  
; PRIOR APPLICATION NUMBER: US 60/459,782  
; PRIOR FILING DATE: 2003-04-03  
; PRIOR APPLICATION NUMBER: US 60/427,982  
; PRIOR FILING DATE: 2002-11-21  
; NUMBER OF SEQ ID NOS: 4904  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 1318  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-717-597-1318

Query Match 1.5%; Score 25; DB 1; Length 25;  
Best Local Similarity 100.0%; Pred. No. 72;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1262 GGTCTGAAGCTCTTTGACTCTGAT 1286  
|||||  
DB 1 GGTCTGAAGCTCTTTGACTCTGAT 25

RESULT 6  
US-10-717-597-1319  
; Sequence 1319, Application US/10717597

```
; Publication No. US20040110221A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Burczynski, Michael E.
; APPLICANT: Twine, Natalie C.
; APPLICANT: Dörner, Andrew J.
; APPLICANT: Trepicchio, William L.
; APPLICANT: Slonim, Donna K.
; APPLICANT: Stover, Jennifer A.
; TITLE OF INVENTION: METHODS FOR DIAGNOSING RCC AND OTHER SOLID TUMORS
; FILE REFERENCE: AM101080L
; CURRENT APPLICATION NUMBER: US/10/717,597
; CURRENT FILING DATE: 2003-11-21
; PRIOR APPLICATION NUMBER: US 60/459,782
; PRIOR FILING DATE: 2003-04-03
; PRIOR APPLICATION NUMBER: US 60/427,982
; PRIOR FILING DATE: 2002-11-21
; NUMBER OF SEQ ID NOS: 4904
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1319
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-717-597-1319

Query Match          1.5%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 72;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1268 GAAGCTCTTTGACTCTGATCCCATC 1292
      |||||
Db 1 GAAGCTCTTTGACTCTGATCCCATC 25

RESULT 7
US-10-717-597-1320
; Sequence 1320, Application US/10717597
; Publication No. US20040110221A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Burczynski, Michael E.
; APPLICANT: Twine, Natalie C.
; APPLICANT: Dörner, Andrew J.
; APPLICANT: Trepicchio, William L.
; APPLICANT: Slonim, Donna K.
; APPLICANT: Stover, Jennifer A.
; TITLE OF INVENTION: METHODS FOR DIAGNOSING RCC AND OTHER SOLID TUMORS
; FILE REFERENCE: AM101080L
; CURRENT APPLICATION NUMBER: US/10/717,597
; CURRENT FILING DATE: 2003-11-21
; PRIOR APPLICATION NUMBER: US 60/459,782
; PRIOR FILING DATE: 2003-04-03
; PRIOR APPLICATION NUMBER: US 60/427,982
; PRIOR FILING DATE: 2002-11-21
; NUMBER OF SEQ ID NOS: 4904
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1320
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-717-597-1320

Query Match          1.5%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 72;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1274 CTTTGACTCTGATCCCATCACTGTG 1298
      |||||
Db 1 CTTTGACTCTGATCCCATCACTGTG 25

RESULT 8
US-10-717-597-1321
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; Sequence 1321, Application US/10717597
; Publication No. US20040110221A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Burczynski, Michael E.
; APPLICANT: Twine, Natalie C.
; APPLICANT: Dörner, Andrew J.
; APPLICANT: Trepicchio, William L.
; APPLICANT: Slonim, Donna K.
; APPLICANT: Stover, Jennifer A.
; TITLE OF INVENTION: METHODS FOR DIAGNOSING RCC AND OTHER SOLID TUMORS
; FILE REFERENCE: AM101080L
; CURRENT APPLICATION NUMBER: US/10/717,597
; CURRENT FILING DATE: 2003-11-21
; PRIOR APPLICATION NUMBER: US 60/459,782
; PRIOR FILING DATE: 2003-04-03
; PRIOR APPLICATION NUMBER: US 60/427,982
; PRIOR FILING DATE: 2002-11-21
; NUMBER OF SEQ ID NOS: 4904
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1321
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-717-597-1321

Query Match          1.5%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 72;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1397 AGATGTGGATGTGCTTTTGCACCT 1421
      |||||
Db 1 AGATGTGGATGTGCTTTTGCACCT 25

RESULT 9
US-10-717-597-1322
; Sequence 1322, Application US/10717597
; Publication No. US20040110221A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Burczynski, Michael E.
; APPLICANT: Twine, Natalie C.
; APPLICANT: Dörner, Andrew J.
; APPLICANT: Trepicchio, William L.
; APPLICANT: Slonim, Donna K.
; APPLICANT: Stover, Jennifer A.
; TITLE OF INVENTION: METHODS FOR DIAGNOSING RCC AND OTHER SOLID TUMORS
; FILE REFERENCE: AM101080L
; CURRENT APPLICATION NUMBER: US/10/717,597
; CURRENT FILING DATE: 2003-11-21
; PRIOR APPLICATION NUMBER: US 60/459,782
; PRIOR FILING DATE: 2003-04-03
; PRIOR APPLICATION NUMBER: US 60/427,982
; PRIOR FILING DATE: 2002-11-21
; NUMBER OF SEQ ID NOS: 4904
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1322
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-717-597-1322

Query Match          1.5%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 72;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1470 CCAGAGAGAGCTCTGCACGTCACCA 1494
      |||||
Db 1 CCAGAGAGAGCTCTGCACGTCACCA 25

RESULT 10
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US-10-717-597-1323  
; Sequence 1323, Application US/10717597  
; Publication No. US20040110221A1  
; GENERAL INFORMATION:  
; APPLICANT: Wyeth  
; APPLICANT: Burczynski, Michael E.  
; APPLICANT: Twine, Natalie C.  
; APPLICANT: Dörner, Andrew J.  
; APPLICANT: Trepicchio, William L.  
; APPLICANT: Slonim, Donna K.  
; APPLICANT: Stover, Jennifer A.  
; TITLE OF INVENTION: METHODS FOR DIAGNOSING RCC AND OTHER SOLID TUMORS  
; FILE REFERENCE: AM101080L  
; CURRENT APPLICATION NUMBER: US/10/717,597  
; CURRENT FILING DATE: 2003-11-21  
; PRIOR APPLICATION NUMBER: US 60/459,782  
; PRIOR FILING DATE: 2003-04-03  
; PRIOR APPLICATION NUMBER: US 60/427,982  
; PRIOR FILING DATE: 2002-11-21  
; NUMBER OF SEQ ID NOS: 4904  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 1323  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-717-597-1323

Query Match 1.5%; Score 25; DB 1; Length 25;  
Best Local Similarity 100.0%; Pred. No. 72; Indels 0; Gaps 0;  
Matches 25; Conservative 0; Mismatches 0;  
QY 1474 AGAGAGCTCTGCACGTCACCAAGTA 1498  
|||||  
DB 1 AGAGAGCTCTGCACGTCACCAAGTA 25

RESULT 11  
US-10-717-597-1324  
; Sequence 1324, Application US/10717597  
; Publication No. US20040110221A1  
; GENERAL INFORMATION:  
; APPLICANT: Wyeth  
; APPLICANT: Burczynski, Michael E.  
; APPLICANT: Twine, Natalie C.  
; APPLICANT: Dörner, Andrew J.  
; APPLICANT: Trepicchio, William L.  
; APPLICANT: Slonim, Donna K.  
; APPLICANT: Stover, Jennifer A.  
; TITLE OF INVENTION: METHODS FOR DIAGNOSING RCC AND OTHER SOLID TUMORS  
; FILE REFERENCE: AM101080L  
; CURRENT APPLICATION NUMBER: US/10/717,597  
; CURRENT FILING DATE: 2003-11-21  
; PRIOR APPLICATION NUMBER: US 60/459,782  
; PRIOR FILING DATE: 2003-04-03  
; PRIOR APPLICATION NUMBER: US 60/427,982  
; PRIOR FILING DATE: 2002-11-21  
; NUMBER OF SEQ ID NOS: 4904  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 1324  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-717-597-1324

Query Match 1.5%; Score 25; DB 1; Length 25;  
Best Local Similarity 100.0%; Pred. No. 72; Indels 0; Gaps 0;  
Matches 25; Conservative 0; Mismatches 0;  
QY 1480 CTCTGCACGTCACCAAGTAACCCAGG 1504  
|||||  
DB 1 CTCTGCACGTCACCAAGTAACCCAGG 25

RESULT 12  
US-10-717-597-1325  
; Sequence 1325, Application US/10717597  
; Publication No. US20040110221A1  
; GENERAL INFORMATION:  
; APPLICANT: Wyeth  
; APPLICANT: Burczynski, Michael E.  
; APPLICANT: Twine, Natalie C.  
; APPLICANT: Dörner, Andrew J.  
; APPLICANT: Trepicchio, William L.  
; APPLICANT: Slonim, Donna K.  
; APPLICANT: Stover, Jennifer A.  
; TITLE OF INVENTION: METHODS FOR DIAGNOSING RCC AND OTHER SOLID TUMORS  
; FILE REFERENCE: AM101080L  
; CURRENT APPLICATION NUMBER: US/10/717,597  
; CURRENT FILING DATE: 2003-11-21  
; PRIOR APPLICATION NUMBER: US 60/459,782  
; PRIOR FILING DATE: 2003-04-03  
; PRIOR APPLICATION NUMBER: US 60/427,982  
; PRIOR FILING DATE: 2002-11-21  
; NUMBER OF SEQ ID NOS: 4904  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 1325  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-717-597-1325

Query Match 1.5%; Score 25; DB 1; Length 25;  
Best Local Similarity 100.0%; Pred. No. 72; Indels 0; Gaps 0;  
Matches 25; Conservative 0; Mismatches 0;  
QY 1550 GGATCCTGCACTCTAACACTCGACT 1574  
|||||  
DB 1 GGATCCTGCACTCTAACACTCGACT 25

RESULT 13  
US-10-717-597-1326  
; Sequence 1326, Application US/10717597  
; Publication No. US20040110221A1  
; GENERAL INFORMATION:  
; APPLICANT: Wyeth  
; APPLICANT: Burczynski, Michael E.  
; APPLICANT: Twine, Natalie C.  
; APPLICANT: Dörner, Andrew J.  
; APPLICANT: Trepicchio, William L.  
; APPLICANT: Slonim, Donna K.  
; APPLICANT: Stover, Jennifer A.  
; TITLE OF INVENTION: METHODS FOR DIAGNOSING RCC AND OTHER SOLID TUMORS  
; FILE REFERENCE: AM101080L  
; CURRENT APPLICATION NUMBER: US/10/717,597  
; CURRENT FILING DATE: 2003-11-21  
; PRIOR APPLICATION NUMBER: US 60/459,782  
; PRIOR FILING DATE: 2003-04-03  
; PRIOR APPLICATION NUMBER: US 60/427,982  
; PRIOR FILING DATE: 2002-11-21  
; NUMBER OF SEQ ID NOS: 4904  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 1326  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-717-597-1326

Query Match 1.5%; Score 25; DB 1; Length 25;  
Best Local Similarity 100.0%; Pred. No. 72; Indels 0; Gaps 0;  
Matches 25; Conservative 0; Mismatches 0;  
QY 1556 TGCACCTCTAACACTCGACTCTGCTG 1580  
|||||  
DB 1 TGCACCTCTAACACTCGACTCTGCTG 25

## RESULT 14

US-10-717-597-1327  
; Sequence 1327, Application US/10717597  
; Publication No. US20040110221A1  
; GENERAL INFORMATION:  
; APPLICANT: Wyeth  
; APPLICANT: Burczynski, Michael E.  
; APPLICANT: Twine, Natalie C.  
; APPLICANT: Dörner, Andrew J.  
; APPLICANT: Trepicchio, William L.  
; APPLICANT: Slonim, Donna K.  
; APPLICANT: Stover, Jennifer A.  
; TITLE OF INVENTION: METHODS FOR DIAGNOSING RCC AND OTHER SOLID TUMORS  
; FILE REFERENCE: AM101080L  
; CURRENT APPLICATION NUMBER: US/10/717,597  
; PRIOR FILING DATE: 2003-11-21  
; PRIOR APPLICATION NUMBER: US 60/459,782  
; PRIOR FILING DATE: 2003-04-03  
; PRIOR APPLICATION NUMBER: US 60/427,982  
; PRIOR FILING DATE: 2002-11-21  
; NUMBER OF SEQ ID NOS: 4904  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 1327  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-717-597-1327

Query Match 1.5%; Score 25; DB 1; Length 25;  
Best Local Similarity 100.0%; Pred. No. 72;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1562 CTAACACTCGACTCTGCTGCTCATG 1586  
|||||  
Db 1 CTAACACTCGACTCTGCTGCTCATG 25

## RESULT 15

US-10-717-597-1328  
; Sequence 1328, Application US/10717597  
; Publication No. US20040110221A1  
; GENERAL INFORMATION:  
; APPLICANT: Wyeth  
; APPLICANT: Burczynski, Michael E.  
; APPLICANT: Twine, Natalie C.  
; APPLICANT: Dörner, Andrew J.  
; APPLICANT: Trepicchio, William L.  
; APPLICANT: Slonim, Donna K.  
; APPLICANT: Stover, Jennifer A.  
; TITLE OF INVENTION: METHODS FOR DIAGNOSING RCC AND OTHER SOLID TUMORS  
; FILE REFERENCE: AM101080L  
; CURRENT APPLICATION NUMBER: US/10/717,597  
; PRIOR FILING DATE: 2003-11-21  
; PRIOR APPLICATION NUMBER: US 60/459,782  
; PRIOR FILING DATE: 2003-04-03  
; PRIOR APPLICATION NUMBER: US 60/427,982  
; PRIOR FILING DATE: 2002-11-21  
; NUMBER OF SEQ ID NOS: 4904  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 1328  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-717-597-1328

Query Match 1.5%; Score 25; DB 1; Length 25;  
Best Local Similarity 100.0%; Pred. No. 72;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1563 TAAACACTCGACTCTGCTGCTCATGG 1587  
|||||  
Db 1 TAAACACTCGACTCTGCTGCTCATGG 25

## RESULT 16

US-10-717-597-1329  
; Sequence 1329, Application US/10717597  
; Publication No. US20040110221A1  
; GENERAL INFORMATION:  
; APPLICANT: Wyeth  
; APPLICANT: Burczynski, Michael E.  
; APPLICANT: Twine, Natalie C.  
; APPLICANT: Dörner, Andrew J.  
; APPLICANT: Trepicchio, William L.  
; APPLICANT: Slonim, Donna K.  
; APPLICANT: Stover, Jennifer A.  
; TITLE OF INVENTION: METHODS FOR DIAGNOSING RCC AND OTHER SOLID TUMORS  
; FILE REFERENCE: AM101080L  
; CURRENT APPLICATION NUMBER: US/10/717,597  
; PRIOR FILING DATE: 2003-11-21  
; PRIOR APPLICATION NUMBER: US 60/459,782  
; PRIOR FILING DATE: 2003-04-03  
; PRIOR APPLICATION NUMBER: US 60/427,982  
; PRIOR FILING DATE: 2002-11-21  
; NUMBER OF SEQ ID NOS: 4904  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 1329  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-717-597-1329

Query Match 1.5%; Score 25; DB 1; Length 25;  
Best Local Similarity 100.0%; Pred. No. 72;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1564 AACACTCGACTCTGCTGCTCATGG 1588  
|||||  
Db 1 AACACTCGACTCTGCTGCTCATGG 25

## RESULT 17

US-10-956-157-25933  
; Sequence 25933, Application US/10956157  
; Publication No. US20050118625A1  
; GENERAL INFORMATION:  
; APPLICANT: Wyeth  
; APPLICANT: Mounts, William  
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH  
; TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES  
; FILE REFERENCE: 031896-043000 (AM 101081)  
; CURRENT APPLICATION NUMBER: US/10/956,157  
; CURRENT FILING DATE: 2004-10-04  
; NUMBER OF SEQ ID NOS: 319805  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 25933  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Probe Sequence  
US-10-956-157-25933

Query Match 1.5%; Score 25; DB 1; Length 25;  
Best Local Similarity 100.0%; Pred. No. 72;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 494 CTTCTACTTCTGGATGAATGGTGAC 518  
|||||  
Db 1 CTTCTACTTCTGGATGAATGGTGAC 25

## RESULT 18

US-10-956-157-25934  
; Sequence 25934, Application US/10956157  
; Publication No. US20050118625A1  
; GENERAL INFORMATION:

```
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 25934
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-25934

Query Match      1.5%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 72;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 493 CTTCTACTTCTGGATGAATGGTGA 517
      |||||
Db 1 CTTCTACTTCTGGATGAATGGTGA 25

RESULT 19
US-10-956-157-25935
; Sequence 25935, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 25935
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-25935

Query Match      1.5%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 72;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 495 TTCTACTTCTGGATGAATGGTGACC 519
      |||||
Db 1 TTCTACTTCTGGATGAATGGTGACC 25

RESULT 20
US-10-956-157-25936
; Sequence 25936, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 25936
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-25936
```

```
Query Match      1.5%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 72;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 300 CTAATGAGACCGAGGAATCAGAGA 324
      |||||
Db 1 CTAATGAGACCGAGGAATCAGAGA 25

RESULT 21
US-10-956-157-25937
; Sequence 25937, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 25937
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-25937

Query Match      1.5%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 72;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 301 TAAATGAGACCGAGGAATCAGAGAC 325
      |||||
Db 1 TAAATGAGACCGAGGAATCAGAGAC 25

RESULT 22
US-10-956-157-25938
; Sequence 25938, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 25938
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-25938

Query Match      1.5%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 72;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 281 GAAGAAGAAAGAGGATGCCCTAAAT 305
      |||||
Db 1 GAAGAAGAAAGAGGATGCCCTAAAT 25

RESULT 23
US-10-956-157-25939
; Sequence 25939, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
```

Tue Sep 13 10:53:21 2005

```
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 25939
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-25939

Query Match      1.5%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 72;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 282 AAGAGAAAGAGGATGCCCTAAATG 306
    |||||||
Db 1 AAGAGAAAGAGGATGCCCTAAATG 25

RESULT 24
US-10-956-157-25940
; Sequence 25940, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 25940
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-25940

Query Match      1.5%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 72;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 283 AGAAGAAAGAGGATGCCCTAAATGA 307
    |||||||
Db 1 AGAAGAAAGAGGATGCCCTAAATGA 25

RESULT 25
US-10-956-157-25941
; Sequence 25941, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 25941
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-25941

Query Match      1.5%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 72;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 284 GAAGAAGAGGATGCCCTAAATGAG 308
    |||||||
Db 1 GAAGAAGAGGATGCCCTAAATGAG 25

RESULT 26
US-10-956-157-25942
; Sequence 25942, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 25942
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-25942

Query Match      1.5%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 72;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 285 AAGAAAGAGGATGCCCTAAATGAGA 309
    |||||||
Db 1 AAGAAAGAGGATGCCCTAAATGAGA 25

RESULT 27
US-10-956-157-25943
; Sequence 25943, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 25943
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-25943

Query Match      1.5%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 72;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 280 AGAAGAAAGAGGATGCCCTAAAA 304
    |||||||
Db 1 AGAAGAAAGAGGATGCCCTAAAA 25

RESULT 28
US-10-956-157-25944
; Sequence 25944, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
```

```
Best Local Similarity 100.0%; Pred. No. 72;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 285 AAGAAAGAGGATGCCCTAAATGAGA 309
    |||||||
Db 1 AAGAAAGAGGATGCCCTAAATGAGA 25

RESULT 26
US-10-956-157-25942
; Sequence 25942, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 25942
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-25942

Query Match      1.5%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 72;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 283 AGAAGAAAGAGGATGCCCTAAATGA 307
    |||||||
Db 1 AGAAGAAAGAGGATGCCCTAAATGA 25

RESULT 27
US-10-956-157-25943
; Sequence 25943, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 25943
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-25943

Query Match      1.5%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 72;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 280 AGAAGAAAGAGGATGCCCTAAAA 304
    |||||||
Db 1 AGAAGAAAGAGGATGCCCTAAAA 25

RESULT 28
US-10-956-157-25944
; Sequence 25944, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
```

```

; APPLICANT: Wyeth
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 25948
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-25948

Query Match          1.5%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 72;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      278 CAAGAAGAAAGAGGATGCCCTA 302
        ||||||||||||||||||||
DB       1 CAAGAAGAAAGAGGATGCCCTA 25

RESULT 33
US-10-956-157-25949
; Sequence 25949, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH

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; TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 25949
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-25949

Query Match      1.5%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 72;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1066 AATAACACGAGCTGCTAAAGTCCTA 1090
      |||||||
Db 1 AATAACACGAGCTGCTAAAGTCCTA 25

RESULT 34
US-10-956-157-25950
; Sequence 25950, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 25950
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-25950

Query Match      1.5%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 72;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 299 CCTAATGACACGACGGAATCAGAG 323
      |||||||
Db 1 CCTAATGACACGACGGAATCAGAG 25

RESULT 35
US-10-956-157-25951
; Sequence 25951, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 25951
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-25951

Query Match      1.5%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 72;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1066 AATAACACGAGCTGCTAAAGTC 1087
      |||||||
Db 1 GGAATACACGAGCTGCTAAAGTC 25

RESULT 36
US-10-956-157-25952
; Sequence 25952, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 25952
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-25952

Query Match      1.5%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 72;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1064 GAAATACACGAGCTGCTAAAGTCC 1088
      |||||||
Db 1 GAAATACACGAGCTGCTAAAGTCC 25

RESULT 37
US-10-956-157-25953
; Sequence 25953, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 25953
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-25953

Query Match      1.5%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 72;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1063 GGAATACACGAGCTGCTAAAGTC 1087
      |||||||
Db 1 GGAATACACGAGCTGCTAAAGTC 25

RESULT 38
US-10-956-157-25954
; Sequence 25954, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
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Qy 1048 CTGAGAGGTTGACCGAAATACAA 1072
      |||||||
Db 1 CTGAGAGGTTGACCGAAATACAA 25

RESULT 36
US-10-956-157-25952
; Sequence 25952, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 25952
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-25952

Query Match      1.5%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 72;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1064 GAAATACACGAGCTGCTAAAGTCC 1088
      |||||||
Db 1 GAAATACACGAGCTGCTAAAGTCC 25

RESULT 37
US-10-956-157-25953
; Sequence 25953, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 25953
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-25953

Query Match      1.5%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 72;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1063 GGAATACACGAGCTGCTAAAGTC 1087
      |||||||
Db 1 GGAATACACGAGCTGCTAAAGTC 25

RESULT 38
US-10-956-157-25954
; Sequence 25954, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
```



; FILE REFERENCE: 031896-043000 (AM 101081)  
; CURRENT APPLICATION NUMBER: US/10/956,157  
; CURRENT FILING DATE: 2004-10-04  
; NUMBER OF SEQ ID NOS: 319805  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 25954  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Probe Sequence  
US-10-956-157-25954

Query Match 1.5%; Score 25; DB 1; Length 25;  
Best Local Similarity 100.0%; Pred. No. 72;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1067 ATACAACGAGCTGCTAAAGTCTCTAC 1091  
|||||  
Db 1 ATACAACGAGCTGCTAAAGTCTCTAC 25

## RESULT 39

US-10-956-157-25955  
; Sequence 25955, Application US/10956157  
; Publication No. US20050118625A1  
; GENERAL INFORMATION:  
; APPLICANT: Wyeth  
; APPLICANT: Mounts, William  
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH

; TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES  
; FILE REFERENCE: 031896-043000 (AM 101081)  
; CURRENT APPLICATION NUMBER: US/10/956,157  
; CURRENT FILING DATE: 2004-10-04  
; NUMBER OF SEQ ID NOS: 319805  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 25955  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Probe Sequence  
US-10-956-157-25955

Query Match 1.5%; Score 25; DB 1; Length 25;  
Best Local Similarity 100.0%; Pred. No. 72;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 398 GAAACAGACCTGCGATGAAGTTCTAC 422  
|||||  
Db 1 GAAACAGACCTGCGATGAAGTTCTAC 25

## RESULT 40

US-10-956-157-25956  
; Sequence 25956, Application US/10956157  
; Publication No. US20050118625A1  
; GENERAL INFORMATION:  
; APPLICANT: Wyeth  
; APPLICANT: Mounts, William  
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH

; TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES  
; FILE REFERENCE: 031896-043000 (AM 101081)  
; CURRENT APPLICATION NUMBER: US/10/956,157  
; CURRENT FILING DATE: 2004-10-04  
; NUMBER OF SEQ ID NOS: 319805  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 25956  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Probe Sequence  
US-10-956-157-25956

Query Match 1.5%; Score 25; DB 1; Length 25;  
Best Local Similarity 100.0%; Pred. No. 72;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 304 ATGAGACCAGGAATCAGAGACAAA 328  
|||||  
Db 1 ATGAGACCAGGAATCAGAGACAAA 25

## RESULT 41

US-10-956-157-122144  
; Sequence 122144, Application US/10956157  
; Publication No. US20050118625A1  
; GENERAL INFORMATION:  
; APPLICANT: Wyeth  
; APPLICANT: Mounts, William  
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH

; TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES  
; FILE REFERENCE: 031896-043000 (AM 101081)  
; CURRENT APPLICATION NUMBER: US/10/956,157  
; CURRENT FILING DATE: 2004-10-04  
; NUMBER OF SEQ ID NOS: 319805  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 122144  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Probe Sequence  
US-10-956-157-122144

Query Match 1.5%; Score 25; DB 1; Length 25;  
Best Local Similarity 100.0%; Pred. No. 72;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 850 AGCACCCGCCAACAGAATTCATACG 874  
|||||  
Db 1 AGCACCCGCCAACAGAATTCATACG 25

## RESULT 42

US-10-956-157-127897  
; Sequence 127897, Application US/10956157  
; Publication No. US20050118625A1  
; GENERAL INFORMATION:  
; APPLICANT: Wyeth  
; APPLICANT: Mounts, William  
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH

; TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES  
; FILE REFERENCE: 031896-043000 (AM 101081)  
; CURRENT APPLICATION NUMBER: US/10/956,157  
; CURRENT FILING DATE: 2004-10-04  
; NUMBER OF SEQ ID NOS: 319805  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 127897  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Probe Sequence  
US-10-956-157-127897

Query Match 1.5%; Score 25; DB 1; Length 25;  
Best Local Similarity 100.0%; Pred. No. 72;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 411 ATGAAGTTCTACGACGCGTCTGCA 435  
|||||  
Db 1 ATGAAGTTCTACGACGCGTCTGCA 25

## RESULT 43

US-10-956-157-131009  
; Sequence 131009, Application US/10956157  
; Publication No. US20050118625A1  
; GENERAL INFORMATION:  
; APPLICANT: Wyeth  
; APPLICANT: Mounts, William  
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH

; TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES  
; FILE REFERENCE: 031896-043000 (AM 101081)

; CURRENT APPLICATION NUMBER: US/10/956,157  
; CURRENT FILING DATE: 2004-10-04  
; NUMBER OF SEQ ID NOS: 319805  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 131009  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Probe Sequence  
US-10-956-157-131009

Query Match 1.5%; Score 25; DB 1; Length 25;  
Best Local Similarity 100.0%; Pred. No. 72;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 561 ATGCTGGATGTCATGCAGGACCACT 585  
|||||  
Db 1 ATGCTGGATGTCATGCAGGACCACT 25

## RESULT 44

US-10-956-157-134947  
; Sequence 134947, Application US/10956157  
; Publication No. US20050118625A1  
; GENERAL INFORMATION:

; APPLICANT: Wyeth  
; APPLICANT: Mounts, William  
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH  
; TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES  
; FILE REFERENCE: 031896-043000 (AM 101081)  
; CURRENT APPLICATION NUMBER: US/10/956,157  
; CURRENT FILING DATE: 2004-10-04  
; NUMBER OF SEQ ID NOS: 319805  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 134947  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Probe Sequence  
US-10-956-157-134947

Query Match 1.5%; Score 25; DB 1; Length 25;  
Best Local Similarity 100.0%; Pred. No. 72;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 334 AGGAGCTCCCAGGAGTGTCGAATGA 358  
|||||  
Db 1 AGGAGCTCCCAGGAGTGTCGAATGA 25

## RESULT 45

US-10-956-157-135244  
; Sequence 135244, Application US/10956157  
; Publication No. US20050118625A1  
; GENERAL INFORMATION:

; APPLICANT: Wyeth  
; APPLICANT: Mounts, William  
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH  
; TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES  
; FILE REFERENCE: 031896-043000 (AM 101081)  
; CURRENT APPLICATION NUMBER: US/10/956,157  
; CURRENT FILING DATE: 2004-10-04  
; NUMBER OF SEQ ID NOS: 319805  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 135244  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Probe Sequence  
US-10-956-157-135244

Query Match 1.5%; Score 25; DB 1; Length 25;  
Best Local Similarity 100.0%; Pred. No. 72;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 292 AGGATGCCCTAAATGACGACGGA 316

Db 1 AGGATGCCCTAAATGACGACGGA 25  
|||||

## RESULT 46

US-10-956-157-139926  
; Sequence 139926, Application US/10956157  
; Publication No. US20050118625A1  
; GENERAL INFORMATION:

; APPLICANT: Wyeth  
; APPLICANT: Mounts, William  
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH  
; TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES  
; FILE REFERENCE: 031896-043000 (AM 101081)  
; CURRENT APPLICATION NUMBER: US/10/956,157  
; CURRENT FILING DATE: 2004-10-04  
; NUMBER OF SEQ ID NOS: 319805  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 139926  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Probe Sequence  
US-10-956-157-139926

Query Match 1.5%; Score 25; DB 1; Length 25;  
Best Local Similarity 100.0%; Pred. No. 72;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 307 AGACCAGGGAATCAGACAAAGCT 331  
|||||  
Db 1 AGACCAGGGAATCAGACAAAGCT 25

## RESULT 47

US-10-956-157-140752  
; Sequence 140752, Application US/10956157  
; Publication No. US20050118625A1  
; GENERAL INFORMATION:

; APPLICANT: Wyeth  
; APPLICANT: Mounts, William  
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH  
; TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES  
; FILE REFERENCE: 031896-043000 (AM 101081)  
; CURRENT APPLICATION NUMBER: US/10/956,157  
; CURRENT FILING DATE: 2004-10-04  
; NUMBER OF SEQ ID NOS: 319805  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 140752  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Probe Sequence  
US-10-956-157-140752

Query Match 1.5%; Score 25; DB 1; Length 25;  
Best Local Similarity 100.0%; Pred. No. 72;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 875 AGAAGCGGACGATGACCGGACTGTG 899  
|||||  
Db 1 AGAAGCGGACGATGACCGGACTGTG 25

## RESULT 48

US-10-956-157-141327  
; Sequence 141327, Application US/10956157  
; Publication No. US20050118625A1  
; GENERAL INFORMATION:

; APPLICANT: Wyeth  
; APPLICANT: Mounts, William  
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH  
; TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES  
; FILE REFERENCE: 031896-043000 (AM 101081)  
; CURRENT APPLICATION NUMBER: US/10/956,157

; CURRENT FILING DATE: 2004-10-04  
; NUMBER OF SEQ ID NOS: 319805  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 141327  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Probe Sequence  
US-10-956-157-141327

Query Match 1.5%; Score 25; DB 1; Length 25;  
Best Local Similarity 100.0%; Pred. No. 72;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1299 ACGGTCCCTGTAGAGTCTCCAGGA 1323  
|||||

Db 1 ACGGTCCCTGTAGAGTCTCCAGGA 25

RESULT 49  
US-10-956-157-146594  
; Sequence 146594, Application US/10956157  
; Publication No. US20050118625A1  
; GENERAL INFORMATION:

; APPLICANT: Wyeth  
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH  
; FILE REFERENCE: 031896-043000 (AM 101081)  
; CURRENT APPLICATION NUMBER: US/10/956,157  
; CURRENT FILING DATE: 2004-10-04  
; NUMBER OF SEQ ID NOS: 319805  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 146594  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Probe Sequence  
US-10-956-157-146594

Query Match 1.5%; Score 25; DB 1; Length 25;  
Best Local Similarity 100.0%; Pred. No. 72;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 889 ACCGGACTGTGTGCCGGGAGATCCG 913  
|||||

Db 1 ACCGGACTGTGTGCCGGGAGATCCG 25

RESULT 50  
US-10-956-157-146923  
; Sequence 146923, Application US/10956157  
; Publication No. US20050118625A1  
; GENERAL INFORMATION:

; APPLICANT: Wyeth  
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH  
; FILE REFERENCE: 031896-043000 (AM 101081)  
; CURRENT APPLICATION NUMBER: US/10/956,157  
; CURRENT FILING DATE: 2004-10-04  
; NUMBER OF SEQ ID NOS: 319805  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 146923  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Probe Sequence  
US-10-956-157-146923

Query Match 1.5%; Score 25; DB 1; Length 25;  
Best Local Similarity 100.0%; Pred. No. 72;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 544 ACCGGCAGCAGCAGCATGTCTGGA 568  
|||||

Db 1 ACCGGCAGCAGCAGCATGTCTGGA 25

RESULT 51  
US-10-956-157-156812  
; Sequence 156812, Application US/10956157  
; Publication No. US20050118625A1  
; GENERAL INFORMATION:

; APPLICANT: Wyeth  
; APPLICANT: Mounts, William  
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH  
; FILE REFERENCE: 031896-043000 (AM 101081)  
; CURRENT APPLICATION NUMBER: US/10/956,157  
; CURRENT FILING DATE: 2004-10-04  
; NUMBER OF SEQ ID NOS: 319805  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 156812  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Probe Sequence  
US-10-956-157-156812

Query Match 1.5%; Score 25; DB 1; Length 25;  
Best Local Similarity 100.0%; Pred. No. 72;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1379 AAAGCACCAGGAGGAGTGATGTG 1403  
|||||

Db 1 AAAGCACCAGGAGGAGTGATGTG 25

RESULT 52  
US-10-956-157-158656  
; Sequence 158656, Application US/10956157  
; Publication No. US20050118625A1  
; GENERAL INFORMATION:

; APPLICANT: Wyeth  
; APPLICANT: Mounts, William  
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH  
; FILE REFERENCE: 031896-043000 (AM 101081)  
; CURRENT APPLICATION NUMBER: US/10/956,157  
; CURRENT FILING DATE: 2004-10-04  
; NUMBER OF SEQ ID NOS: 319805  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 158656  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Probe Sequence  
US-10-956-157-158656

Query Match 1.5%; Score 25; DB 1; Length 25;  
Best Local Similarity 100.0%; Pred. No. 72;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1083 AAGTCCTACCAAGTGAAGATGCTCA 1107  
|||||

Db 1 AAGTCCTACCAAGTGAAGATGCTCA 25

RESULT 53  
US-10-956-157-159440  
; Sequence 159440, Application US/10956157  
; Publication No. US20050118625A1  
; GENERAL INFORMATION:

; APPLICANT: Wyeth  
; APPLICANT: Mounts, William  
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH  
; FILE REFERENCE: 031896-043000 (AM 101081)  
; CURRENT APPLICATION NUMBER: US/10/956,157  
; CURRENT FILING DATE: 2004-10-04

; NUMBER OF SEQ ID NOS: 319805  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 159440  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Probe Sequence  
US-10-956-157-159440

Query Match 1.5%; Score 25; DB 1; Length 25;  
Best Local Similarity 100.0%; Pred. No. 72;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1071 AACGAGCTGCTAAAGTCTTACCAGT 1095  
|||||  
Db 1 AACGAGCTGCTAAAGTCTTACCAGT 25

RESULT 54  
US-10-956-157-168291  
; Sequence 168291, Application US/10956157  
; Publication No. US20050118625A1  
; GENERAL INFORMATION:  
; APPLICANT: Wyeth  
; APPLICANT: Mounts, William  
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH  
; FILE REFERENCE: 031896-043000 (AM 101081)  
; CURRENT APPLICATION NUMBER: US/10/956,157  
; CURRENT FILING DATE: 2004-10-04  
; NUMBER OF SEQ ID NOS: 319805  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 168291  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Probe Sequence  
US-10-956-157-168291

Query Match 1.5%; Score 25; DB 1; Length 25;  
Best Local Similarity 100.0%; Pred. No. 72;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 182 AATTCAAATGCTGTCAACGGGGTG 206  
|||||  
Db 1 AATTCAAATGCTGTCAACGGGGTG 25

RESULT 55  
US-10-956-157-172467  
; Sequence 172467, Application US/10956157  
; Publication No. US20050118625A1  
; GENERAL INFORMATION:  
; APPLICANT: Wyeth  
; APPLICANT: Mounts, William  
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH  
; FILE REFERENCE: 031896-043000 (AM 101081)  
; CURRENT APPLICATION NUMBER: US/10/956,157  
; CURRENT FILING DATE: 2004-10-04  
; NUMBER OF SEQ ID NOS: 319805  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 172467  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Probe Sequence  
US-10-956-157-172467

Query Match 1.5%; Score 25; DB 1; Length 25;  
Best Local Similarity 100.0%; Pred. No. 72;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1140 CAGTTTAACGTGGGTGCCGGCTGG 1164  
|||||  
Db 1 CAGTTTAACGTGGGTGCCGGCTGG 25

## RESULT 56

US-10-956-157-174696  
; Sequence 174696, Application US/10956157  
; Publication No. US20050118625A1  
; GENERAL INFORMATION:  
; APPLICANT: Wyeth  
; APPLICANT: Mounts, William  
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH  
; FILE REFERENCE: 031896-043000 (AM 101081)  
; CURRENT APPLICATION NUMBER: US/10/956,157  
; CURRENT FILING DATE: 2004-10-04  
; NUMBER OF SEQ ID NOS: 319805  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 174696  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Probe Sequence  
US-10-956-157-174696

Query Match 1.5%; Score 25; DB 1; Length 25;  
Best Local Similarity 100.0%; Pred. No. 72;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 462 CAGCTTGAGGAGTTCCTGAACACAGA 486  
|||||  
Db 1 CAGCTTGAGGAGTTCCTGAACACAGA 25

## RESULT 57

US-10-956-157-174708  
; Sequence 174708, Application US/10956157  
; Publication No. US20050118625A1  
; GENERAL INFORMATION:  
; APPLICANT: Wyeth  
; APPLICANT: Mounts, William  
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH  
; FILE REFERENCE: 031896-043000 (AM 101081)  
; CURRENT APPLICATION NUMBER: US/10/956,157  
; CURRENT FILING DATE: 2004-10-04  
; NUMBER OF SEQ ID NOS: 319805  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 174708  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Probe Sequence  
US-10-956-157-174708

Query Match 1.5%; Score 25; DB 1; Length 25;  
Best Local Similarity 100.0%; Pred. No. 72;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 780 CAGCCCTTCCTTGAGATGATACACG 804  
|||||  
Db 1 CAGCCCTTCCTTGAGATGATACACG 25

## RESULT 58

US-10-956-157-174902  
; Sequence 174902, Application US/10956157  
; Publication No. US20050118625A1  
; GENERAL INFORMATION:  
; APPLICANT: Wyeth  
; APPLICANT: Mounts, William  
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH  
; FILE REFERENCE: 031896-043000 (AM 101081)  
; CURRENT APPLICATION NUMBER: US/10/956,157  
; CURRENT FILING DATE: 2004-10-04  
; NUMBER OF SEQ ID NOS: 319805

; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 174902  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Probe Sequence  
US-10-956-157-174902

Query Match 1.5%; Score 25; DB 1; Length 25;  
Best Local Similarity 100.0%; Pred. No. 72;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1441 CAGCTCCCCCAGAGTACTGCAG 1465  
|||  
Db 1 CAGCTCCCCCAGAGTACTGCAG 25

## RESULT 59

US-10-956-157-176821  
; Sequence 176821, Application US/10956157  
; Publication No. US20050118625A1  
; GENERAL INFORMATION:

; APPLICANT: Wyeth

; APPLICANT: Mounts, William

; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH

; FILE REFERENCE: 031896-043000 (AM 101081)

; CURRENT APPLICATION NUMBER: US/10/956,157

; CURRENT FILING DATE: 2004-10-04

; NUMBER OF SEQ ID NOS: 319805

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 176821

; LENGTH: 25

; TYPE: DNA

; ORGANISM: Probe Sequence

US-10-956-157-176821

Query Match 1.5%; Score 25; DB 1; Length 25;  
Best Local Similarity 100.0%; Pred. No. 72;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 948 CAGTGTGACAGTCCGGGAGATCT 972  
|||  
Db 1 CAGTGTGACAGTCCGGGAGATCT 25

## RESULT 60

US-10-956-157-178550  
; Sequence 178550, Application US/10956157  
; Publication No. US20050118625A1  
; GENERAL INFORMATION:

; APPLICANT: Wyeth

; APPLICANT: Mounts, William

; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH

; FILE REFERENCE: 031896-043000 (AM 101081)

; CURRENT APPLICATION NUMBER: US/10/956,157

; CURRENT FILING DATE: 2004-10-04

; NUMBER OF SEQ ID NOS: 319805

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 178550

; LENGTH: 25

; TYPE: DNA

; ORGANISM: Probe Sequence

US-10-956-157-178550

Query Match 1.5%; Score 25; DB 1; Length 25;  
Best Local Similarity 100.0%; Pred. No. 72;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 602 CATCATAGACGAGCTCTCCAGGAC 626  
|||  
Db 1 CATCATAGACGAGCTCTCCAGGAC 25

## RESULT 61

US-10-956-157-178867  
; Sequence 178867, Application US/10956157  
; Publication No. US20050118625A1  
; GENERAL INFORMATION:

; APPLICANT: Wyeth

; APPLICANT: Mounts, William

; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH

; FILE REFERENCE: 031896-043000 (AM 101081)

; CURRENT APPLICATION NUMBER: US/10/956,157

; CURRENT FILING DATE: 2004-10-04

; NUMBER OF SEQ ID NOS: 319805

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 178867

; LENGTH: 25

; TYPE: DNA

; ORGANISM: Probe Sequence

US-10-956-157-178867

Query Match 1.5%; Score 25; DB 1; Length 25;  
Best Local Similarity 100.0%; Pred. No. 72;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1289 CATCACTGTGACGGTCCCTGTAGAA 1313  
|||  
Db 1 CATCACTGTGACGGTCCCTGTAGAA 25

## RESULT 62

US-10-956-157-186901  
; Sequence 186901, Application US/10956157  
; Publication No. US20050118625A1  
; GENERAL INFORMATION:

; APPLICANT: Wyeth

; APPLICANT: Mounts, William

; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH

; FILE REFERENCE: 031896-043000 (AM 101081)

; CURRENT APPLICATION NUMBER: US/10/956,157

; CURRENT FILING DATE: 2004-10-04

; NUMBER OF SEQ ID NOS: 319805

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 186901

; LENGTH: 25

; TYPE: DNA

; ORGANISM: Probe Sequence

US-10-956-157-186901

Query Match 1.5%; Score 25; DB 1; Length 25;  
Best Local Similarity 100.0%; Pred. No. 72;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1602 CTCCTGCATGCAACTTAATTCATATA 1626  
|||  
Db 1 CTCCTGCATGCAACTTAATTCATATA 25

## RESULT 63

US-10-956-157-186902  
; Sequence 186902, Application US/10956157  
; Publication No. US20050118625A1  
; GENERAL INFORMATION:

; APPLICANT: Wyeth

; APPLICANT: Mounts, William

; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH

; FILE REFERENCE: 031896-043000 (AM 101081)

; CURRENT APPLICATION NUMBER: US/10/956,157

; CURRENT FILING DATE: 2004-10-04

; NUMBER OF SEQ ID NOS: 319805

; SOFTWARE: PatentIn version 3.2

```

; SEQ ID NO 186902
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-186902

Query Match      1.5%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 72;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1602 CTCCTGCATGCAACTAATTCATAA 1626
      |||
Db 1 CTCCTGCATGCAACTAATTCATAA 25

RESULT 64
US-10-956-157-186903
; Sequence 186903, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956.157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 186903
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-186903

Query Match      1.5%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 72;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1602 CTCCTGCATGCAACTAATTCATAA 1626
      |||
Db 1 CTCCTGCATGCAACTAATTCATAA 25

RESULT 65
US-10-956-157-186908
; Sequence 186908, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956.157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 186908
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-186908

Query Match      1.5%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 72;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1482 CTCACGTCACCAAGTAACCAAGCC 1506
      |||
Db 1 CTCACGTCACCAAGTAACCAAGCC 25

RESULT 66
US-10-956-157-186914
; Sequence 186914, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956.157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 186914
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-186914

Query Match      1.5%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 72;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1038 CTCACGTCGCTGAGAGTTGACCA 1062
      |||
Db 1 CTCACGTCGCTGAGAGTTGACCA 25

RESULT 67
US-10-956-157-188008
; Sequence 188008, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956.157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 188008
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-188008

Query Match      1.5%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 72;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 78 CTGCTGCTGACCTGGGAGAGTGGGC 102
      |||
Db 1 CTGCTGCTGACCTGGGAGAGTGGGC 25

RESULT 68
US-10-956-157-188038
; Sequence 188038, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956.157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 188038
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-188038

Query Match      1.5%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 72;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 78 CTGCTGCTGACCTGGGAGAGTGGGC 102
      |||
Db 1 CTGCTGCTGACCTGGGAGAGTGGGC 25
```

; LENGTH: 25

; TYPE: DNA

; ORGANISM: Probe Sequence

US-10-956-157-188038

Query Match 1.5%; Score 25; DB 1; Length 25;

Best Local Similarity 100.0%; Pred. No. 72;

Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 407 CTGCATGAAGTTCTACGACGGTC 431

Db 1 CTGCATGAAGTTCTACGACGGTC 25

RESULT 69

US-10-956-157-189641

; Sequence 189641, Application US/10956157

; Publication No. US20050118625A1

; GENERAL INFORMATION:

; APPLICANT: Wyeth

; APPLICANT: Mounts, William

; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH

; TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES

; FILE REFERENCE: 031896-043000 (AM 101081)

; CURRENT APPLICATION NUMBER: US/10/956,157

; CURRENT FILING DATE: 2004-10-04

; NUMBER OF SEQ ID NOS: 319805

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 189641

; LENGTH: 25

; TYPE: DNA

; ORGANISM: Probe Sequence

US-10-956-157-189641

Query Match 1.5%; Score 25; DB 1; Length 25;

Best Local Similarity 100.0%; Pred. No. 72;

Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 976 CTGTGGACTGTTCCACCAACACC 1000

Db 1 CTGTGGACTGTTCCACCAACACC 25

RESULT 70

US-10-956-157-191487

; Sequence 191487, Application US/10956157

; Publication No. US20050118625A1

; GENERAL INFORMATION:

; APPLICANT: Wyeth

; APPLICANT: Mounts, William

; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH

; TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES

; FILE REFERENCE: 031896-043000 (AM 101081)

; CURRENT APPLICATION NUMBER: US/10/956,157

; CURRENT FILING DATE: 2004-10-04

; NUMBER OF SEQ ID NOS: 319805

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 191487

; LENGTH: 25

; TYPE: DNA

; ORGANISM: Probe Sequence

US-10-956-157-191487

Query Match 1.5%; Score 25; DB 1; Length 25;

Best Local Similarity 100.0%; Pred. No. 72;

Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 884 CGATGACCGGACTGTGTCCCGGGAG 908

Db 1 CGATGACCGGACTGTGTCCCGGGAG 25

RESULT 71

US-10-956-157-193107

; Sequence 193107, Application US/10956157

; Publication No. US20050118625A1

; GENERAL INFORMATION:

; APPLICANT: Wyeth

; APPLICANT: Mounts, William

; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH

; TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES

; FILE REFERENCE: 031896-043000 (AM 101081)

; CURRENT APPLICATION NUMBER: US/10/956,157

; CURRENT FILING DATE: 2004-10-04

; NUMBER OF SEQ ID NOS: 319805

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 193107

; LENGTH: 25

; TYPE: DNA

; ORGANISM: Probe Sequence

US-10-956-157-193107

Query Match 1.5%; Score 25; DB 1; Length 25;

Best Local Similarity 100.0%; Pred. No. 72;

Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 490 CGCCCTTCTACTTCTGGATGATGG 514

Db 1 CGCCCTTCTACTTCTGGATGATGG 25

RESULT 72

US-10-956-157-193726

; Sequence 193726, Application US/10956157

; Publication No. US20050118625A1

; GENERAL INFORMATION:

; APPLICANT: Wyeth

; APPLICANT: Mounts, William

; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH

; TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES

; FILE REFERENCE: 031896-043000 (AM 101081)

; CURRENT APPLICATION NUMBER: US/10/956,157

; CURRENT FILING DATE: 2004-10-04

; NUMBER OF SEQ ID NOS: 319805

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 193726

; LENGTH: 25

; TYPE: DNA

; ORGANISM: Probe Sequence

US-10-956-157-193726

Query Match 1.5%; Score 25; DB 1; Length 25;

Best Local Similarity 100.0%; Pred. No. 72;

Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 341 CCCAGGAGTGTGCAATGAGACCATG 365

Db 1 CCCAGGAGTGTGCAATGAGACCATG 25

RESULT 73

US-10-956-157-194937

; Sequence 194937, Application US/10956157

; Publication No. US20050118625A1

; GENERAL INFORMATION:

; APPLICANT: Wyeth

; APPLICANT: Mounts, William

; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH

; TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES

; FILE REFERENCE: 031896-043000 (AM 101081)

; CURRENT APPLICATION NUMBER: US/10/956,157

; CURRENT FILING DATE: 2004-10-04

; NUMBER OF SEQ ID NOS: 319805

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 194937

; LENGTH: 25

```
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-194937

Query Match      1.5%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 72;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 390 CCCTGCTGAAACAGACCTGCATGA 414
Db 1 CCCTGCTGAAACAGACCTGCATGA 25

RESULT 74
US-10-956-157-195328
; Sequence 195328, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 195328
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-195328

Query Match      1.5%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 72;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 854 CCCGCCAACAGAAATTCATACGAGAA 878
Db 1 CCCGCCAACAGAAATTCATACGAGAA 25

RESULT 75
US-10-956-157-195368
; Sequence 195368, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 195368
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-195368

Query Match      1.5%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 72;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1467 CCCCCAGAGAGCTCTGCACGTCA 1491
Db 1 CCCCCAGAGAGCTCTGCACGTCA 25

RESULT 76
US-10-956-157-196424
```

```
; Sequence 196424, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 196424
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-196424

Query Match      1.5%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 72;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 590 CCGCGCGTCCAGCATCATAGACGAG 614
Db 1 CCGCGCGTCCAGCATCATAGACGAG 25

RESULT 77
US-10-956-157-199713
; Sequence 199713, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 199713
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-199713

Query Match      1.5%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 72;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 106 TCCTGGGGGACACGCGTCTCAGA 130
Db 1 TCCTGGGGGACACGCGTCTCAGA 25

RESULT 78
US-10-956-157-206442
; Sequence 206442, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 206442
; LENGTH: 25
; TYPE: DNA
```



```
; ORGANISM: Probe Sequence
US-10-956-157-206442

Query Match      1.5%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 72;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 782 GCCCTTCCTTCGAGTATACACGAG 806
      |||||
Db 1 GCCCTTCCTTCGAGTATACACGAG 25

RESULT 79
US-10-956-157-208499
; Sequence 208499, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 208499
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-208499

Query Match      1.5%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 72;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1121 GCTGAGCAGCTGAACGAGCAGTTT 1145
      |||||
Db 1 GCTGAGCAGCTGAACGAGCAGTTT 25

RESULT 80
US-10-956-157-212934
; Sequence 212934, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 212934
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-212934

Query Match      1.5%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 72;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1364 GCAGGAATACCGCAAAAGCACCGG 1388
      |||||
Db 1 GCAGGAATACCGCAAAAGCACCGG 25

RESULT 81
US-10-956-157-215054
; Sequence 215054, Application US/10956157
```

```
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 215054
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-215054

Query Match      1.5%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 72;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 551 GCAGACGCACATGCTGGATGTCATG 575
      |||||
Db 1 GCAGACGCACATGCTGGATGTCATG 25

RESULT 82
US-10-956-157-216983
; Sequence 216983, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 216983
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-216983

Query Match      1.5%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 72;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 247 GCAAGACACTGCTCAGCAACCTAGA 271
      |||||
Db 1 GCAAGACACTGCTCAGCAACCTAGA 25

RESULT 83
US-10-956-157-218349
; Sequence 218349, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 218349
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
```

US-10-956-157-218349

Query Match 1.5%; Score 25; DB 1; Length 25;  
Best Local Similarity 100.0%; Pred. No. 72;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1596 GAATTGCTCTCGCATGCAACTAATT 1620  
|||||  
Db 1 GAATTGCTCTCGCATGCAACTAATT 25

## RESULT 84

US-10-956-157-218350  
; Sequence 218350, Application US/10956157  
; Publication No. US20050118625A1  
; GENERAL INFORMATION:

; APPLICANT: Wyeth  
; APPLICANT: Mounts, William  
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH  
; FILE REFERENCE: 031896-043000 (AM 101081)  
; CURRENT APPLICATION NUMBER: US/10/956,157  
; CURRENT FILING DATE: 2004-10-04  
; NUMBER OF SEQ ID NOS: 319805  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 218350  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Probe Sequence  
US-10-956-157-218350

Query Match 1.5%; Score 25; DB 1; Length 25;  
Best Local Similarity 100.0%; Pred. No. 72;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1596 GAATTGCTCTCGCATGCAACTAATT 1620  
|||||  
Db 1 GAATTGCTCTCGCATGCAACTAATT 25

## RESULT 85

US-10-956-157-218351  
; Sequence 218351, Application US/10956157  
; Publication No. US20050118625A1  
; GENERAL INFORMATION:

; APPLICANT: Wyeth  
; APPLICANT: Mounts, William  
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH  
; FILE REFERENCE: 031896-043000 (AM 101081)  
; CURRENT APPLICATION NUMBER: US/10/956,157  
; CURRENT FILING DATE: 2004-10-04  
; NUMBER OF SEQ ID NOS: 319805  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 218351  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Probe Sequence  
US-10-956-157-218351

Query Match 1.5%; Score 25; DB 1; Length 25;  
Best Local Similarity 100.0%; Pred. No. 72;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1596 GAATTGCTCTCGCATGCAACTAATT 1620  
|||||  
Db 1 GAATTGCTCTCGCATGCAACTAATT 25

## RESULT 86

US-10-956-157-219734  
; Sequence 219734, Application US/10956157  
; Publication No. US20050118625A1

; GENERAL INFORMATION:

; APPLICANT: Wyeth  
; APPLICANT: Mounts, William  
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH  
; FILE REFERENCE: 031896-043000 (AM 101081)  
; CURRENT APPLICATION NUMBER: US/10/956,157  
; CURRENT FILING DATE: 2004-10-04  
; NUMBER OF SEQ ID NOS: 319805  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 219734  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Probe Sequence  
US-10-956-157-219734

Query Match 1.5%; Score 25; DB 1; Length 25;  
Best Local Similarity 100.0%; Pred. No. 72;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1311 GAAGTCTCCAGGAAGAACCTAAAT 1335  
|||||  
Db 1 GAAGTCTCCAGGAAGAACCTAAAT 25

## RESULT 87

US-10-956-157-220245  
; Sequence 220245, Application US/10956157  
; Publication No. US20050118625A1  
; GENERAL INFORMATION:

; APPLICANT: Wyeth  
; APPLICANT: Mounts, William  
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH  
; FILE REFERENCE: 031896-043000 (AM 101081)  
; CURRENT APPLICATION NUMBER: US/10/956,157  
; CURRENT FILING DATE: 2004-10-04  
; NUMBER OF SEQ ID NOS: 319805  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 220245  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Probe Sequence  
US-10-956-157-220245

Query Match 1.5%; Score 25; DB 1; Length 25;  
Best Local Similarity 100.0%; Pred. No. 72;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 941 GAAGGACCAAGTGACAAAGTGCCGG 965  
|||||  
Db 1 GAAGGACCAAGTGACAAAGTGCCGG 25

## RESULT 88

US-10-956-157-221279  
; Sequence 221279, Application US/10956157  
; Publication No. US20050118625A1  
; GENERAL INFORMATION:

; APPLICANT: Wyeth  
; APPLICANT: Mounts, William  
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH  
; FILE REFERENCE: 031896-043000 (AM 101081)  
; CURRENT APPLICATION NUMBER: US/10/956,157  
; CURRENT FILING DATE: 2004-10-04  
; NUMBER OF SEQ ID NOS: 319805  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 221279  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Probe Sequence  
US-10-956-157-221279

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; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 221280
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-221280
Query Match      1.5%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 72;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1588 GAAGAACAGAAATTGCTCTGCGATGC 1612
|||||
Db 1 GAAGAACAGAAATTGCTCTGCGATGC 25

RESULT 89
US-10-956-157-221280
; Sequence 221280, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 221280
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-221280

Query Match      1.5%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 72;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1588 GAAGAACAGAAATTGCTCTGCGATGC 1612
|||||
Db 1 GAAGAACAGAAATTGCTCTGCGATGC 25

RESULT 90
US-10-956-157-222407
; Sequence 222407, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 222407
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-222407

Query Match      1.5%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 72;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1325 GAACCCAAATTTATGGAGACCGTG 1349
|||||
Db 1 GAACCCAAATTTATGGAGACCGTG 25

RESULT 91
US-10-956-157-225352
; Sequence 225352, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
```

```
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 225352
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-225352
Query Match      1.5%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 72;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1355 GAAAGCGCTGCAGGAATACCGCAA 1379
|||||
Db 1 GAAAGCGCTGCAGGAATACCGCAA 25

RESULT 92
US-10-956-157-228789
; Sequence 228789, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 228789
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-228789
Query Match      1.5%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 72;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1571 GACTCTGCTGCTCATGGAGAACA 1595
|||||
Db 1 GACTCTGCTGCTCATGGAGAACA 25

RESULT 93
US-10-956-157-229312
; Sequence 229312, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 229312
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-229312
```

```
Query Match      1.5%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 72;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 119 GACGGTCTCAGACAATGAGCTCCAG 143
|||||
Db 1 GACGGTCTCAGACAATGAGCTCCAG 25
|||||

RESULT 94
US-10-956-157-230136
; Sequence 230136, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 230136
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-230136

Query Match      1.5%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 72;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 404 GACCTGCATGAAGTCTTACGCACGC 428
|||||
Db 1 GACCTGCATGAAGTCTTACGCACGC 25
|||||

RESULT 95
US-10-956-157-230317
; Sequence 230317, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 230317
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-230317

Query Match      1.5%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 72;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1185 GACCAGTACTATCTGCGGGTCACCA 1209
|||||
Db 1 GACCAGTACTATCTGCGGGTCACCA 25
|||||

RESULT 96
US-10-956-157-231573
; Sequence 231573, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
```

```
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 231573
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-231573
```

```
Query Match      1.5%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 72;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 135 GAGCTCCAGGAATGTCCAATCAGG 159
|||||
Db 1 GAGCTCCAGGAATGTCCAATCAGG 25
|||||
```

```
RESULT 97
US-10-956-157-231724
; Sequence 231724, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 231724
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-231724
```

```
Query Match      1.5%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 72;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1074 GAGCTGCTAAAGTCCTTACCAGTGGG 1098
|||||
Db 1 GAGCTGCTAAAGTCCTTACCAGTGGG 25
|||||
```

```
RESULT 98
US-10-956-157-231783
; Sequence 231783, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 231783
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-231783
```

```
Query Match      1.5%; Score 25; DB 1; Length 25;
```

Best Local Similarity 100.0%; Pred. No. 72;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1137 GAGCAGTTTAACTGGGTGTCGCCGC 1161  
|||||  
Db 1 GAGCAGTTTAACTGGGTGTCGCCGC 25

RESULT 99  
US-10-956-157-232704  
; Sequence 232704, Application US/10956157  
; Publication No. US20050118625A1  
; GENERAL INFORMATION:  
; APPLICANT: Wyeth  
; APPLICANT: Mounts, William  
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH  
; FILE REFERENCE: 031896-043000 (AM 101081)  
; CURRENT APPLICATION NUMBER: US/10/956,157  
; CURRENT FILING DATE: 2004-10-04  
; NUMBER OF SEQ ID NOS: 319805  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 232704  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Probe Sequence  
US-10-956-157-232704

Query Match 1.5%; Score 25; DB 1; Length 25;  
Best Local Similarity 100.0%; Pred. No. 72;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1341 GAGACCGTGGCGGAGAAAGCGCTGC 1365  
|||||  
Db 1 GAGACCGTGGCGGAGAAAGCGCTGC 25

RESULT 100  
US-10-956-157-233030  
; Sequence 233030, Application US/10956157  
; Publication No. US20050118625A1  
; GENERAL INFORMATION:  
; APPLICANT: Wyeth  
; APPLICANT: Mounts, William  
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH  
; FILE REFERENCE: 031896-043000 (AM 101081)  
; CURRENT APPLICATION NUMBER: US/10/956,157  
; CURRENT FILING DATE: 2004-10-04  
; NUMBER OF SEQ ID NOS: 319805  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 233030  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Probe Sequence  
US-10-956-157-233030

Query Match 1.5%; Score 25; DB 1; Length 25;  
Best Local Similarity 100.0%; Pred. No. 72;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 321 GAGACAAAGCTGAAGAGCTCCAG 345  
|||||  
Db 1 GAGACAAAGCTGAAGAGCTCCAG 25

RESULT 101  
US-10-956-157-233762  
; Sequence 233762, Application US/10956157  
; Publication No. US20050118625A1  
; GENERAL INFORMATION:  
; APPLICANT: Wyeth  
; APPLICANT: Mounts, William

; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH  
; TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES  
; FILE REFERENCE: 031896-043000 (AM 101081)  
; CURRENT APPLICATION NUMBER: US/10/956,157  
; CURRENT FILING DATE: 2004-10-04  
; NUMBER OF SEQ ID NOS: 319805  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 233762  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Probe Sequence  
US-10-956-157-233762

Query Match 1.5%; Score 25; DB 1; Length 25;  
Best Local Similarity 100.0%; Pred. No. 72;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 966 GAGATCTTGTCTGTGGACTGTCCA 990  
|||||  
Db 1 GAGATCTTGTCTGTGGACTGTCCA 25

RESULT 102  
US-10-956-157-235882  
; Sequence 235882, Application US/10956157  
; Publication No. US20050118625A1  
; GENERAL INFORMATION:  
; APPLICANT: Wyeth  
; APPLICANT: Mounts, William  
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH  
; FILE REFERENCE: 031896-043000 (AM 101081)  
; CURRENT APPLICATION NUMBER: US/10/956,157  
; CURRENT FILING DATE: 2004-10-04  
; NUMBER OF SEQ ID NOS: 319805  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 235882  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Probe Sequence  
US-10-956-157-235882

Query Match 1.5%; Score 25; DB 1; Length 25;  
Best Local Similarity 100.0%; Pred. No. 72;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 468 GAGGAGTTCTCTGAACCGAGCTCGC 492  
|||||  
Db 1 GAGGAGTTCTCTGAACCGAGCTCGC 25

RESULT 103  
US-10-956-157-236817  
; Sequence 236817, Application US/10956157  
; Publication No. US20050118625A1  
; GENERAL INFORMATION:  
; APPLICANT: Wyeth  
; APPLICANT: Mounts, William  
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH  
; FILE REFERENCE: 031896-043000 (AM 101081)  
; CURRENT APPLICATION NUMBER: US/10/956,157  
; CURRENT FILING DATE: 2004-10-04  
; NUMBER OF SEQ ID NOS: 319805  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 236817  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Probe Sequence  
US-10-956-157-236817

Query Match 1.5%; Score 25; DB 1; Length 25;  
Best Local Similarity 100.0%; Pred. No. 72;

Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
Qy 43	GAGGCATGATGAGACTCTCTGCT 67
Db 1	GAGGCATGATGAGACTCTCTGCT 25
RESULT 104	
US-10-956-157-237638	
; Sequence 237638, Application US/10956157	
; Publication No. US20050118625A1	
; GENERAL INFORMATION:	
; APPLICANT: Wyeth	
; APPLICANT: Mounts, William	
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH	
; TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES	
; FILE REFERENCE: 031896-043000 (AM 101081)	
; CURRENT APPLICATION NUMBER: US/10/956,157	
; CURRENT FILING DATE: 2004-10-04	
; NUMBER OF SEQ ID NOS: 319805	
; SOFTWARE: PatentIn version 3.2	
; SEQ ID NO 237638	
; LENGTH: 25	
; TYPE: DNA	
; ORGANISM: Probe Sequence	
US-10-956-157-237638	
Query Match 1.5%; Score 25; DB 1; Length 25;	
Best Local Similarity 100.0%; Pred. No. 72;	
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
Qy 794	GATGATACACGAGGCTCAGCAGGCC 818
Db 1	GATGATACACGAGGCTCAGCAGGCC 25
RESULT 105	
US-10-956-157-238337	
; Sequence 238337, Application US/10956157	
; Publication No. US20050118625A1	
; GENERAL INFORMATION:	
; APPLICANT: Wyeth	
; APPLICANT: Mounts, William	
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH	
; TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES	
; FILE REFERENCE: 031896-043000 (AM 101081)	
; CURRENT APPLICATION NUMBER: US/10/956,157	
; CURRENT FILING DATE: 2004-10-04	
; NUMBER OF SEQ ID NOS: 319805	
; SOFTWARE: PatentIn version 3.2	
; SEQ ID NO 238337	
; LENGTH: 25	
; TYPE: DNA	
; ORGANISM: Probe Sequence	
US-10-956-157-238337	
Query Match 1.5%; Score 25; DB 1; Length 25;	
Best Local Similarity 100.0%; Pred. No. 72;	
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
Qy 506	GATGAATGGTGACCGCATGACTCC 530
Db 1	GATGAATGGTGACCGCATGACTCC 25
RESULT 106	
US-10-956-157-243092	
; Sequence 243092, Application US/10956157	
; Publication No. US20050118625A1	
; GENERAL INFORMATION:	
; APPLICANT: Wyeth	
; APPLICANT: Mounts, William	
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH	

; TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES	
; FILE REFERENCE: 031896-043000 (AM 101081)	
; CURRENT APPLICATION NUMBER: US/10/956,157	
; CURRENT FILING DATE: 2004-10-04	
; NUMBER OF SEQ ID NOS: 319805	
; SOFTWARE: PatentIn version 3.2	
; SEQ ID NO 243092	
; LENGTH: 25	
; TYPE: DNA	
; ORGANISM: Probe Sequence	
US-10-956-157-243092	
Query Match 1.5%; Score 25; DB 1; Length 25;	
Best Local Similarity 100.0%; Pred. No. 72;	
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
Qy 416	GTCTACGCACGCGTCTGCAGAAGT 440
Db 1	GTCTACGCACGCGTCTGCAGAAGT 25
RESULT 107	
US-10-956-157-252760	
; Sequence 252760, Application US/10956157	
; Publication No. US20050118625A1	
; GENERAL INFORMATION:	
; APPLICANT: Wyeth	
; APPLICANT: Mounts, William	
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH	
; TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES	
; FILE REFERENCE: 031896-043000 (AM 101081)	
; CURRENT APPLICATION NUMBER: US/10/956,157	
; CURRENT FILING DATE: 2004-10-04	
; NUMBER OF SEQ ID NOS: 319805	
; SOFTWARE: PatentIn version 3.2	
; SEQ ID NO 252760	
; LENGTH: 25	
; TYPE: DNA	
; ORGANISM: Probe Sequence	
US-10-956-157-252760	
Query Match 1.5%; Score 25; DB 1; Length 25;	
Best Local Similarity 100.0%; Pred. No. 72;	
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
Qy 1044	GTGCTGAGAGGTTGACCAGAAAT 1068
Db 1	GTGCTGAGAGGTTGACCAGAAAT 25
RESULT 108	
US-10-956-157-253138	
; Sequence 253138, Application US/10956157	
; Publication No. US20050118625A1	
; GENERAL INFORMATION:	
; APPLICANT: Wyeth	
; APPLICANT: Mounts, William	
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH	
; TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES	
; FILE REFERENCE: 031896-043000 (AM 101081)	
; CURRENT APPLICATION NUMBER: US/10/956,157	
; CURRENT FILING DATE: 2004-10-04	
; NUMBER OF SEQ ID NOS: 319805	
; SOFTWARE: PatentIn version 3.2	
; SEQ ID NO 253138	
; LENGTH: 25	
; TYPE: DNA	
; ORGANISM: Probe Sequence	
US-10-956-157-253138	
Query Match 1.5%; Score 25; DB 1; Length 25;	
Best Local Similarity 100.0%; Pred. No. 72;	
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	

```
QY 596 GTCCAGCATCATAGACGAGCTCTTC 620
      |||||
Db 1 GTCCAGCATCATAGACGAGCTCTTC 25

RESULT 109
US-10-956-157-255424
; Sequence 255424, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; FILE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 255424
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-255424

Query Match 1.5%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 72;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1394 GTGAGATGTGGATGTTGCTTTTGCA 1418
      |||||
Db 1 GTGAGATGTGGATGTTGCTTTTGCA 25

RESULT 110
US-10-956-157-255957
; Sequence 255957, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; FILE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 255957
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-255957

Query Match 1.5%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 72;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 383 GTGTAAGCCCTGCCTGAACAGACC 407
      |||||
Db 1 GTGTAAGCCCTGCCTGAACAGACC 25

RESULT 111
US-10-956-157-256203
; Sequence 256203, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; FILE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
```

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; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 256203
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-256203

Query Match 1.5%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 72;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 348 GTGTGCAATGAGACCATGATGCCCC 372
      |||||
Db 1 GTGTGCAATGAGACCATGATGCCCC 25

RESULT 112
US-10-956-157-261789
; Sequence 261789, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; FILE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 261789
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-261789

Query Match 1.5%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 72;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1259 GGTGTCGTGAGCTCTTTGACTCT 1283
      |||||
Db 1 GGTGTCGTGAGCTCTTTGACTCT 25

RESULT 113
US-10-956-157-266662
; Sequence 266662, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; FILE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 266662
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-266662

Query Match 1.5%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 72;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

Qy 566 GGATGTCATGCAGGACCACTTCAGC 590  
|||  
Db 1 GGATGTCATGCAGGACCACTTCAGC 25

RESULT 114

US-10-956-157-268124  
; Sequence 268124, Application US/10956157  
; Publication No. US20050118625A1

```

; Applicant:
; Applicant: Wyeth
; Applicant: Mounts, William
; Title of Invention: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; Title of Invention: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES

```

RESULT 115

US-10-956-157-269972  
; Sequence 269972, Application US/10956157  
; Publication No. US20050118625A1

Query Match	1.5%;	Score 25;	DB 1;	Length 25;
Best Local Similarity	100.0%;	Pred. No. 72;		
Matches 25:	Conservative	0:	Mismatches	0:
	Indels	0:	Gaps	0:

RESULT 116

US-10-956-157-273702  
; Sequence 273702, Application US/10956157  
; Publication No. US20050118625A1

```

; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 273702

```

Query Match	1.5%;	Score 25;	DB 1;	Length 25;
Best Local Similarity	100.0%;	Pred. No. 72;		
Matches 25;	Conservative	0;	Mismatches	0;
Gaps	0;	Indels	0;	Gaps

RESULT 117

US-10-956-157-274079  
; Sequence 274079, Application US/10956157  
; Publication No. US20050118625A1

Query Match	1.5%	Score 25;	DB 1;	Length 25;
Best Local Similarity	100.0%;	pred. No. 72;		
Matches 25;	Conservative	0;	Mismatches	0;
			Indels	0;
			Gaps	0;

RESULT 118

US-10-956-157-274264  
; Sequence 274264, Application US/10956157  
; Publication No. US20050118625A1

Query Match	1.5%;	Score 25;	DB 1;	Length 25;
Best Local Similarity	100.0%;	Pred. No. 72;		
Matches 25: Conservative	0;	Mismatches	0;	Gaps 0;
Indels	0;			



Db 1 GCGGAGACAGTACTATCTGCGG 25  
|||||

## RESULT 119

US-10-956-157-274647  
; Sequence 274647, Application US/10956157  
; Publication No. US20050118625A1

## GENERAL INFORMATION:

; APPLICANT: Wyeth  
; APPLICANT: Mounts, William  
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH  
; TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES  
; FILE REFERENCE: 031896-043000 (AM 101081)  
; CURRENT APPLICATION NUMBER: US/10/956,157  
; CURRENT FILING DATE: 2004-10-04  
; NUMBER OF SEQ ID NOS: 319805  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 274647  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Probe Sequence  
US-10-956-157-274647

Query Match 1.5%; Score 25; DB 1; Length 25;  
Best Local Similarity 100.0%; Pred. No. 72;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 20 GCGTGCGCAAGACTCCAGAAATTGGA 44  
|||||

Db 1 GCGTGCGCAAGACTCCAGAAATTGGA 25  
|||||

## RESULT 120

US-10-956-157-279222  
; Sequence 279222, Application US/10956157  
; Publication No. US20050118625A1

## GENERAL INFORMATION:

; APPLICANT: Wyeth  
; APPLICANT: Mounts, William  
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH  
; TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES  
; FILE REFERENCE: 031896-043000 (AM 101081)  
; CURRENT APPLICATION NUMBER: US/10/956,157  
; CURRENT FILING DATE: 2004-10-04  
; NUMBER OF SEQ ID NOS: 319805  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 279222  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Probe Sequence  
US-10-956-157-279222

Query Match 1.5%; Score 25; DB 1; Length 25;  
Best Local Similarity 100.0%; Pred. No. 72;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1295 TGTGACGGTCCCTGAGAGTCTCC 1319  
|||||

Db 1 TGTGACGGTCCCTGAGAGTCTCC 25  
|||||

## RESULT 121

US-10-956-157-281215  
; Sequence 281215, Application US/10956157  
; Publication No. US20050118625A1

## GENERAL INFORMATION:

; APPLICANT: Wyeth  
; APPLICANT: Mounts, William  
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH  
; TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES  
; FILE REFERENCE: 031896-043000 (AM 101081)  
; CURRENT APPLICATION NUMBER: US/10/956,157

; CURRENT FILING DATE: 2004-10-04  
; NUMBER OF SEQ ID NOS: 319805  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 281215  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Probe Sequence  
US-10-956-157-281215

Query Match 1.5%; Score 25; DB 1; Length 25;  
Best Local Similarity 100.0%; Pred. No. 72;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 150 TCCAATCAGGAAGTAAGTACGTCA 174  
|||||

Db 1 TCCAATCAGGAAGTAAGTACGTCA 25  
|||||

## RESULT 122

US-10-956-157-285427  
; Sequence 285427, Application US/10956157  
; Publication No. US20050118625A1

## GENERAL INFORMATION:

; APPLICANT: Wyeth  
; APPLICANT: Mounts, William  
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH  
; TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES  
; FILE REFERENCE: 031896-043000 (AM 101081)  
; CURRENT APPLICATION NUMBER: US/10/956,157  
; CURRENT FILING DATE: 2004-10-04  
; NUMBER OF SEQ ID NOS: 319805  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 285427  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Probe Sequence  
US-10-956-157-285427

Query Match 1.5%; Score 25; DB 1; Length 25;  
Best Local Similarity 100.0%; Pred. No. 72;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 52 TGAAGACTCTCTGCTGTTTGTGGG 76  
|||||

Db 1 TGAAGACTCTCTGCTGTTTGTGGG 25  
|||||

## RESULT 123

US-10-956-157-285561  
; Sequence 285561, Application US/10956157  
; Publication No. US20050118625A1

## GENERAL INFORMATION:

; APPLICANT: Wyeth  
; APPLICANT: Mounts, William  
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH  
; TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES  
; FILE REFERENCE: 031896-043000 (AM 101081)  
; CURRENT APPLICATION NUMBER: US/10/956,157  
; CURRENT FILING DATE: 2004-10-04  
; NUMBER OF SEQ ID NOS: 319805  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 285561  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Probe Sequence  
US-10-956-157-285561

Query Match 1.5%; Score 25; DB 1; Length 25;  
Best Local Similarity 100.0%; Pred. No. 72;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 351 TGCATGAGACCATGATGGCCCTCT 375  
|||||

```
Db      1  TGCATGAGACCATGATGCCCTCT 25

RESULT 124
US-10-956-157-285688
; Sequence 285688, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 285688
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-285688

Query Match      1.5%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 72;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      256  TGCTCAGCAACTAGAGAGCCAA 280
|||||
Db      1  TGCTCAGCAACTAGAGAGCCAA 25

RESULT 125
US-10-956-157-287832
; Sequence 287832, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 287832
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-287832

Query Match      1.5%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 72;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      960  TGCCGGGAGATCTTGTCTGTGGACT 984
|||||
Db      1  TGCCGGGAGATCTTGTCTGTGGACT 25

RESULT 126
US-10-956-157-291738
; Sequence 291738, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
```

```
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 291738
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-291738

Query Match      1.5%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 72;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1002  TCCAGGCTAAGCTGCGGCGGAGC 1026
|||||
Db      1  TCCAGGCTAAGCTGCGGCGGAGC 25

RESULT 127
US-10-956-157-292100
; Sequence 292100, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 292100
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-292100

Query Match      1.5%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 72;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1264  TCGTGAAGCTCTTTGACTCTGATCC 1288
|||||
Db      1  TCGTGAAGCTCTTTGACTCTGATCC 25

RESULT 128
US-10-956-157-292272
; Sequence 292272, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 292272
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-292272

Query Match      1.5%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 72;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1569  TCGACTCTCTGCTCATGGAGAA 1593
|||||
Db      1  TCGACTCTCTGCTCATGGAGAA 25
```

```

; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 316681
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-316681

Query Match          1.5%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 72;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1244  TTCGGGTGTCACGTAGGTGTCGTG 1268
Db       1      TTTCCGGTGTCACGTAGGTGTCGTG 25

RESULT 132
US-10-956-157-317598
; Sequence 317598, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 317598
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-317598

Query Match          1.5%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 72;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1240  TTCCTTCCGGGTGTCACGTAGGTGTT 1264
Db       1      TTTCCCTTCCGGGTGTCACGTAGGTGTT 25

RESULT 133
US-10-956-157-287991
; Sequence 287991, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 287991
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-287991

Query Match          1.5%; Score 24; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 90;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      8      GCCGCTGACCGAGGGGTGCAAGA 31
Db       2      GCCGCTGACCGAGGGGTGCAAGA 25

```

## RESULT 134

US-10-719-956-187214  
; Sequence 187214, Application US/10719956  
; Publication No. US20040146910A1  
; GENERAL INFORMATION:  
; APPLICANT: Xue Mei Zhou  
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat  
; FILE REFERENCE: 3527.1  
; CURRENT APPLICATION NUMBER: US/10/719,956  
; CURRENT FILING DATE: 2003-11-20  
; PRIOR APPLICATION NUMBER: 60/427,836  
; PRIOR FILING DATE: 2002-11-20  
; NUMBER OF SEQ ID NOS: 699466  
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1  
; SEQ ID NO 187214  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Rattus norvegicus  
US-10-719-956-187214

Query Match 1.4%; Score 23.4; DB 1; Length 25;  
Best Local Similarity 96.0%; Pred. No. 1e+02;  
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 969 ATCTTGTCGTGGACTGTTCCACCA 993  
Db 1 ATCTTGTCGTGGACTGTTCCACCA 25  
|||||

## RESULT 135

US-10-080-794-16  
; Sequence 16, Application US/10080794  
; Publication No. US20030166591A1  
; GENERAL INFORMATION:  
; APPLICANT: Gleave, Martin  
; APPLICANT: Rennie, Paul S.  
; APPLICANT: Miyake, Hideaki  
; APPLICANT: Nelson, Colleen  
; APPLICANT: Monia, Brett P.  
; TITLE OF INVENTION: TRPM-2 ANTISENSE THERAPY USING AN OLIGONUCLEOTIDE  
; FILE REFERENCE: UBC P-020-3  
; CURRENT APPLICATION NUMBER: US/10/080,794  
; CURRENT FILING DATE: 2002-02-22  
; PRIOR APPLICATION NUMBER: 60/121,726  
; PRIOR FILING DATE: 1999-02-26  
; PRIOR APPLICATION NUMBER: 09/913,325  
; PRIOR FILING DATE: 2001-08-10  
; PRIOR APPLICATION NUMBER: 09/944,326  
; PRIOR FILING DATE: 2001-08-30  
; NUMBER OF SEQ ID NOS: 19  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 16  
; LENGTH: 23  
; TYPE: DNA  
; ORGANISM: HUMAN  
US-10-080-794-16

Query Match 1.4%; Score 23; DB 1; Length 23;  
Best Local Similarity 100.0%; Pred. No. 93;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 177 AAGGAAATTCAAATGCTGCA 199  
Db 1 AAGGAAATTCAAATGCTGCA 23  
|||||

## RESULT 136

US-10-080-794-17/c  
; Sequence 17, Application US/10080794  
; Publication No. US20030166591A1  
; GENERAL INFORMATION:

; APPLICANT: Gleave, Martin  
; APPLICANT: Rennie, Paul S.  
; APPLICANT: Miyake, Hideaki  
; APPLICANT: Nelson, Colleen  
; APPLICANT: Monia, Brett P.  
; TITLE OF INVENTION: TRPM-2 ANTISENSE THERAPY USING AN OLIGONUCLEOTIDE  
; FILE REFERENCE: UBC P-020-3  
; CURRENT APPLICATION NUMBER: US/10/080,794  
; CURRENT FILING DATE: 2002-02-22  
; PRIOR APPLICATION NUMBER: 60/121,726  
; PRIOR FILING DATE: 1999-02-26  
; PRIOR APPLICATION NUMBER: 09/913,325  
; PRIOR FILING DATE: 2001-08-10  
; PRIOR APPLICATION NUMBER: 09/944,326  
; PRIOR FILING DATE: 2001-08-30  
; NUMBER OF SEQ ID NOS: 19  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 17  
; LENGTH: 23  
; TYPE: DNA  
; ORGANISM: HUMAN  
US-10-080-794-17

Query Match 1.4%; Score 23; DB 1; Length 23;  
Best Local Similarity 100.0%; Pred. No. 93;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 957 AAGTCCCGGAGATCTTGTGT 979  
Db 23 AAGTCCCGGAGATCTTGTGT 1  
|||||

## RESULT 137

US-10-380-124-5/c  
; Sequence 5, Application US/10380124  
; Publication No. US20040053874A1  
; GENERAL INFORMATION:  
; APPLICANT: Isis Pharmaceuticals, Inc.  
; APPLICANT: Brett P. Monia  
; APPLICANT: Susan M. Freier  
; TITLE OF INVENTION: ANTISENSE MODULATION OF CLUSTERIN EXPRESSION  
; FILE REFERENCE: RTS-0156  
; CURRENT APPLICATION NUMBER: US/10/380,124  
; CURRENT FILING DATE: 2003-03-10  
; NUMBER OF SEQ ID NOS: 90  
; SEQ ID NO 5  
; LENGTH: 23  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: PCR Primer  
US-10-380-124-5

Query Match 1.4%; Score 23; DB 1; Length 23;  
Best Local Similarity 100.0%; Pred. No. 93;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 789 CTTGAGATGATACACGAGGCTCA 811  
Db 23 CTTGAGATGATACACGAGGCTCA 1  
|||||

## RESULT 138

US-10-646-436-57  
; Sequence 57, Application US/10646436  
; Publication No. US20040096882A1  
; GENERAL INFORMATION:  
; APPLICANT: Jansen, Burkhard  
; APPLICANT: Gleave, Martin  
; APPLICANT: Signaevsky, Maxim  
; APPLICANT: Beraldi, Eliana  
; APPLICANT: Trougakos, Ioannis



```
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 291041
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-291041

Query Match      1.3%; Score 23; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1114 CCTCCTTGCTGGAGCAGCTGAAC 1136
      |||||||
Db 3 CCTCCTTGCTGGAGCAGCTGAAC 25

RESULT 143
US-10-980-850-34/c
; Sequence 34, Application US/10980850
; Publication No. US20050152908A1
; GENERAL INFORMATION:
; APPLICANT: Liew, Choong-Chin
; TITLE OF INVENTION: LIVER CANCER BIOMARKERS
; FILE REFERENCE: 4231/2072
; CURRENT APPLICATION NUMBER: US/10/980,850
; CURRENT FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/516,853
; PRIOR FILING DATE: 2003-11-03
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 34
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Reverse Primer for OAS1
US-10-980-850-34

Query Match      1.3%; Score 22; DB 1; Length 22;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1072 ACGAGCTGCTAAAGTCTTACCA 1093
      |||||||
Db 22 ACGAGCTGCTAAAGTCTTACCA 1

RESULT 144
US-10-956-157-167169
; Sequence 167169, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 167169
; LENGTH: 25
; TYPE: DNA
```

```
; ORGANISM: Probe Sequence
US-10-956-157-167169

Query Match      1.3%; Score 22; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1622 AATAAAACTGCTCTGTGAGCTG 1643
      |||||||
Db 1 AATAAAACTGCTCTGTGAGCTG 22

RESULT 145
US-10-956-157-167170
; Sequence 167170, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 167170
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-167170

Query Match      1.3%; Score 22; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1622 AATAAAACTGCTCTGTGAGCTG 1643
      |||||||
Db 1 AATAAAACTGCTCTGTGAGCTG 22

RESULT 146
US-10-956-157-167171
; Sequence 167171, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 167171
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-167171

Query Match      1.3%; Score 22; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1622 AATAAAACTGCTCTGTGAGCTG 1643
      |||||||
Db 1 AATAAAACTGCTCTGTGAGCTG 22

RESULT 147
US-10-956-157-228788
; Sequence 228788, Application US/10956157
```

```
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 228788
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-228788

Query Match      1.3%; Score 22; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1571 GACTCTGCTGCTCATGGGAAGA 1592
Db 1 GACTCTGCTGCTCATGGGAAGA 22

RESULT 148
US-10-956-157-279365
; Sequence 279365, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 279365
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-279365

Query Match      1.3%; Score 22; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1400 TGTGATGTTGCTTTTGACACT 1421
Db 1 TGTGATGTTGCTTTTGACACT 22

RESULT 149
US-10-719-900-56804
; Sequence 56804, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 56804
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
```

```
US-10-719-900-56804

Query Match      1.3%; Score 21.8; DB 1; Length 25;
Best Local Similarity 92.0%; Pred. No. 1.4e+02;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1269 AAGCTCTTTGACTCTGATCCCATCA 1293
Db 1 AAGCTGTTTGACTCTGACCCCATCA 25

RESULT 150
US-10-719-900-417945
; Sequence 417945, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 417945
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-417945

Query Match      1.3%; Score 21.8; DB 1; Length 25;
Best Local Similarity 92.0%; Pred. No. 1.4e+02;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1133 GAACGACGAGTTTAACCTGGGTGTC 1157
Db 1 GAACGACGAGTTCAACTGGGTGTC 25

RESULT 151
US-10-719-900-417946
; Sequence 417946, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 417946
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-417946

Query Match      1.3%; Score 21.8; DB 1; Length 25;
Best Local Similarity 92.0%; Pred. No. 1.4e+02;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1133 GAACGACGAGTTTAACCTGGGTGTC 1157
Db 1 GAACGACGAGTTGAACCTGGGTGTC 25

RESULT 152
US-10-719-900-815718
; Sequence 815718, Application US/10719900
; Publication No. US20050026164A1
```

```
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 815718
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-815718

Query Match      1.3%; Score 21.8; DB 1; Length 25;
Best Local Similarity 92.0%; Pred. No. 1.4e+02;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1245 TCCGGTGTCACTGAGGTGGTGTGA 1269
Db      1 TCCCGTGTCACTGAGGTGGTGTGA 25

RESULT 153
US-10-719-900-892165
; Sequence 892165, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 892165
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-892165

Query Match      1.3%; Score 21.8; DB 1; Length 25;
Best Local Similarity 92.0%; Pred. No. 1.4e+02;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1149 TGGGTGTCCCGCTGGCAACCTCA 1173
Db      1 TGGGTGTCCAGCTGGCTAACCTCA 25

RESULT 154
US-10-809-189-31760
; Sequence 31760, Application US/10809189
; Publication No. US20050048531A1
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/10/809,189
; CURRENT FILING DATE: 2004-03-25
; PRIOR APPLICATION NUMBER: US/09/396,196
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO 31760
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-809-189-31760

Query Match      1.3%; Score 21.8; DB 1; Length 25;
Best Local Similarity 92.0%; Pred. No. 1.4e+02;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1270 AGCTCTTTGACTCTGATCCCATCAC 1294
Db      1 AGCTGTTTGACTCTGACCCCATCAC 25

RESULT 155
US-10-719-956-30749/c
; Sequence 30749, Application US/10719956
; Publication No. US20040146910A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527.1
; CURRENT APPLICATION NUMBER: US/10/719,956
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,836
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 30749
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-10-719-956-30749

Query Match      1.3%; Score 21.8; DB 1; Length 25;
Best Local Similarity 92.0%; Pred. No. 1.4e+02;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1120 TGCTGGAGCAGCTGAACGAGCAGTT 1144
Db      25 TGCTGGAACAGCTGAACGACCAGTT 1

RESULT 156
US-10-719-956-187213
; Sequence 187213, Application US/10719956
; Publication No. US20040146910A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527.1
; CURRENT APPLICATION NUMBER: US/10/719,956
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,836
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 187213
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-10-719-956-187213

Query Match      1.3%; Score 21.8; DB 1; Length 25;
Best Local Similarity 92.0%; Pred. No. 1.4e+02;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      969 ATCTTGTCTGTGGACTGTTCACCA 993
Db      1 ATCTTGTCTGTGCACCTGTTCACCA 25
```



```
RESULT 157
US-10-719-956-374026/c
; Sequence 374026, Application US/10719956
; Publication No. US20040146910A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527.1
; CURRENT APPLICATION NUMBER: US/10/719,956
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,836
; PRIOR FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 374026
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-10-719-956-374026
Query Match      1.3%; Score 21.8; DB 1; Length 25;
Best Local Similarity 92.0%; Pred. No. 1.4e+02;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 975 TCTGTGGACTGTTCCACCAACCC 999
Db 25 TCTGTGGACTGTTCCACCAACATC 1

RESULT 158
US-10-719-956-501381
; Sequence 501381, Application US/10719956
; Publication No. US20040146910A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527.1
; CURRENT APPLICATION NUMBER: US/10/719,956
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,836
; PRIOR FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 501381
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-10-719-956-501381
Query Match      1.3%; Score 21.8; DB 1; Length 25;
Best Local Similarity 92.0%; Pred. No. 1.4e+02;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1266 GTGAAGCTCTTTGACTGATCTGATCCCA 1290
Db 1 GTGAAGCTCTTTGACTGATCTGATCCCA 25

RESULT 159
US-10-719-956-612442/c
; Sequence 612442, Application US/10719956
; Publication No. US20040146910A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527.1
; CURRENT APPLICATION NUMBER: US/10/719,956
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,836
; PRIOR FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 612442
```

```
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-10-719-956-612442
Query Match      1.3%; Score 21.8; DB 1; Length 25;
Best Local Similarity 92.0%; Pred. No. 1.4e+02;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1149 TGGGTGTCCCGCTGGCAAACTCA 1173
Db 25 TGGGTGTCCCGCTGGCTTAACCTCA 1

RESULT 160
US-09-944-326-3/c
; Sequence 3, Application US/09944326
; Patent No. US20020128220A1
; GENERAL INFORMATION:
; APPLICANT: Gleave, Martin
; APPLICANT: Rennie, Paul S.
; APPLICANT: Miyake, Hideaki
; APPLICANT: Nelson, Colleen
; TITLE OF INVENTION: TRPM-2 ANTISENSE THERAPY
; FILE REFERENCE: UBC.P-020-2
; CURRENT APPLICATION NUMBER: US/09/944,326
; CURRENT FILING DATE: 2001-08-30
; PRIOR APPLICATION NUMBER: 60/121,726
; PRIOR FILING DATE: 1999-02-26
; PRIOR APPLICATION NUMBER: 09/913,325
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 21
; TYPE: DNA
; ORGANISM: HUMAN
; FEATURE:
; OTHER INFORMATION: antisense TRPM-2 ODN
US-09-944-326-3
Query Match      1.3%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 CCGAGGCGTGCAAGACTCCA 36
Db 21 CCGAGGCGTGCAAGACTCCA 1

RESULT 161
US-09-944-326-4/c
; Sequence 4, Application US/09944326
; Patent No. US20020128220A1
; GENERAL INFORMATION:
; APPLICANT: Gleave, Martin
; APPLICANT: Rennie, Paul S.
; APPLICANT: Miyake, Hideaki
; APPLICANT: Nelson, Colleen
; TITLE OF INVENTION: TRPM-2 ANTISENSE THERAPY
; FILE REFERENCE: UBC.P-020-2
; CURRENT APPLICATION NUMBER: US/09/944,326
; CURRENT FILING DATE: 2001-08-30
; PRIOR APPLICATION NUMBER: 60/121,726
; PRIOR FILING DATE: 1999-02-26
; PRIOR APPLICATION NUMBER: 09/913,325
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 21
; TYPE: DNA
; ORGANISM: HUMAN
```

```
;
; FEATURE:
; OTHER INFORMATION: antisense TRPM-2 ODN
US-09-944-326-4
Query Match      1.3%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 48 ATGATGAAGACTCTGCTGCTG 68
Db 21 ATGATGAAGACTCTGCTGCTG 1

RESULT 162
US-09-944-326-5/c
; Sequence 5, Application US/09944326
; Patent No. US20020128220A1
; GENERAL INFORMATION:
; APPLICANT: Gleave, Martin
; APPLICANT: Rennie, Paul S.
; APPLICANT: Miyake, Hideaki
; APPLICANT: Nelson, Colleen
; TITLE OF INVENTION: TRPM-2 ANTISENSE THERAPY
; FILE REFERENCE: UBC P-020-2
; CURRENT APPLICATION NUMBER: US/09/944,326
; PRIOR FILING DATE: 2001-08-30
; PRIOR APPLICATION NUMBER: 60/121,726
; PRIOR FILING DATE: 1999-02-26
; PRIOR APPLICATION NUMBER: 09/913,325
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 21
; TYPE: DNA
; ORGANISM: HUMAN
; FEATURE:
; OTHER INFORMATION: antisense TRPM-2 ODN
US-09-944-326-5
Query Match      1.3%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 114 GACCAGACGGTCTCAGACAAT 134
Db 21 GACCAGACGGTCTCAGACAAT 1

RESULT 163
US-09-944-326-6/c
; Sequence 6, Application US/09944326
; Patent No. US20020128220A1
; GENERAL INFORMATION:
; APPLICANT: Gleave, Martin
; APPLICANT: Rennie, Paul S.
; APPLICANT: Miyake, Hideaki
; APPLICANT: Nelson, Colleen
; TITLE OF INVENTION: TRPM-2 ANTISENSE THERAPY
; FILE REFERENCE: UBC P-020-2
; CURRENT APPLICATION NUMBER: US/09/944,326
; PRIOR FILING DATE: 2001-08-30
; PRIOR APPLICATION NUMBER: 60/121,726
; PRIOR FILING DATE: 1999-02-26
; PRIOR APPLICATION NUMBER: 09/913,325
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 21
; TYPE: DNA
; ORGANISM: HUMAN
; FEATURE:
; OTHER INFORMATION: antisense TRPM-2 ODN
US-09-944-326-6/c
Query Match      1.3%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 515 TGACCGCATCGACTCCCTGCT 535
Db 21 TGACCGCATCGACTCCCTGCT 1

RESULT 165
US-09-944-326-8/c
; Sequence 8, Application US/09944326
; Patent No. US20020128220A1
; GENERAL INFORMATION:
; APPLICANT: Gleave, Martin
; APPLICANT: Rennie, Paul S.
; APPLICANT: Miyake, Hideaki
; APPLICANT: Nelson, Colleen
; TITLE OF INVENTION: TRPM-2 ANTISENSE THERAPY
; FILE REFERENCE: UBC P-020-2
; CURRENT APPLICATION NUMBER: US/09/944,326
; PRIOR FILING DATE: 2001-08-30
; PRIOR APPLICATION NUMBER: 60/121,726
; PRIOR FILING DATE: 1999-02-26
; PRIOR APPLICATION NUMBER: 09/913,325
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 21
; TYPE: DNA
; ORGANISM: HUMAN
; FEATURE:
; OTHER INFORMATION: antisense TRPM-2 ODN
US-09-944-326-8/c
Query Match      1.3%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 515 TGACCGCATCGACTCCCTGCT 535
Db 21 TGACCGCATCGACTCCCTGCT 1

RESULT 166
US-09-944-326-7/c
; Sequence 7, Application US/09944326
; Patent No. US20020128220A1
; GENERAL INFORMATION:
; APPLICANT: Gleave, Martin
; APPLICANT: Rennie, Paul S.
; APPLICANT: Miyake, Hideaki
; APPLICANT: Nelson, Colleen
; TITLE OF INVENTION: TRPM-2 ANTISENSE THERAPY
; FILE REFERENCE: UBC P-020-2
; CURRENT APPLICATION NUMBER: US/09/944,326
; PRIOR FILING DATE: 2001-08-30
; PRIOR APPLICATION NUMBER: 60/121,726
; PRIOR FILING DATE: 1999-02-26
; PRIOR APPLICATION NUMBER: 09/913,325
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 21
; TYPE: DNA
; ORGANISM: HUMAN
; FEATURE:
; OTHER INFORMATION: antisense TRPM-2 ODN
US-09-944-326-7
Query Match      1.3%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 515 TGACCGCATCGACTCCCTGCT 535
Db 21 TGACCGCATCGACTCCCTGCT 1
```

## US-09-944-326-8

Query Match 1.3%; Score 21; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 1.2e+02;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 716 CCGCATCGTCGCGAGCTTGAT 736  
Db 21 CCGCATCGTCGCGAGCTTGAT 1

## RESULT 166

US-09-944-326-9/c  
; Sequence 9, Application US/09944326  
; Patent No. US20020128220A1  
; GENERAL INFORMATION:  
; APPLICANT: Gleave, Martin  
; APPLICANT: Rennie, Paul S.  
; APPLICANT: Miyake, Hideaki  
; APPLICANT: Nelson, Colleen  
; TITLE OF INVENTION: TRPM-2 ANTISENSE THERAPY  
; FILE REFERENCE: UBC.P-020-2  
; CURRENT APPLICATION NUMBER: US/09/944,326  
; CURRENT FILING DATE: 2001-08-30  
; PRIOR APPLICATION NUMBER: 60/121,726  
; PRIOR FILING DATE: 1999-02-26  
; PRIOR APPLICATION NUMBER: 09/913,325  
; PRIOR FILING DATE: 2001-08-10  
; NUMBER OF SEQ ID NOS: 14  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 9  
; LENGTH: 21  
; TYPE: DNA  
; ORGANISM: HUMAN  
; FEATURE:  
; OTHER INFORMATION: antisense TRPM-2 ODN  
US-09-944-326-9

Query Match 1.3%; Score 21; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 1.2e+02;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 916 ACAACTCCACGGGCTGCTGC 936  
Db 21 ACAACTCCACGGGCTGCTGC 1

## RESULT 167

US-09-944-326-10/c  
; Sequence 10, Application US/09944326  
; Patent No. US20020128220A1  
; GENERAL INFORMATION:  
; APPLICANT: Gleave, Martin  
; APPLICANT: Rennie, Paul S.  
; APPLICANT: Miyake, Hideaki  
; APPLICANT: Nelson, Colleen  
; TITLE OF INVENTION: TRPM-2 ANTISENSE THERAPY  
; FILE REFERENCE: UBC.P-020-2  
; CURRENT APPLICATION NUMBER: US/09/944,326  
; CURRENT FILING DATE: 2001-08-30  
; PRIOR APPLICATION NUMBER: 60/121,726  
; PRIOR FILING DATE: 1999-02-26  
; PRIOR APPLICATION NUMBER: 09/913,325  
; PRIOR FILING DATE: 2001-08-10  
; NUMBER OF SEQ ID NOS: 14  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 10  
; LENGTH: 21  
; TYPE: DNA  
; ORGANISM: HUMAN  
; FEATURE:  
; OTHER INFORMATION: antisense TRPM-2 ODN  
US-09-944-326-10

Query Match 1.3%; Score 21; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 1.2e+02;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1115 CTCCTTCTGCGAGCAGCTGAA 1135  
Db 21 CTCCTTCTGCGAGCAGCTGAA 1

## RESULT 168

US-09-944-326-11/c  
; Sequence 11, Application US/09944326  
; Patent No. US20020128220A1  
; GENERAL INFORMATION:  
; APPLICANT: Gleave, Martin  
; APPLICANT: Rennie, Paul S.  
; APPLICANT: Miyake, Hideaki  
; APPLICANT: Nelson, Colleen  
; TITLE OF INVENTION: TRPM-2 ANTISENSE THERAPY  
; FILE REFERENCE: UBC.P-020-2  
; CURRENT APPLICATION NUMBER: US/09/944,326  
; CURRENT FILING DATE: 2001-08-30  
; PRIOR APPLICATION NUMBER: 60/121,726  
; PRIOR FILING DATE: 1999-02-26  
; PRIOR APPLICATION NUMBER: 09/913,325  
; PRIOR FILING DATE: 2001-08-10  
; NUMBER OF SEQ ID NOS: 14  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 11  
; LENGTH: 21  
; TYPE: DNA  
; ORGANISM: HUMAN  
; FEATURE:  
; OTHER INFORMATION: antisense TRPM-2 ODN  
US-09-944-326-11

Query Match 1.3%; Score 21; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 1.2e+02;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1316 CTCGAGGAAGAACCCCTAAATT 1336  
Db 21 CTCGAGGAAGAACCCCTAAATT 1

## RESULT 169

US-09-944-326-12/c  
; Sequence 12, Application US/09944326  
; Patent No. US20020128220A1  
; GENERAL INFORMATION:  
; APPLICANT: Gleave, Martin  
; APPLICANT: Rennie, Paul S.  
; APPLICANT: Miyake, Hideaki  
; APPLICANT: Nelson, Colleen  
; TITLE OF INVENTION: TRPM-2 ANTISENSE THERAPY  
; FILE REFERENCE: UBC.P-020-2  
; CURRENT APPLICATION NUMBER: US/09/944,326  
; CURRENT FILING DATE: 2001-08-30  
; PRIOR APPLICATION NUMBER: 60/121,726  
; PRIOR FILING DATE: 1999-02-26  
; PRIOR APPLICATION NUMBER: 09/913,325  
; PRIOR FILING DATE: 2001-08-10  
; NUMBER OF SEQ ID NOS: 14  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 12  
; LENGTH: 21  
; TYPE: DNA  
; ORGANISM: HUMAN  
; FEATURE:  
; OTHER INFORMATION: antisense TRPM-2 ODN  
US-09-944-326-12



```
; APPLICANT: Zellweger, Tobias
; TITLE OF INVENTION: Chemo- and Radiation-Sensitization of Cancer by Antisense TRPM-2
; FILE OF INVENTION: Oligonucleotides
; FILE REFERENCE: UBC.P-022
; CURRENT APPLICATION NUMBER: US/09/967,726A
; CURRENT FILING DATE: 2001-09-28
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 21
; TYPE: DNA
; ORGANISM: human
US-09-967-726A-6

Query Match      1.3%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      316 AATCAGAGACAAGCTGAAGG 336
Db      21 AATCAGAGACAAGCTGAAGG 1

RESULT 175
US-09-967-726A-7/c
; Sequence 7, Application US/09967726A
; Publication No. US20030158130A1
; GENERAL INFORMATION:
; APPLICANT: Gleave, Martin
; APPLICANT: Rennie, Paul S.
; APPLICANT: Miyake, Hideaki
; APPLICANT: Nelson, Colleen
; APPLICANT: Zellweger, Tobias
; TITLE OF INVENTION: Chemo- and Radiation-Sensitization of Cancer by Antisense TRPM-2
; FILE REFERENCE: UBC.P-022
; CURRENT APPLICATION NUMBER: US/09/967,726A
; CURRENT FILING DATE: 2001-09-28
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
; LENGTH: 21
; TYPE: DNA
; ORGANISM: human
US-09-967-726A-7

Query Match      1.3%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      515 TGACCGCATCGACTCCCTGCT 535
Db      21 TGACCGCATCGACTCCCTGCT 1

RESULT 176
US-09-967-726A-8/c
; Sequence 8, Application US/09967726A
; Publication No. US20030158130A1
; GENERAL INFORMATION:
; APPLICANT: Gleave, Martin
; APPLICANT: Rennie, Paul S.
; APPLICANT: Miyake, Hideaki
; APPLICANT: Nelson, Colleen
; APPLICANT: Zellweger, Tobias
; TITLE OF INVENTION: Chemo- and Radiation-Sensitization of Cancer by Antisense TRPM-2
; FILE REFERENCE: UBC.P-022
; CURRENT APPLICATION NUMBER: US/09/967,726A
; CURRENT FILING DATE: 2001-09-28
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
```

```
; LENGTH: 21
; TYPE: DNA
; ORGANISM: human
US-09-967-726A-8

Query Match      1.3%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      716 CCGCATCGTCGCGAGCTTGAT 736
Db      21 CCGCATCGTCGCGAGCTTGAT 1

RESULT 177
US-09-967-726A-9/c
; Sequence 9, Application US/09967726A
; Publication No. US20030158130A1
; GENERAL INFORMATION:
; APPLICANT: Gleave, Martin
; APPLICANT: Rennie, Paul S.
; APPLICANT: Miyake, Hideaki
; APPLICANT: Nelson, Colleen
; APPLICANT: Zellweger, Tobias
; TITLE OF INVENTION: Chemo- and Radiation-Sensitization of Cancer by Antisense TRPM-2
; FILE REFERENCE: UBC.P-022
; CURRENT APPLICATION NUMBER: US/09/967,726A
; CURRENT FILING DATE: 2001-09-28
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9
; LENGTH: 21
; TYPE: DNA
; ORGANISM: human
US-09-967-726A-9

Query Match      1.3%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      916 ACAACTCCACGGCTGCTGC 936
Db      21 ACAACTCCACGGCTGCTGC 1

RESULT 178
US-09-967-726A-10/c
; Sequence 10, Application US/09967726A
; Publication No. US20030158130A1
; GENERAL INFORMATION:
; APPLICANT: Gleave, Martin
; APPLICANT: Rennie, Paul S.
; APPLICANT: Miyake, Hideaki
; APPLICANT: Nelson, Colleen
; APPLICANT: Zellweger, Tobias
; TITLE OF INVENTION: Chemo- and Radiation-Sensitization of Cancer by Antisense TRPM-2
; FILE REFERENCE: UBC.P-022
; CURRENT APPLICATION NUMBER: US/09/967,726A
; CURRENT FILING DATE: 2001-09-28
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
; LENGTH: 21
; TYPE: DNA
; ORGANISM: human
US-09-967-726A-10

Query Match      1.3%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1115 CTCCTTGCTGGAGCAGCTGAA 1135
Db 21 CTCCTTGCTGGAGCAGCTGAA 1

RESULT 179
US-09-967-726A-11/c
; Sequence 11, Application US/09967726A
; Publication No. US20030158130A1
; GENERAL INFORMATION:
; APPLICANT: Gleave, Martin
; APPLICANT: Rennie, Paul S.
; APPLICANT: Miyake, Hideaki
; APPLICANT: Nelson, Colleen
; APPLICANT: Zellweger, Tobias
; TITLE OF INVENTION: Chemo- and Radiation-Sensitization of Cancer by Antisense TRPM-2
; TITLE OF INVENTION: Oligonucleotides
; FILE REFERENCE: UBC.P-022
; CURRENT APPLICATION NUMBER: US/09/967,726A
; CURRENT FILING DATE: 2001-09-28
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 11
; LENGTH: 21
; TYPE: DNA
; ORGANISM: human
US-09-967-726A-11

Query Match 1.3%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1316 CTCACGAGGAAGACCTTAATT 1336
Db 21 CTCACGAGGAAGACCTTAATT 1

RESULT 180
US-09-967-726A-12/c
; Sequence 12, Application US/09967726A
; Publication No. US20030158130A1
; GENERAL INFORMATION:
; APPLICANT: Gleave, Martin
; APPLICANT: Rennie, Paul S.
; APPLICANT: Miyake, Hideaki
; APPLICANT: Nelson, Colleen
; APPLICANT: Zellweger, Tobias
; TITLE OF INVENTION: Chemo- and Radiation-Sensitization of Cancer by Antisense TRPM-2
; TITLE OF INVENTION: Oligonucleotides
; FILE REFERENCE: UBC.P-022
; CURRENT APPLICATION NUMBER: US/09/967,726A
; CURRENT FILING DATE: 2001-09-28
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 12
; LENGTH: 21
; TYPE: DNA
; ORGANISM: human
US-09-967-726A-12

Query Match 1.3%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1516 AGGCCCCCAACTCCGCCAGC 1536
Db 21 AGGCCCCCAACTCCGCCAGC 1

RESULT 181
US-10-270-871-14
; Sequence 14, Application US/10270871
; Publication No. US20030162702A1
```

```
; GENERAL INFORMATION:
; APPLICANT: Millis, Albert J. T.
; TITLE OF INVENTION: Compositions and Methods For Altering Cell Migration
; FILE REFERENCE: 0794.016A
; CURRENT APPLICATION NUMBER: US/10/270,871
; CURRENT FILING DATE: 2002-10-15
; PRIOR APPLICATION NUMBER: US/09/459,749D
; PRIOR FILING DATE: 1999-12-10
; PRIOR APPLICATION NUMBER: 60/111,856
; PRIOR FILING DATE: 1998-12-11
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 14
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:primer_bind
; FEATURE:
; OTHER INFORMATION: synthetic sense primer based on porcine clusterin
US-10-270-871-14
```

```
Query Match 1.3%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 274 AAGCCCAAGAGAAGAGAGG 294
Db 1 AAGCCCAAGAGAAGAGAGG 21
```

```
RESULT 182
US-10-080-794-3/c
; Sequence 3, Application US/10080794
; Publication No. US20030166591A1
; GENERAL INFORMATION:
; APPLICANT: Gleave, Martin
; APPLICANT: Rennie, Paul S.
; APPLICANT: Miyake, Hideaki
; APPLICANT: Nelson, Colleen
; APPLICANT: Monia, Brett P.
; TITLE OF INVENTION: TRPM-2 ANTISENSE THERAPY USING AN OLIGONUCLEOTIDE
; FILE REFERENCE: UBC.P-020-3
; CURRENT APPLICATION NUMBER: US/10/080,794
; CURRENT FILING DATE: 2002-02-22
; PRIOR APPLICATION NUMBER: 60/121,726
; PRIOR FILING DATE: 1999-02-26
; PRIOR APPLICATION NUMBER: 09/913,325
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: 09/944,326
; PRIOR FILING DATE: 2001-08-30
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 21
; TYPE: DNA
; ORGANISM: HUMAN
; FEATURE:
; OTHER INFORMATION: antisense TRPM-2 ODN
```

```
Query Match 1.3%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 16 CCGAGGCGTGCAAGAGCTCCA 16
Db 21 CCGAGGCGTGCAAGAGCTCCA 1
```

```
RESULT 183
US-10-080-794-4/c
```

Sequence 4, Application US/10080794  
Publication No. US20030166591A1  
GENERAL INFORMATION:  
APPLICANT: Gleave, Martin  
APPLICANT: Rennie, Paul S.  
APPLICANT: Miyake, Hideaki  
APPLICANT: Nelson, Colleen  
APPLICANT: Monia, Brett P.  
TITLE OF INVENTION: TRPM-2 ANTISENSE THERAPY USING AN OLIGONUCLEOTIDE  
FILE REFERENCE: UBC P-020-3  
CURRENT APPLICATION NUMBER: US/10/080,794  
CURRENT FILING DATE: 2002-02-22  
PRIOR APPLICATION NUMBER: 60/121,726  
PRIOR FILING DATE: 1999-02-26  
PRIOR APPLICATION NUMBER: 09/913,325  
PRIOR FILING DATE: 2001-08-10  
PRIOR APPLICATION NUMBER: 09/944,326  
PRIOR FILING DATE: 2001-08-30  
NUMBER OF SEQ ID NOS: 19  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 4  
LENGTH: 21  
TYPE: DNA  
ORGANISM: HUMAN  
FEATURE:  
OTHER INFORMATION: antisense TRPM-2 ODN  
US-10-080-794-4

Query Match 1.3%; Score 21; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 1.2e+02;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 48 ATGATGAAGACTGCTGCTG 68  
DB 21 ATGATGAAGACTGCTGCTG 1

## RESULT 184

US-10-080-794-5/c  
Sequence 5, Application US/10080794  
Publication No. US20030166591A1  
GENERAL INFORMATION:  
APPLICANT: Gleave, Martin  
APPLICANT: Rennie, Paul S.  
APPLICANT: Miyake, Hideaki  
APPLICANT: Nelson, Colleen  
APPLICANT: Monia, Brett P.  
TITLE OF INVENTION: TRPM-2 ANTISENSE THERAPY USING AN OLIGONUCLEOTIDE  
FILE REFERENCE: UBC P-020-3  
CURRENT APPLICATION NUMBER: US/10/080,794  
CURRENT FILING DATE: 2002-02-22  
PRIOR APPLICATION NUMBER: 60/121,726  
PRIOR FILING DATE: 1999-02-26  
PRIOR APPLICATION NUMBER: 09/913,325  
PRIOR FILING DATE: 2001-08-10  
PRIOR APPLICATION NUMBER: 09/944,326  
PRIOR FILING DATE: 2001-08-30  
NUMBER OF SEQ ID NOS: 19  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 5  
LENGTH: 21  
TYPE: DNA  
ORGANISM: HUMAN  
FEATURE:  
OTHER INFORMATION: antisense TRPM-2 ODN  
US-10-080-794-5

Query Match 1.3%; Score 21; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 1.2e+02;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 114 GACCAGACGGTCTCAGACAAT 134  
DB 21 GACCAGACGGTCTCAGACAAT 1

## RESULT 185

US-10-080-794-6/c  
Sequence 6, Application US/10080794  
Publication No. US20030166591A1  
GENERAL INFORMATION:  
APPLICANT: Gleave, Martin  
APPLICANT: Rennie, Paul S.  
APPLICANT: Miyake, Hideaki  
APPLICANT: Nelson, Colleen  
APPLICANT: Monia, Brett P.  
TITLE OF INVENTION: TRPM-2 ANTISENSE THERAPY USING AN OLIGONUCLEOTIDE  
FILE REFERENCE: UBC P-020-3  
CURRENT APPLICATION NUMBER: US/10/080,794  
CURRENT FILING DATE: 2002-02-22  
PRIOR APPLICATION NUMBER: 60/121,726  
PRIOR FILING DATE: 1999-02-26  
PRIOR APPLICATION NUMBER: 09/913,325  
PRIOR FILING DATE: 2001-08-10  
PRIOR APPLICATION NUMBER: 09/944,326  
PRIOR FILING DATE: 2001-08-30  
NUMBER OF SEQ ID NOS: 19  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 6  
LENGTH: 21  
TYPE: DNA  
ORGANISM: HUMAN  
FEATURE:  
OTHER INFORMATION: antisense TRPM-2 ODN  
US-10-080-794-6

Query Match 1.3%; Score 21; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 1.2e+02;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 316 AATCAGACAAAGCTGAAGG 336  
DB 21 AATCAGACAAAGCTGAAGG 1

## RESULT 186

US-10-080-794-7/c  
Sequence 7, Application US/10080794  
Publication No. US20030166591A1  
GENERAL INFORMATION:  
APPLICANT: Gleave, Martin  
APPLICANT: Rennie, Paul S.  
APPLICANT: Miyake, Hideaki  
APPLICANT: Nelson, Colleen  
APPLICANT: Monia, Brett P.  
TITLE OF INVENTION: TRPM-2 ANTISENSE THERAPY USING AN OLIGONUCLEOTIDE  
FILE REFERENCE: UBC P-020-3  
CURRENT APPLICATION NUMBER: US/10/080,794  
CURRENT FILING DATE: 2002-02-22  
PRIOR APPLICATION NUMBER: 60/121,726  
PRIOR FILING DATE: 1999-02-26  
PRIOR APPLICATION NUMBER: 09/913,325  
PRIOR FILING DATE: 2001-08-10  
PRIOR APPLICATION NUMBER: 09/944,326  
PRIOR FILING DATE: 2001-08-30  
NUMBER OF SEQ ID NOS: 19  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 7  
LENGTH: 21  
TYPE: DNA  
ORGANISM: HUMAN  
FEATURE:  
OTHER INFORMATION: antisense TRPM-2 ODN  
US-10-080-794-7

Query Match 1.3%; Score 21; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 1.2e+02;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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; OTHER INFORMATION: antisense TRPM-2 ODN
US-10-080-794-7

Query Match      1.3%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 515 TGACGGCATCGACTCCCTGCT 535
      |||||
Db 21 TGACGGCATCGACTCCCTGCT 1

RESULT 187
US-10-080-794-8/c
; Sequence 8, Application US/10080794
; Publication No. US20030166591A1
; GENERAL INFORMATION:
; APPLICANT: Gleave, Martin
; APPLICANT: Rennie, Paul S.
; APPLICANT: Miyake, Hideaki
; APPLICANT: Nelson, Colleen
; APPLICANT: Monia, Brett P.
; TITLE OF INVENTION: TRPM-2 ANTISENSE THERAPY USING AN OLIGONUCLEOTIDE
; FILE REFERENCE: UBC P-020-3
; CURRENT APPLICATION NUMBER: US/10/080,794
; CURRENT FILING DATE: 2002-02-22
; PRIOR FILING DATE: 1999-02-26
; PRIOR APPLICATION NUMBER: 09/913,325
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: 09/944,326
; PRIOR FILING DATE: 2001-08-30
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; TYPE: DNA
; ORGANISM: HUMAN
; FEATURE:
; OTHER INFORMATION: antisense TRPM-2 ODN
US-10-080-794-8

Query Match      1.3%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 716 CCGCATCGTCCGAGCTTGAT 736
      |||||
Db 21 CCGCATCGTCCGAGCTTGAT 1

RESULT 188
US-10-080-794-9/c
; Sequence 9, Application US/10080794
; Publication No. US20030166591A1
; GENERAL INFORMATION:
; APPLICANT: Gleave, Martin
; APPLICANT: Rennie, Paul S.
; APPLICANT: Miyake, Hideaki
; APPLICANT: Nelson, Colleen
; APPLICANT: Monia, Brett P.
; TITLE OF INVENTION: TRPM-2 ANTISENSE THERAPY USING AN OLIGONUCLEOTIDE
; FILE REFERENCE: UBC P-020-3
; CURRENT APPLICATION NUMBER: US/10/080,794
; CURRENT FILING DATE: 2002-02-22
; PRIOR FILING DATE: 1999-02-26
; PRIOR APPLICATION NUMBER: 09/913,325
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: 09/944,326
; PRIOR FILING DATE: 2001-08-30
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
; TYPE: DNA
; ORGANISM: HUMAN
; FEATURE:
; OTHER INFORMATION: antisense TRPM-2 ODN
US-10-080-794-9

Query Match      1.3%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1115 CTCCTTGCTGGAGCAGCTGAA 1135
      |||||
Db 21 CTCCTTGCTGGAGCAGCTGAA 1

RESULT 190
US-10-080-794-11/c
; Sequence 11, Application US/10080794
; Publication No. US20030166591A1
; GENERAL INFORMATION:
; APPLICANT: Gleave, Martin
; APPLICANT: Rennie, Paul S.
; APPLICANT: Miyake, Hideaki
; APPLICANT: Nelson, Colleen
; APPLICANT: Monia, Brett P.
; TITLE OF INVENTION: TRPM-2 ANTISENSE THERAPY USING AN OLIGONUCLEOTIDE
; FILE REFERENCE: UBC P-020-3
; CURRENT APPLICATION NUMBER: US/10/080,794
; CURRENT FILING DATE: 2001-08-30
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 10
; TYPE: DNA
; ORGANISM: HUMAN
; FEATURE:
; OTHER INFORMATION: antisense TRPM-2 ODN
US-10-080-794-10

Query Match      1.3%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1115 CTCCTTGCTGGAGCAGCTGAA 1135
      |||||
Db 21 CTCCTTGCTGGAGCAGCTGAA 1

RESULT 190
US-10-080-794-11/c
; Sequence 11, Application US/10080794
; Publication No. US20030166591A1
; GENERAL INFORMATION:
; APPLICANT: Gleave, Martin
; APPLICANT: Rennie, Paul S.
; APPLICANT: Miyake, Hideaki
; APPLICANT: Nelson, Colleen
; APPLICANT: Monia, Brett P.
; TITLE OF INVENTION: TRPM-2 ANTISENSE THERAPY USING AN OLIGONUCLEOTIDE
; FILE REFERENCE: UBC P-020-3
; CURRENT APPLICATION NUMBER: US/10/080,794
; CURRENT FILING DATE: 2001-08-30
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 10
; TYPE: DNA
; ORGANISM: HUMAN
; FEATURE:
; OTHER INFORMATION: antisense TRPM-2 ODN
US-10-080-794-10
```



```
; CURRENT FILING DATE: 2002-02-22
; PRIOR APPLICATION NUMBER: 60/121,726
; PRIOR FILING DATE: 1999-02-26
; PRIOR APPLICATION NUMBER: 09/913,325
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: 09/944,326
; PRIOR FILING DATE: 2001-08-30
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 11
; LENGTH: 21
; TYPE: DNA
; ORGANISM: HUMAN
; FEATURE:
; OTHER INFORMATION: antisense TRPM-2 ODN
US-10-080-794-11

Query Match          1.3%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1316 CTCAGGAGAACCCCTAAATT 1336
Db      21 CTCAGGAGAACCCCTAAATT 1

RESULT 191
US-10-080-794-12/c
; Sequence 12, Application US/10080794
; Publication No. US20030166591A1
; GENERAL INFORMATION:
; APPLICANT: Gleave, Martin
; APPLICANT: Rennie, Paul S.
; APPLICANT: Miyake, Hideaki
; APPLICANT: Nelson, Colleen
; APPLICANT: Monia, Brett P.
; TITLE OF INVENTION: TRPM-2 ANTISENSE THERAPY USING AN OLIGONUCLEOTIDE
; TITLE OF INVENTION: HAVING 2'-O-(2-METHOXY)ETHYL MODIFICATIONS
; FILE REFERENCE: UBC P-020-3
; CURRENT APPLICATION NUMBER: US/10/080,794
; CURRENT FILING DATE: 2002-02-22
; PRIOR APPLICATION NUMBER: 60/121,726
; PRIOR FILING DATE: 1999-02-26
; PRIOR APPLICATION NUMBER: 09/913,325
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: 09/944,326
; PRIOR FILING DATE: 2001-08-30
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 12
; LENGTH: 21
; TYPE: DNA
; ORGANISM: HUMAN
; FEATURE:
; OTHER INFORMATION: antisense TRPM-2 ODN
US-10-080-794-12

Query Match          1.3%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1516 AGGCCCCCAACTCCGCCGAGC 1536
Db      21 AGGCCCCCAACTCCGCCGAGC 1

RESULT 192
US-10-380-124-6
; Sequence 6, Application US/10380124
; Publication No. US20040053674A1
; GENERAL INFORMATION:
; APPLICANT: Isis Pharmaceuticals, Inc.
; APPLICANT: Brett P. Monia
```

```
; APPLICANT: Susan M. Freier
; TITLE OF INVENTION: ANTISENSE MODULATION OF CLUSTERIN EXPRESSION
; FILE REFERENCE: RTS-0156
; CURRENT APPLICATION NUMBER: US/10/380,124
; CURRENT FILING DATE: 2003-03-10
; NUMBER OF SEQ ID NOS: 90
; SEQ ID NO 6
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: PCR Probe
US-10-380-124-6

Query Match          1.3%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      766 TCCAGGCCATGTTCCAGCCCT 786
Db      1 TCCAGGCCATGTTCCAGCCCT 21

RESULT 193
US-10-383-864-27
; Sequence 27, Application US/10383864
; Publication No. US20040081976A1
; GENERAL INFORMATION:
; APPLICANT: SIDRANSKY, David
; APPLICANT: THE JOHNS HOPKINS UNIVERSITY SCHOOL OF MEDICINE
; TITLE OF INVENTION: GENOMIC SCREEN FOR EPIGENETICALLY SILENCED TUMOR SUPPRESSOR GENES
; FILE REFERENCE: JHU1860-1
; CURRENT APPLICATION NUMBER: US/10/383,864
; CURRENT FILING DATE: 2003-07-25
; PRIOR APPLICATION NUMBER: US 60/362,577
; PRIOR FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 127
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 27
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: PCR primer
US-10-383-864-27

Query Match          1.3%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      994 ACAACCCCTCCAGGCTAAGC 1014
Db      1 ACAACCCCTCCAGGCTAAGC 21

RESULT 194
US-10-383-864-28/c
; Sequence 28, Application US/10383864
; Publication No. US20040081976A1
; GENERAL INFORMATION:
; APPLICANT: SIDRANSKY, David
; APPLICANT: THE JOHNS HOPKINS UNIVERSITY SCHOOL OF MEDICINE
; TITLE OF INVENTION: GENOMIC SCREEN FOR EPIGENETICALLY SILENCED TUMOR SUPPRESSOR GENES
; FILE REFERENCE: JHU1860-1
; CURRENT APPLICATION NUMBER: US/10/383,864
; CURRENT FILING DATE: 2003-07-25
; PRIOR APPLICATION NUMBER: US 60/362,577
; PRIOR FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 127
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 28
; LENGTH: 21
; TYPE: DNA
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```
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: PCR primer
US-10-383-864-28

Query Match          1.3%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1334 ATTATGAGACCGTGGCGGA 1354
      |||||
DB 21 ATTATGAGACCGTGGCGGA 1

RESULT 195
US-10-646-391A-3/c
; Sequence 3, Application US/10646391A
; Publication No. US20040082534A1
; GENERAL INFORMATION:
; APPLICANT: Jansen, Burkhard
; TITLE OF INVENTION: Treatment of Melanoma by Reduction in Clusterin Levels
; FILE REFERENCE: UBC.P-035
; CURRENT APPLICATION NUMBER: US/10/646,391A
; CURRENT FILING DATE: 2003-08-21
; PRIOR APPLICATION NUMBER: US 60/405,193
; PRIOR FILING DATE: 2002-08-21
; PRIOR APPLICATION NUMBER: US 60/319,748
; PRIOR FILING DATE: 2002-12-02
; PRIOR APPLICATION NUMBER: US 60/408,152
; PRIOR FILING DATE: 2002-09-03
; PRIOR APPLICATION NUMBER: US 60/473,387
; PRIOR FILING DATE: 2003-05-20
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3
; LENGTH: 21
; TYPE: DNA
; ORGANISM: human
US-10-646-391A-3

Query Match          1.3%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 CCGAGGCGTGCAAGACTCCA 36
      |||||
DB 21 CCGAGGCGTGCAAGACTCCA 1

RESULT 196
US-10-646-391A-4/c
; Sequence 4, Application US/10646391A
; Publication No. US20040082534A1
; GENERAL INFORMATION:
; APPLICANT: Jansen, Burkhard
; TITLE OF INVENTION: Treatment of Melanoma by Reduction in Clusterin Levels
; FILE REFERENCE: UBC.P-035
; CURRENT APPLICATION NUMBER: US/10/646,391A
; CURRENT FILING DATE: 2003-08-21
; PRIOR APPLICATION NUMBER: US 60/405,193
; PRIOR FILING DATE: 2002-08-21
; PRIOR APPLICATION NUMBER: US 60/319,748
; PRIOR FILING DATE: 2002-12-02
; PRIOR APPLICATION NUMBER: US 60/408,152
; PRIOR FILING DATE: 2002-09-03
; PRIOR APPLICATION NUMBER: US 60/473,387
; PRIOR FILING DATE: 2003-05-20
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4
; LENGTH: 21
; TYPE: DNA
; ORGANISM: human
US-10-646-391A-4

Query Match          1.3%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 114 GACCAGACGGTCTCAGACAAT 134
      |||||
DB 21 GACCAGACGGTCTCAGACAAT 1

RESULT 198
US-10-646-391A-6/c
; Sequence 6, Application US/10646391A
; Publication No. US20040082534A1
; GENERAL INFORMATION:
; APPLICANT: Jansen, Burkhard
; TITLE OF INVENTION: Treatment of Melanoma by Reduction in Clusterin Levels
; FILE REFERENCE: UBC.P-035
; CURRENT APPLICATION NUMBER: US/10/646,391A
; CURRENT FILING DATE: 2003-08-21
; PRIOR APPLICATION NUMBER: US 60/405,193
; PRIOR FILING DATE: 2002-08-21
; PRIOR APPLICATION NUMBER: US 60/319,748
; PRIOR FILING DATE: 2002-12-02
; PRIOR APPLICATION NUMBER: US 60/408,152
; PRIOR FILING DATE: 2002-09-03
; PRIOR APPLICATION NUMBER: US 60/473,387
; PRIOR FILING DATE: 2003-05-20
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 6
; LENGTH: 21
; TYPE: DNA
; ORGANISM: human
US-10-646-391A-6
```

```
; ORGANISM: human
US-10-646-391A-6

Query Match          1.3%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 316 AATCAGAGACAAAGCTGAAGG 336
   |||||
Db 21 AATCAGAGACAAAGCTGAAGG 1

RESULT 199
US-10-646-391A-7/c
; Sequence 7, Application US/10646391A
; Publication No. US20040082534A1
; GENERAL INFORMATION:
; APPLICANT: Gleave, Martin
; APPLICANT: Jansen, Burkhard
; TITLE OF INVENTION: Treatment of Melanoma by Reduction in Clusterin Levels
; FILE REFERENCE: UBC.P-035
; CURRENT APPLICATION NUMBER: US/10/646,391A
; CURRENT FILING DATE: 2003-08-21
; PRIOR APPLICATION NUMBER: US 60/405,193
; PRIOR FILING DATE: 2002-08-21
; PRIOR APPLICATION NUMBER: US 60/319,748
; PRIOR FILING DATE: 2002-12-02
; PRIOR APPLICATION NUMBER: US 60/408,152
; PRIOR FILING DATE: 2002-09-03
; PRIOR APPLICATION NUMBER: US 60/473,387
; PRIOR FILING DATE: 2003-05-20
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 7
; LENGTH: 21
; TYPE: DNA
; ORGANISM: human
US-10-646-391A-7

Query Match          1.3%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 515 TGACCGCATCGACTCCCTGCT 535
   |||||
Db 21 TGACCGCATCGACTCCCTGCT 1

RESULT 200
US-10-646-391A-8/c
; Sequence 8, Application US/10646391A
; Publication No. US20040082534A1
; GENERAL INFORMATION:
; APPLICANT: Gleave, Martin
; APPLICANT: Jansen, Burkhard
; TITLE OF INVENTION: Treatment of Melanoma by Reduction in Clusterin Levels
; FILE REFERENCE: UBC.P-035
; CURRENT APPLICATION NUMBER: US/10/646,391A
; CURRENT FILING DATE: 2003-08-21
; PRIOR APPLICATION NUMBER: US 60/405,193
; PRIOR FILING DATE: 2002-08-21
; PRIOR APPLICATION NUMBER: US 60/319,748
; PRIOR FILING DATE: 2002-12-02
; PRIOR APPLICATION NUMBER: US 60/408,152
; PRIOR FILING DATE: 2002-09-03
; PRIOR APPLICATION NUMBER: US 60/473,387
; PRIOR FILING DATE: 2003-05-20
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 8
; LENGTH: 21
; TYPE: DNA
; ORGANISM: human
US-10-646-391A-8

Query Match          1.3%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 716 CCGCATCGTCCGACGCTTGAT 736
   |||||
Db 21 CCGCATCGTCCGACGCTTGAT 1

RESULT 201
US-10-646-391A-9/c
; Sequence 9, Application US/10646391A
; Publication No. US20040082534A1
; GENERAL INFORMATION:
; APPLICANT: Gleave, Martin
; APPLICANT: Jansen, Burkhard
; TITLE OF INVENTION: Treatment of Melanoma by Reduction in Clusterin Levels
; FILE REFERENCE: UBC.P-035
; CURRENT APPLICATION NUMBER: US/10/646,391A
; CURRENT FILING DATE: 2003-08-21
; PRIOR APPLICATION NUMBER: US 60/405,193
; PRIOR FILING DATE: 2002-08-21
; PRIOR APPLICATION NUMBER: US 60/319,748
; PRIOR FILING DATE: 2002-12-02
; PRIOR APPLICATION NUMBER: US 60/408,152
; PRIOR FILING DATE: 2002-09-03
; PRIOR APPLICATION NUMBER: US 60/473,387
; PRIOR FILING DATE: 2003-05-20
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 9
; LENGTH: 21
; TYPE: DNA
; ORGANISM: human
US-10-646-391A-9

Query Match          1.3%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 916 ACAACTCCACGGGCTGCTGC 936
   |||||
Db 21 ACAACTCCACGGGCTGCTGC 1

RESULT 202
US-10-646-391A-10/c
; Sequence 10, Application US/10646391A
; Publication No. US20040082534A1
; GENERAL INFORMATION:
; APPLICANT: Gleave, Martin
; APPLICANT: Jansen, Burkhard
; TITLE OF INVENTION: Treatment of Melanoma by Reduction in Clusterin Levels
; FILE REFERENCE: UBC.P-035
; CURRENT APPLICATION NUMBER: US/10/646,391A
; CURRENT FILING DATE: 2003-08-21
; PRIOR APPLICATION NUMBER: US 60/405,193
; PRIOR FILING DATE: 2002-08-21
; PRIOR APPLICATION NUMBER: US 60/319,748
; PRIOR FILING DATE: 2002-12-02
; PRIOR APPLICATION NUMBER: US 60/408,152
; PRIOR FILING DATE: 2002-09-03
; PRIOR APPLICATION NUMBER: US 60/473,387
; PRIOR FILING DATE: 2003-05-20
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 10
; LENGTH: 21
; TYPE: DNA
; ORGANISM: human
US-10-646-391A-10
```

```
Query Match      1.3%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1115 CTCCTTGCTGGAGCAGCTGAA 1135
    |||||
Db 21 CTCCTTGCTGGAGCAGCTGAA 1

RESULT 203
US-10-646-391A-11/c
; Sequence 11, Application US/10646391A
; Publication No. US20040082534A1
; GENERAL INFORMATION:
; APPLICANT: Jansen, Burkhard
; TITLE OF INVENTION: Treatment of Melanoma by Reduction in Clusterin Levels
; FILE REFERENCE: UBC.P-035
; CURRENT APPLICATION NUMBER: US/10/646,391A
; PRIOR FILING DATE: 2003-08-21
; PRIOR APPLICATION NUMBER: US 60/405,193
; PRIOR FILING DATE: 2002-08-21
; PRIOR APPLICATION NUMBER: US 60/319,748
; PRIOR FILING DATE: 2002-12-02
; PRIOR APPLICATION NUMBER: US 60/408,152
; PRIOR FILING DATE: 2002-09-03
; PRIOR APPLICATION NUMBER: US 60/473,387
; PRIOR FILING DATE: 2003-05-20
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 11
; LENGTH: 21
; TYPE: DNA
; ORGANISM: human
US-10-646-391A-11

Query Match      1.3%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1316 CTCAGGAGGAACCCCTAAATT 1336
    |||||
Db 21 CTCAGGAGGAACCCCTAAATT 1

RESULT 204
US-10-646-391A-12/c
; Sequence 12, Application US/10646391A
; Publication No. US20040082534A1
; GENERAL INFORMATION:
; APPLICANT: Jansen, Burkhard
; TITLE OF INVENTION: Treatment of Melanoma by Reduction in Clusterin Levels
; FILE REFERENCE: UBC.P-035
; CURRENT APPLICATION NUMBER: US/10/646,391A
; PRIOR FILING DATE: 2003-08-21
; PRIOR APPLICATION NUMBER: US 60/405,193
; PRIOR FILING DATE: 2002-08-21
; PRIOR APPLICATION NUMBER: US 60/319,748
; PRIOR FILING DATE: 2002-12-02
; PRIOR APPLICATION NUMBER: US 60/408,152
; PRIOR FILING DATE: 2002-09-03
; PRIOR APPLICATION NUMBER: US 60/473,387
; PRIOR FILING DATE: 2003-05-20
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 12
; LENGTH: 21
; TYPE: DNA
; ORGANISM: human
US-10-646-391A-12

Query Match      1.3%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1516 AGGCCCCCAACTCCGCCCCAGC 1536
    |||||
Db 21 AGGCCCCCAACTCCGCCCCAGC 1

RESULT 205
US-10-646-391A-20
; Sequence 20, Application US/10646391A
; Publication No. US20040082534A1
; GENERAL INFORMATION:
; APPLICANT: Jansen, Burkhard
; TITLE OF INVENTION: Treatment of Melanoma by Reduction in Clusterin Levels
; FILE REFERENCE: UBC.P-035
; CURRENT APPLICATION NUMBER: US/10/646,391A
; PRIOR FILING DATE: 2003-08-21
; PRIOR APPLICATION NUMBER: US 60/405,193
; PRIOR FILING DATE: 2002-08-21
; PRIOR APPLICATION NUMBER: US 60/319,748
; PRIOR FILING DATE: 2002-12-02
; PRIOR APPLICATION NUMBER: US 60/408,152
; PRIOR FILING DATE: 2002-09-03
; PRIOR APPLICATION NUMBER: US 60/473,387
; PRIOR FILING DATE: 2003-05-20
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 20
; LENGTH: 21
; TYPE: DNA
; ORGANISM: artificial
; FEATURE:
; OTHER INFORMATION: RNAi for human clusterin
US-10-646-391A-20

Query Match      1.3%; Score 21; DB 1; Length 21;
Best Local Similarity 81.0%; Pred. No. 1.2e+02;
Matches 17; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 482 CCAGAGCTCGCCCTTCTACTT 502
    |||||
Db 1 CCAGAGCTCGCCCTTCTACTT 21

RESULT 206
US-10-646-391A-21/c
; Sequence 21, Application US/10646391A
; Publication No. US20040082534A1
; GENERAL INFORMATION:
; APPLICANT: Jansen, Burkhard
; TITLE OF INVENTION: Treatment of Melanoma by Reduction in Clusterin Levels
; FILE REFERENCE: UBC.P-035
; CURRENT APPLICATION NUMBER: US/10/646,391A
; PRIOR FILING DATE: 2003-08-21
; PRIOR APPLICATION NUMBER: US 60/405,193
; PRIOR FILING DATE: 2002-08-21
; PRIOR APPLICATION NUMBER: US 60/319,748
; PRIOR FILING DATE: 2002-12-02
; PRIOR APPLICATION NUMBER: US 60/408,152
; PRIOR FILING DATE: 2002-09-03
; PRIOR APPLICATION NUMBER: US 60/473,387
; PRIOR FILING DATE: 2003-05-20
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 21
; LENGTH: 21
; TYPE: DNA
; ORGANISM: artificial
; FEATURE:
```

```
; OTHER INFORMATION: RNAi for human clusterin
US-10-646-391A-21

Query Match      1.3%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 480 AACAGAGTCCGCTTCTAC 500
Db 21 AACAGAGTCCGCTTCTAC 1

RESULT 207
US-10-646-391A-22
; Sequence 22, Application US/10646391A
; Publication No. US20040082534A1
; GENERAL INFORMATION:
; APPLICANT: Gleave, Martin
; TITLE OF INVENTION: Treatment of Melanoma by Reduction in Clusterin Levels
; FILE REFERENCE: UBC.P-035
; CURRENT APPLICATION NUMBER: US/10/646,391A
; CURRENT FILING DATE: 2003-08-21
; PRIOR APPLICATION NUMBER: US 60/405,193
; PRIOR FILING DATE: 2002-08-21
; PRIOR APPLICATION NUMBER: US 60/319,748
; PRIOR FILING DATE: 2002-12-02
; PRIOR APPLICATION NUMBER: US 60/408,152
; PRIOR FILING DATE: 2002-09-03
; PRIOR APPLICATION NUMBER: US 60/473,387
; PRIOR FILING DATE: 2003-05-20
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 22
; LENGTH: 21
; TYPE: DNA
; ORGANISM: artificial
; FEATURE:
; OTHER INFORMATION: RNAi for human clusterin
US-10-646-391A-22

Query Match      1.3%; Score 21; DB 1; Length 21;
Best Local Similarity 81.0%; Pred. No. 1.2e+02;
Matches 17; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1100 GATGCTCAACACTCTCTCTT 1120
Db 1 GAUGCUCAACACCCUCCUCC 21

RESULT 208
US-10-646-391A-23/c
; Sequence 23, Application US/10646391A
; Publication No. US20040082534A1
; GENERAL INFORMATION:
; APPLICANT: Gleave, Martin
; TITLE OF INVENTION: Treatment of Melanoma by Reduction in Clusterin Levels
; FILE REFERENCE: UBC.P-035
; CURRENT APPLICATION NUMBER: US/10/646,391A
; CURRENT FILING DATE: 2003-08-21
; PRIOR APPLICATION NUMBER: US 60/405,193
; PRIOR FILING DATE: 2002-08-21
; PRIOR APPLICATION NUMBER: US 60/319,748
; PRIOR FILING DATE: 2002-12-02
; PRIOR APPLICATION NUMBER: US 60/408,152
; PRIOR FILING DATE: 2002-09-03
; PRIOR APPLICATION NUMBER: US 60/473,387
; PRIOR FILING DATE: 2003-05-20
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 23
; LENGTH: 21
; TYPE: DNA
; ORGANISM: artificial
; FEATURE:
; OTHER INFORMATION: RNAi for human clusterin
US-10-646-391A-23/c

Query Match      1.3%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1613 AACTAATTCAATAAACTGTC 1633
Db 21 AACTAATTCAATAAACTGTC 1

RESULT 210
US-10-646-391A-36
; Sequence 36, Application US/10646391A
; Publication No. US20040082534A1
; GENERAL INFORMATION:
; APPLICANT: Gleave, Martin
; TITLE OF INVENTION: Treatment of Melanoma by Reduction in Clusterin Levels
; FILE REFERENCE: UBC.P-035
; CURRENT APPLICATION NUMBER: US/10/646,391A
; CURRENT FILING DATE: 2003-08-21
; PRIOR APPLICATION NUMBER: US 60/405,193
; PRIOR FILING DATE: 2002-08-21
; PRIOR APPLICATION NUMBER: US 60/319,748
; PRIOR FILING DATE: 2002-12-02
; PRIOR APPLICATION NUMBER: US 60/408,152
; PRIOR FILING DATE: 2002-09-03
; PRIOR APPLICATION NUMBER: US 60/473,387
; PRIOR FILING DATE: 2003-05-20
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 24
; LENGTH: 21
; TYPE: DNA
; ORGANISM: artificial
; FEATURE:
; OTHER INFORMATION: RNAi for human clusterin
US-10-646-391A-25

Query Match      1.3%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1098 AAGATGCTCAACACCTCTCTCC 1118
Db 21 AAGATGCTCAACACCTCTCTCC 1

RESULT 209
US-10-646-391A-25/c
; Sequence 25, Application US/10646391A
; Publication No. US20040082534A1
; GENERAL INFORMATION:
; APPLICANT: Jansen, Burkhard
; TITLE OF INVENTION: Treatment of Melanoma by Reduction in Clusterin Levels
; FILE REFERENCE: UBC.P-035
; CURRENT APPLICATION NUMBER: US/10/646,391A
; CURRENT FILING DATE: 2003-08-21
; PRIOR APPLICATION NUMBER: US 60/405,193
; PRIOR FILING DATE: 2002-08-21
; PRIOR APPLICATION NUMBER: US 60/319,748
; PRIOR FILING DATE: 2002-12-02
; PRIOR APPLICATION NUMBER: US 60/408,152
; PRIOR FILING DATE: 2002-09-03
; PRIOR APPLICATION NUMBER: US 60/473,387
; PRIOR FILING DATE: 2003-05-20
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 25
; LENGTH: 21
; TYPE: DNA
; ORGANISM: artificial
; FEATURE:
; OTHER INFORMATION: RNAi for human clusterin
US-10-646-391A-25
```

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; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 36
; LENGTH: 21
; TYPE: DNA
; ORGANISM: artificial
; FEATURE:
; OTHER INFORMATION: RNAi for human clusterin
US-10-646-391A-36

Query Match          1.3%; Score 21; DB 1; Length 21;
Best Local Similarity 81.0%; Pred. No. 1.2e+02;
Matches 17; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 482 CCAGAGCTCGCCCTTCTTACTT 502
      |||||:||||:||||:||||:
Db 1 CCAGAGCTCGCCCUUUACTT 21

RESULT 211
US-10-646-391A-37/c
; Sequence 37, Application US/10646391A
; Publication No. US20040082534A1
; GENERAL INFORMATION:
; APPLICANT: Gleave, Martin
; TITLE OF INVENTION: Treatment of Melanoma by Reduction in Clusterin Levels
; FILE REFERENCE: UBC.P-035
; CURRENT APPLICATION NUMBER: US/10/646,391A
; CURRENT FILING DATE: 2003-08-21
; PRIOR APPLICATION NUMBER: US 60/405,193
; PRIOR FILING DATE: 2002-08-21
; PRIOR APPLICATION NUMBER: US 60/319,748
; PRIOR FILING DATE: 2002-12-02
; PRIOR APPLICATION NUMBER: US 60/408,152
; PRIOR FILING DATE: 2002-09-03
; PRIOR APPLICATION NUMBER: US 60/473,387
; PRIOR FILING DATE: 2003-05-20
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 37
; LENGTH: 21
; TYPE: DNA
; ORGANISM: artificial
; FEATURE:
; OTHER INFORMATION: RNAi for human clusterin
US-10-646-391A-37

Query Match          1.3%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 480 AACGAGCTCGCCCTTCTTAC 500
      |||||:||||:||||:||||:
Db 21 AACGAGCTCGCCCTTCTTAC 1

RESULT 212
US-10-646-391A-38
; Sequence 38, Application US/10646391A
; Publication No. US20040082534A1
; GENERAL INFORMATION:
; APPLICANT: Gleave, Martin
; TITLE OF INVENTION: Treatment of Melanoma by Reduction in Clusterin Levels
; FILE REFERENCE: UBC.P-035
; CURRENT APPLICATION NUMBER: US/10/646,391A
; CURRENT FILING DATE: 2003-08-21
; PRIOR APPLICATION NUMBER: US 60/405,193
; PRIOR FILING DATE: 2002-08-21
; PRIOR APPLICATION NUMBER: US 60/319,748
; PRIOR FILING DATE: 2002-12-02
; PRIOR APPLICATION NUMBER: US 60/408,152
; PRIOR FILING DATE: 2002-09-03

; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 38
; LENGTH: 21
; TYPE: DNA
; ORGANISM: artificial
; FEATURE:
; OTHER INFORMATION: RNAi for human clusterin
US-10-646-391A-38

Query Match          1.3%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 711 AAGTCCGCGCATCGTCCGAGC 731
      |||||:||||:||||:||||:
Db 21 AAGTCCGCGCATCGTCCGAGC 1

RESULT 214
US-10-646-391A-40
; Sequence 40, Application US/10646391A
; Publication No. US20040082534A1
; GENERAL INFORMATION:
; APPLICANT: Gleave, Martin
; TITLE OF INVENTION: Treatment of Melanoma by Reduction in Clusterin Levels
; FILE REFERENCE: UBC.P-035
; CURRENT APPLICATION NUMBER: US/10/646,391A
; CURRENT FILING DATE: 2003-08-21
; PRIOR APPLICATION NUMBER: US 60/405,193
; PRIOR FILING DATE: 2002-08-21
; PRIOR APPLICATION NUMBER: US 60/319,748
; PRIOR FILING DATE: 2002-09-03

; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 39
; LENGTH: 21
; TYPE: DNA
; ORGANISM: artificial
; FEATURE:
; OTHER INFORMATION: RNAi for human clusterin
US-10-646-391A-39

Query Match          1.3%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 713 GTCCCGCATCGTCCGAGCTT 733
      |||||:||||:||||:||||:
Db 1 GUCCCGCAUGCGCCGAGCTT 21

RESULT 213
US-10-646-391A-39/c
; Sequence 39, Application US/10646391A
; Publication No. US20040082534A1
; GENERAL INFORMATION:
; APPLICANT: Gleave, Martin
; TITLE OF INVENTION: Treatment of Melanoma by Reduction in Clusterin Levels
; FILE REFERENCE: UBC.P-035
; CURRENT APPLICATION NUMBER: US/10/646,391A
; CURRENT FILING DATE: 2003-08-21
; PRIOR APPLICATION NUMBER: US 60/405,193
; PRIOR FILING DATE: 2002-08-21
; PRIOR APPLICATION NUMBER: US 60/319,748
; PRIOR FILING DATE: 2002-12-02
; PRIOR APPLICATION NUMBER: US 60/408,152
; PRIOR FILING DATE: 2002-09-03
; PRIOR APPLICATION NUMBER: US 60/473,387
; PRIOR FILING DATE: 2003-05-20
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 39
; LENGTH: 21
; TYPE: DNA
; ORGANISM: artificial
; FEATURE:
; OTHER INFORMATION: RNAi for human clusterin
US-10-646-391A-39

Query Match          1.3%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 711 AAGTCCGCGCATCGTCCGAGC 731
      |||||:||||:||||:||||:
Db 21 AAGTCCGCGCATCGTCCGAGC 1

RESULT 214
US-10-646-391A-40
; Sequence 40, Application US/10646391A
; Publication No. US20040082534A1
; GENERAL INFORMATION:
; APPLICANT: Gleave, Martin
; TITLE OF INVENTION: Treatment of Melanoma by Reduction in Clusterin Levels
; FILE REFERENCE: UBC.P-035
; CURRENT APPLICATION NUMBER: US/10/646,391A
; CURRENT FILING DATE: 2003-08-21
; PRIOR APPLICATION NUMBER: US 60/405,193
; PRIOR FILING DATE: 2002-08-21
; PRIOR APPLICATION NUMBER: US 60/319,748
; PRIOR FILING DATE: 2002-09-03
```

RESULT 218  
US-10-646-436-3  
; Sequence 3, Application US/10646436  
; Publication No. US20040096882A1

GENERAL INFORMATION:  
; APPLICANT: Jansen, Burkhard  
; APPLICANT: Gleave, Martin  
; APPLICANT: Signaevsky, Maxim  
; APPLICANT: Beraldi, Eliana  
; APPLICANT: Trougakos, Ioannis  
; APPLICANT: Gonos, Efsthios  
; TITLE OF INVENTION: RNAi Probes Targeting Cancer-Related Proteins  
; FILE REFERENCE: UBC.P-030  
; CURRENT APPLICATION NUMBER: US/10/646,436  
; CURRENT FILING DATE: 2003-08-21  
; PRIOR APPLICATION NUMBER: US 60/405,193  
; PRIOR FILING DATE: 2002-08-21  
; PRIOR APPLICATION NUMBER: US 60/408,152  
; PRIOR FILING DATE: 2002-09-03  
; PRIOR APPLICATION NUMBER: US 60/473,387  
; PRIOR FILING DATE: 2003-05-20  
; NUMBER OF SEQ ID NOS: 68  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 3  
; LENGTH: 21  
; TYPE: DNA  
; ORGANISM: artificial  
; FEATURE:  
; OTHER INFORMATION: RNAi for human clusterin  
US-10-646-436-3

Query Match 1.3%; Score 21; DB 1; Length 21;  
Best Local Similarity 81.0%; Pred. No. 1.2e+02;  
Matches 17; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy 1100 GATGCTCAACACCTCTCTT 1120  
||:|||||:-||:-|||  
Db 1 GAUGCUCACACCUCCUCCTT 21

RESULT 219  
US-10-646-436-4/c  
; Sequence 4, Application US/10646436  
; Publication No. US20040096882A1  
; GENERAL INFORMATION:  
; APPLICANT: Jansen, Burkhard  
; APPLICANT: Gleave, Martin  
; APPLICANT: Signaevsky, Maxim  
; APPLICANT: Beraldi, Eliana  
; APPLICANT: Trougakos, Ioannis  
; APPLICANT: Gonos, Efsthios  
; TITLE OF INVENTION: RNAi Probes Targeting Cancer-Related Proteins  
; FILE REFERENCE: UBC.P-030  
; CURRENT APPLICATION NUMBER: US/10/646,436  
; CURRENT FILING DATE: 2003-08-21  
; PRIOR APPLICATION NUMBER: US 60/405,193  
; PRIOR FILING DATE: 2002-08-21  
; PRIOR APPLICATION NUMBER: US 60/408,152  
; PRIOR FILING DATE: 2002-09-03  
; PRIOR APPLICATION NUMBER: US 60/473,387  
; PRIOR FILING DATE: 2003-05-20  
; NUMBER OF SEQ ID NOS: 68  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 4  
; LENGTH: 21  
; TYPE: DNA  
; ORGANISM: artificial  
; FEATURE:  
; OTHER INFORMATION: RNAi for human clusterin  
US-10-646-436-4

Query Match 1.3%; Score 21; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 1.2e+02;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1098 AAGATGCTCAACACCTCTCTCC 1118  
|||||||

Db 21 AAGATGCTCAACACCTCTCTCC 1

RESULT 220  
US-10-646-436-5  
; Sequence 5, Application US/10646436  
; Publication No. US20040096882A1  
; GENERAL INFORMATION:  
; APPLICANT: Jansen, Burkhard  
; APPLICANT: Gleave, Martin  
; APPLICANT: Signaevsky, Maxim  
; APPLICANT: Beraldi, Eliana  
; APPLICANT: Trougakos, Ioannis  
; APPLICANT: Gonos, Efsthios  
; TITLE OF INVENTION: RNAi Probes Targeting Cancer-Related Proteins  
; FILE REFERENCE: UBC.P-030  
; CURRENT APPLICATION NUMBER: US/10/646,436  
; CURRENT FILING DATE: 2003-08-21  
; PRIOR APPLICATION NUMBER: US 60/405,193  
; PRIOR FILING DATE: 2002-08-21  
; PRIOR APPLICATION NUMBER: US 60/408,152  
; PRIOR FILING DATE: 2002-09-03  
; PRIOR APPLICATION NUMBER: US 60/473,387  
; PRIOR FILING DATE: 2003-05-20  
; NUMBER OF SEQ ID NOS: 68  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 5  
; LENGTH: 21  
; TYPE: DNA  
; ORGANISM: artificial  
; FEATURE:  
; OTHER INFORMATION: RNAi for human clusterin  
US-10-646-436-5

Query Match 1.3%; Score 21; DB 1; Length 21;  
Best Local Similarity 71.4%; Pred. No. 1.2e+02;  
Matches 15; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

Qy 1615 CTAAATTCATAATAAACTGTCTT 1635  
|:|||||:-||:-|||  
Db 1 CUAUUCNAUAAACUGUCCTT 21

RESULT 221  
US-10-646-436-6/c  
; Sequence 6, Application US/10646436  
; Publication No. US20040096882A1  
; GENERAL INFORMATION:  
; APPLICANT: Jansen, Burkhard  
; APPLICANT: Gleave, Martin  
; APPLICANT: Signaevsky, Maxim  
; APPLICANT: Beraldi, Eliana  
; APPLICANT: Trougakos, Ioannis  
; APPLICANT: Gonos, Efsthios  
; TITLE OF INVENTION: RNAi Probes Targeting Cancer-Related Proteins  
; FILE REFERENCE: UBC.P-030  
; CURRENT APPLICATION NUMBER: US/10/646,436  
; CURRENT FILING DATE: 2003-08-21  
; PRIOR APPLICATION NUMBER: US 60/405,193  
; PRIOR FILING DATE: 2002-08-21  
; PRIOR APPLICATION NUMBER: US 60/408,152  
; PRIOR FILING DATE: 2002-09-03  
; PRIOR APPLICATION NUMBER: US 60/473,387  
; PRIOR FILING DATE: 2003-05-20  
; NUMBER OF SEQ ID NOS: 68  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 6  
; LENGTH: 21  
; TYPE: DNA  
; ORGANISM: artificial  
; FEATURE:  
; OTHER INFORMATION: RNAi for human clusterin  
US-10-646-436-6



Query Match 1.3%; Score 21; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 1.2e+02;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1613 AACTAATTCATATAACGTC 1633  
Db 21 AACTAATTCATATAAACTGTC 1

## RESULT 222

US-10-646-436-58  
; Sequence 58, Application US/10646436  
; Publication No. US20040096882A1  
; GENERAL INFORMATION:  
; APPLICANT: Jansen, Burkhard  
; APPLICANT: Gleave, Martin  
; APPLICANT: Signaevsky, Maxim  
; APPLICANT: Beraldi, Eliana  
; APPLICANT: Trougakos, Ioannis  
; APPLICANT: Gonos, Efsthios  
; TITLE OF INVENTION: RNAi Probes Targeting Cancer-Related Proteins  
; FILE REFERENCE: UBC P-030  
; CURRENT APPLICATION NUMBER: US/10/646,436  
; CURRENT FILING DATE: 2003-08-21  
; PRIOR APPLICATION NUMBER: US 60/405,193  
; PRIOR FILING DATE: 2002-08-21  
; PRIOR APPLICATION NUMBER: US 60/408,152  
; PRIOR FILING DATE: 2002-09-03  
; PRIOR APPLICATION NUMBER: US 60/473,387  
; PRIOR FILING DATE: 2003-05-20  
; NUMBER OF SEQ ID NOS: 68  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 58  
; LENGTH: 21  
; TYPE: DNA  
; ORGANISM: artificial  
; FEATURE:  
; OTHER INFORMATION: RNAi for human clusterin  
US-10-646-436-58

Query Match 1.3%; Score 21; DB 1; Length 21;  
Best Local Similarity 81.0%; Pred. No. 1.2e+02;  
Matches 17; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy 482 CCAGAGCTCGCCCTTCTACTT 502  
Db 1 CCAGAGCUCGCCCUUUAUACTT 21

## RESULT 223

US-10-646-436-59/c  
; Sequence 59, Application US/10646436  
; Publication No. US20040096882A1  
; GENERAL INFORMATION:  
; APPLICANT: Jansen, Burkhard  
; APPLICANT: Gleave, Martin  
; APPLICANT: Signaevsky, Maxim  
; APPLICANT: Beraldi, Eliana  
; APPLICANT: Trougakos, Ioannis  
; APPLICANT: Gonos, Efsthios  
; TITLE OF INVENTION: RNAi Probes Targeting Cancer-Related Proteins  
; FILE REFERENCE: UBC P-030  
; CURRENT APPLICATION NUMBER: US/10/646,436  
; CURRENT FILING DATE: 2003-08-21  
; PRIOR APPLICATION NUMBER: US 60/405,193  
; PRIOR FILING DATE: 2002-08-21  
; PRIOR APPLICATION NUMBER: US 60/408,152  
; PRIOR FILING DATE: 2002-09-03  
; PRIOR APPLICATION NUMBER: US 60/473,387  
; PRIOR FILING DATE: 2003-05-20  
; NUMBER OF SEQ ID NOS: 68  
; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 59  
; LENGTH: 21  
; TYPE: DNA  
; ORGANISM: artificial  
; FEATURE:  
; OTHER INFORMATION: RNAi for human clusterin  
US-10-646-436-59

Query Match 1.3%; Score 21; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 1.2e+02;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 480 AACGAGCTCGCCCTTCTAC 500  
Db 21 AACGAGCTCGCCCTTCTAC 1

## RESULT 224

US-10-646-436-61  
; Sequence 61, Application US/10646436  
; Publication No. US20040096882A1  
; GENERAL INFORMATION:  
; APPLICANT: Jansen, Burkhard  
; APPLICANT: Gleave, Martin  
; APPLICANT: Signaevsky, Maxim  
; APPLICANT: Beraldi, Eliana  
; APPLICANT: Trougakos, Ioannis  
; APPLICANT: Gonos, Efsthios  
; TITLE OF INVENTION: RNAi Probes Targeting Cancer-Related Proteins  
; FILE REFERENCE: UBC P-030  
; CURRENT APPLICATION NUMBER: US/10/646,436  
; CURRENT FILING DATE: 2003-08-21  
; PRIOR APPLICATION NUMBER: US 60/405,193  
; PRIOR FILING DATE: 2002-08-21  
; PRIOR APPLICATION NUMBER: US 60/408,152  
; PRIOR FILING DATE: 2002-09-03  
; PRIOR APPLICATION NUMBER: US 60/473,387  
; PRIOR FILING DATE: 2003-05-20  
; NUMBER OF SEQ ID NOS: 68  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 61  
; LENGTH: 21  
; TYPE: DNA  
; ORGANISM: artificial  
; FEATURE:  
; OTHER INFORMATION: RNAi for human clusterin  
US-10-646-436-61

Query Match 1.3%; Score 21; DB 1; Length 21;  
Best Local Similarity 85.7%; Pred. No. 1.2e+02;  
Matches 18; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 713 GTCCCGCATGTCGCGAGCTT 733  
Db 1 GUCCCGCAUCGUCGCGAGCTT 21

## RESULT 225

US-10-646-436-62/c  
; Sequence 62, Application US/10646436  
; Publication No. US20040096882A1  
; GENERAL INFORMATION:  
; APPLICANT: Jansen, Burkhard  
; APPLICANT: Gleave, Martin  
; APPLICANT: Signaevsky, Maxim  
; APPLICANT: Beraldi, Eliana  
; APPLICANT: Trougakos, Ioannis  
; APPLICANT: Gonos, Efsthios  
; TITLE OF INVENTION: RNAi Probes Targeting Cancer-Related Proteins  
; FILE REFERENCE: UBC P-030  
; CURRENT APPLICATION NUMBER: US/10/646,436  
; CURRENT FILING DATE: 2003-08-21  
; SOFTWARE: PatentIn version 3.2

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; PRIOR FILING DATE: 2002-08-21
; PRIOR APPLICATION NUMBER: US 60/408,152
; PRIOR FILING DATE: 2002-09-03
; PRIOR APPLICATION NUMBER: US 60/473,387
; PRIOR FILING DATE: 2003-05-20
; NUMBER OF SEQ ID NOS: 68
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 62
; LENGTH: 21
; TYPE: DNA
; ORGANISM: artificial
; FEATURE:
; OTHER INFORMATION: RNAi for human clusterin
US-10-646-436-62

Query Match          1.3%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 711 AAGTCCCGCATCGTCCGCAGC 731
Db 21 AAGTCCCGCATCGTCCGCAGC 1

RESULT 226
US-10-646-436-64
; Sequence 64, Application US/10646436
; Publication No. US20040096882A1
; GENERAL INFORMATION:
; APPLICANT: Jansen, Burkhard
; APPLICANT: Gleave, Martin
; APPLICANT: Signaevsky, Maxim
; APPLICANT: Beraldi, Eliana
; APPLICANT: Trougakos, Ioannis
; APPLICANT: Gonos, Efsthathios
; TITLE OF INVENTION: RNAi Probes Targeting Cancer-Related Proteins
; FILE REFERENCE: UBC.P-030
; CURRENT APPLICATION NUMBER: US/10/646,436
; CURRENT FILING DATE: 2003-08-21
; PRIOR FILING DATE: 2002-08-21
; PRIOR APPLICATION NUMBER: US 60/408,152
; PRIOR FILING DATE: 2002-09-03
; PRIOR APPLICATION NUMBER: US 60/473,387
; PRIOR FILING DATE: 2003-05-20
; NUMBER OF SEQ ID NOS: 68
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 64
; LENGTH: 21
; TYPE: DNA
; ORGANISM: artificial
; FEATURE:
; OTHER INFORMATION: RNAi for human clusterin
US-10-646-436-64

Query Match          1.3%; Score 21; DB 1; Length 21;
Best Local Similarity 71.4%; Pred. No. 1.2e+02;
Matches 15; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

Qy 1615 CTAATTCATTAATAACTGTCTT 1635
Db 1 CUAUAUCAUAAACUGUCTT 21

RESULT 227
US-10-646-436-65/c
; Sequence 65, Application US/10646436
; Publication No. US20040096882A1
; GENERAL INFORMATION:
; APPLICANT: Jansen, Burkhard
; APPLICANT: Gleave, Martin
; APPLICANT: Signaevsky, Maxim
; APPLICANT: Beraldi, Eliana
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; APPLICANT: Trougakos, Ioannis
; APPLICANT: Gonos, Efsthathios
; TITLE OF INVENTION: RNAi Probes Targeting Cancer-Related Proteins
; FILE REFERENCE: UBC.P-030
; CURRENT APPLICATION NUMBER: US/10/646,436
; CURRENT FILING DATE: 2003-08-21
; PRIOR APPLICATION NUMBER: US 60/408,152
; PRIOR FILING DATE: 2002-08-21
; PRIOR APPLICATION NUMBER: US 60/408,152
; PRIOR FILING DATE: 2002-09-03
; PRIOR APPLICATION NUMBER: US 60/473,387
; PRIOR FILING DATE: 2003-05-20
; NUMBER OF SEQ ID NOS: 68
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 65
; LENGTH: 21
; TYPE: DNA
; ORGANISM: artificial
; FEATURE:
; OTHER INFORMATION: RNAi for human clusterin
US-10-646-436-65

Query Match          1.3%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1613 AACTAATTCATTAATAACTGTC 1633
Db 21 AACTAATTCATTAATAACTGTC 1

RESULT 228
US-10-828-394-4/c
; Sequence 4, Application US/10828394
; Publication No. US20040220131A1
; GENERAL INFORMATION:
; APPLICANT: Jackson, John
; APPLICANT: Burt, Helen
; APPLICANT: Springate, Christopher
; APPLICANT: Gleave, Martin
; TITLE OF INVENTION: Method for Treatment of Cancerous Angiogenic Disorders
; FILE REFERENCE: UBC.P-033
; CURRENT APPLICATION NUMBER: US/10/828,394
; CURRENT FILING DATE: 2004-04-19
; PRIOR APPLICATION NUMBER: US 60/464,159
; PRIOR FILING DATE: 2003-04-18
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4
; LENGTH: 21
; TYPE: DNA
; ORGANISM: human
US-10-828-394-4

Query Match          1.3%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 16 CCGAGGCGTGCAGAAAGACTCCA 36
Db 21 CCGAGGCGTGCAGAAAGACTCCA 1

RESULT 229
US-10-828-394-5/c
; Sequence 5, Application US/10828394
; Publication No. US20040220131A1
; GENERAL INFORMATION:
; APPLICANT: Jackson, John
; APPLICANT: Burt, Helen
; APPLICANT: Springate, Christopher
; APPLICANT: Gleave, Martin
; TITLE OF INVENTION: Method for Treatment of Cancerous Angiogenic Disorders
```

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; FILE REFERENCE: UBC.P-033
; CURRENT APPLICATION NUMBER: US/10/828,394
; CURRENT FILING DATE: 2004-04-19
; PRIOR APPLICATION NUMBER: US 60/464,159
; PRIOR FILING DATE: 2003-04-18
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 5
; LENGTH: 21
; TYPE: DNA
; ORGANISM: human
US-10-828-394-5

Query Match      1.3%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      48 ATGATGAAGACTCTGCTGCTG 68
Db      21 ATGATGAAGACTCTGCTGCTG 1

RESULT 230
US-10-828-394-6/c
; Sequence 6, Application US/10828394
; Publication No. US20040220131A1
; GENERAL INFORMATION:
; APPLICANT: Jackson, John
; APPLICANT: Burt, Helen
; APPLICANT: Springate, Christopher
; APPLICANT: Gleave, Martin
; TITLE OF INVENTION: Method for Treatment of Cancerous Angiogenic Disorders
; FILE REFERENCE: UBC.P-033
; CURRENT APPLICATION NUMBER: US/10/828,394
; CURRENT FILING DATE: 2004-04-19
; PRIOR APPLICATION NUMBER: US 60/464,159
; PRIOR FILING DATE: 2003-04-18
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 6
; LENGTH: 21
; TYPE: DNA
; ORGANISM: human
US-10-828-394-6

Query Match      1.3%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      114 GACCAGACGGTCTCAGACAAT 134
Db      21 GACCAGACGGTCTCAGACAAT 1

RESULT 231
US-10-828-394-7/c
; Sequence 7, Application US/10828394
; Publication No. US20040220131A1
; GENERAL INFORMATION:
; APPLICANT: Jackson, John
; APPLICANT: Burt, Helen
; APPLICANT: Springate, Christopher
; APPLICANT: Gleave, Martin
; TITLE OF INVENTION: Method for Treatment of Cancerous Angiogenic Disorders
; FILE REFERENCE: UBC.P-033
; CURRENT APPLICATION NUMBER: US/10/828,394
; CURRENT FILING DATE: 2004-04-19
; PRIOR APPLICATION NUMBER: US 60/464,159
; PRIOR FILING DATE: 2003-04-18
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 7
; LENGTH: 21

; FILE REFERENCE: UBC.P-033
; CURRENT APPLICATION NUMBER: US/10/828,394
; CURRENT FILING DATE: 2004-04-19
; PRIOR APPLICATION NUMBER: US 60/464,159
; PRIOR FILING DATE: 2003-04-18
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 8
; LENGTH: 21
; TYPE: DNA
; ORGANISM: human
US-10-828-394-8/c

Query Match      1.3%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      515 TGACCGCATCGACTCCCTGCT 535
Db      21 TGACCGCATCGACTCCCTGCT 1

RESULT 233
US-10-828-394-9/c
; Sequence 9, Application US/10828394
; Publication No. US20040220131A1
; GENERAL INFORMATION:
; APPLICANT: Jackson, John
; APPLICANT: Burt, Helen
; APPLICANT: Springate, Christopher
; APPLICANT: Gleave, Martin
; TITLE OF INVENTION: Method for Treatment of Cancerous Angiogenic Disorders
; FILE REFERENCE: UBC.P-033
; CURRENT APPLICATION NUMBER: US/10/828,394
; CURRENT FILING DATE: 2004-04-19
; PRIOR APPLICATION NUMBER: US 60/464,159
; PRIOR FILING DATE: 2003-04-18
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 9
; LENGTH: 21
; TYPE: DNA
; ORGANISM: human
US-10-828-394-9

Query Match      1.3%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      716 CCGCATCGTCGCGAGCTTGAT 736
Db      21 CCGCATCGTCGCGAGCTTGAT 1
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Db      21  CCGCATCGTCCGAGCTTGAT 1
|||||
RESULT 234
US-10-828-394-10/c
; Sequence 10, Application US/10828394
; Publication No. US20040220131A1
; GENERAL INFORMATION:
; APPLICANT: Jackson, John
; APPLICANT: Burt, Helen
; APPLICANT: Springate, Christopher
; APPLICANT: Gleave, Martin
; TITLE OF INVENTION: Method for Treatment of Cancerous Angiogenic Disorders
; FILE REFERENCE: UBC.P-033
; CURRENT APPLICATION NUMBER: US/10/828,394
; CURRENT FILING DATE: 2004-04-19
; PRIOR APPLICATION NUMBER: US 60/464,159
; PRIOR FILING DATE: 2003-04-18
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 10
; LENGTH: 21
; TYPE: DNA
; ORGANISM: human
US-10-828-394-10

Query Match      1.3%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      916  ACAACTCCACGGGCTGCTGC 936
|||||
Db      21  ACAACTCCACGGGCTGCTGC 1

RESULT 235
US-10-828-394-11/c
; Sequence 11, Application US/10828394
; Publication No. US20040220131A1
; GENERAL INFORMATION:
; APPLICANT: Jackson, John
; APPLICANT: Burt, Helen
; APPLICANT: Springate, Christopher
; APPLICANT: Gleave, Martin
; TITLE OF INVENTION: Method for Treatment of Cancerous Angiogenic Disorders
; FILE REFERENCE: UBC.P-033
; CURRENT APPLICATION NUMBER: US/10/828,394
; CURRENT FILING DATE: 2004-04-19
; PRIOR APPLICATION NUMBER: US 60/464,159
; PRIOR FILING DATE: 2003-04-18
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 11
; LENGTH: 21
; TYPE: DNA
; ORGANISM: human
US-10-828-394-11

Query Match      1.3%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1115 CTCCTTGCTGGAGCAGCTGAA 1135
|||||
Db      21  CTCCTTGCTGGAGCAGCTGAA 1

RESULT 236
US-10-828-394-12/c
; Sequence 12, Application US/10828394
; Publication No. US20040220131A1
; GENERAL INFORMATION:
; APPLICANT: Jackson, John
; APPLICANT: Burt, Helen
; APPLICANT: Springate, Christopher
; APPLICANT: Gleave, Martin
; TITLE OF INVENTION: Method for Treatment of Cancerous Angiogenic Disorders
; FILE REFERENCE: UBC.P-032
; CURRENT APPLICATION NUMBER: US/10/828,395
; CURRENT FILING DATE: 2004-04-19
; PRIOR APPLICATION NUMBER: US 60/464,159
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 12
; LENGTH: 21
; TYPE: DNA
; ORGANISM: human
US-10-828-394-12

Query Match      1.3%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1516 AGGCCCCCACTCCGCCGAC 1536
|||||
Db      21  AGGCCCCCACTCCGCCGAC 1

RESULT 237
US-10-828-394-13/c
; Sequence 13, Application US/10828394
; Publication No. US20040220131A1
; GENERAL INFORMATION:
; APPLICANT: Jackson, John
; APPLICANT: Burt, Helen
; APPLICANT: Springate, Christopher
; APPLICANT: Gleave, Martin
; TITLE OF INVENTION: Method for Treatment of Cancerous Angiogenic Disorders
; FILE REFERENCE: UBC.P-033
; CURRENT APPLICATION NUMBER: US/10/828,394
; CURRENT FILING DATE: 2004-04-19
; PRIOR APPLICATION NUMBER: US 60/464,159
; PRIOR FILING DATE: 2003-04-18
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 13
; LENGTH: 21
; TYPE: DNA
; ORGANISM: human
US-10-828-394-13

Query Match      1.3%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1316 CTCGAGGAGACCCCTAAATT 1336
|||||
Db      21  CTCGAGGAGACCCCTAAATT 1

RESULT 238
US-10-828-395-4/c
; Sequence 4, Application US/10828395
; Publication No. US20040224914A1
; GENERAL INFORMATION:
; APPLICANT: Jackson, John
; APPLICANT: Burt, Helen
; APPLICANT: Springate, Christopher
; APPLICANT: Gleave, Martin
; TITLE OF INVENTION: Method for Treatment of Angiogenic Disorders
; FILE REFERENCE: UBC.P-032
; CURRENT APPLICATION NUMBER: US/10/828,395
; CURRENT FILING DATE: 2004-04-19
; PRIOR APPLICATION NUMBER: US 60/464,159
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 14
; LENGTH: 21
; TYPE: DNA
; ORGANISM: human
US-10-828-395-4/c

Query Match      1.3%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1516 AGGCCCCCACTCCGCCGAC 1536
|||||
Db      21  AGGCCCCCACTCCGCCGAC 1

RESULT 239
US-10-828-395-4/c
; Sequence 4, Application US/10828395
; Publication No. US20040224914A1
; GENERAL INFORMATION:
; APPLICANT: Jackson, John
; APPLICANT: Burt, Helen
; APPLICANT: Springate, Christopher
; APPLICANT: Gleave, Martin
; TITLE OF INVENTION: Method for Treatment of Angiogenic Disorders
; FILE REFERENCE: UBC.P-032
; CURRENT APPLICATION NUMBER: US/10/828,395
; CURRENT FILING DATE: 2004-04-19
; PRIOR APPLICATION NUMBER: US 60/464,159
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 14
; LENGTH: 21
; TYPE: DNA
; ORGANISM: human
US-10-828-395-4/c
```

; PRIOR FILING DATE: 2003-04-18  
; PRIOR APPLICATION NUMBER: US 60/464,160  
; PRIOR FILING DATE: 2003-04-18  
; NUMBER OF SEQ ID NOS: 23  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 4  
; LENGTH: 21  
; TYPE: DNA  
; ORGANISM: human  
US-10-828-395-4

Query Match 1.3%; Score 21; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 1.2e+02;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 16 CCGAGGCGTGCAGACTCCA 36  
| | | | | | | | | | | | | | | | | | | | | |  
Db 21 CCGAGGCGTGCAGACTCCA 1

RESULT 239  
US-10-828-395-5/c  
; Sequence 5, Application US/10828395  
; Publication No. US20040224914A1  
; GENERAL INFORMATION:  
; APPLICANT: Jackson, John  
; APPLICANT: Burt, Helen  
; APPLICANT: Springate, Christopher  
; APPLICANT: Gleave, Martin  
; TITLE OF INVENTION: Method for Treatment of Angiogenic Disorders  
; FILE REFERENCE: UBC.P-032  
; CURRENT APPLICATION NUMBER: US/10/828,395  
; CURRENT FILING DATE: 2004-04-19  
; PRIOR APPLICATION NUMBER: US 60/464,159  
; PRIOR FILING DATE: 2003-04-18  
; PRIOR APPLICATION NUMBER: US 60/464,160  
; PRIOR FILING DATE: 2003-04-18  
; NUMBER OF SEQ ID NOS: 23  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 5  
; LENGTH: 21  
; TYPE: DNA  
; ORGANISM: human  
US-10-828-395-5

Query Match 1.3%; Score 21; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 1.2e+02;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 48 ATGATGAAGACTGCTGCTG 68  
| | | | | | | | | | | | | | | | | | | | | |  
Db 21 ATGATGAAGACTGCTGCTG 1

RESULT 240  
US-10-828-395-6/c  
; Sequence 6, Application US/10828395  
; Publication No. US20040224914A1  
; GENERAL INFORMATION:  
; APPLICANT: Jackson, John  
; APPLICANT: Burt, Helen  
; APPLICANT: Springate, Christopher  
; APPLICANT: Gleave, Martin  
; TITLE OF INVENTION: Method for Treatment of Angiogenic Disorders  
; FILE REFERENCE: UBC.P-032  
; CURRENT APPLICATION NUMBER: US/10/828,395  
; CURRENT FILING DATE: 2004-04-19  
; PRIOR APPLICATION NUMBER: US 60/464,159  
; PRIOR FILING DATE: 2003-04-18  
; PRIOR APPLICATION NUMBER: US 60/464,160  
; PRIOR FILING DATE: 2003-04-18  
; NUMBER OF SEQ ID NOS: 23  
; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 6  
; LENGTH: 21  
; TYPE: DNA  
; ORGANISM: human  
US-10-828-395-6

Query Match 1.3%; Score 21; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 1.2e+02;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 114 GACCAGACGGTCTCAGACAAT 134  
| | | | | | | | | | | | | | | | | | | | | |  
Db 21 GACCAGACGGTCTCAGACAAT 1

RESULT 241  
US-10-828-395-7/c  
; Sequence 7, Application US/10828395  
; Publication No. US20040224914A1  
; GENERAL INFORMATION:  
; APPLICANT: Jackson, John  
; APPLICANT: Burt, Helen  
; APPLICANT: Springate, Christopher  
; APPLICANT: Gleave, Martin  
; TITLE OF INVENTION: Method for Treatment of Angiogenic Disorders  
; FILE REFERENCE: UBC.P-032  
; CURRENT APPLICATION NUMBER: US/10/828,395  
; CURRENT FILING DATE: 2004-04-19  
; PRIOR APPLICATION NUMBER: US 60/464,159  
; PRIOR FILING DATE: 2003-04-18  
; PRIOR APPLICATION NUMBER: US 60/464,160  
; PRIOR FILING DATE: 2003-04-18  
; NUMBER OF SEQ ID NOS: 23  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 7  
; LENGTH: 21  
; TYPE: DNA  
; ORGANISM: human  
US-10-828-395-7

Query Match 1.3%; Score 21; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 1.2e+02;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 316 AATCAGACAAAGCTGAAGG 336  
| | | | | | | | | | | | | | | | | | | | | |  
Db 21 AATCAGACAAAGCTGAAGG 1

RESULT 242  
US-10-828-395-8/c  
; Sequence 8, Application US/10828395  
; Publication No. US20040224914A1  
; GENERAL INFORMATION:  
; APPLICANT: Jackson, John  
; APPLICANT: Burt, Helen  
; APPLICANT: Springate, Christopher  
; APPLICANT: Gleave, Martin  
; TITLE OF INVENTION: Method for Treatment of Angiogenic Disorders  
; FILE REFERENCE: UBC.P-032  
; CURRENT APPLICATION NUMBER: US/10/828,395  
; CURRENT FILING DATE: 2004-04-19  
; PRIOR APPLICATION NUMBER: US 60/464,159  
; PRIOR FILING DATE: 2003-04-18  
; PRIOR APPLICATION NUMBER: US 60/464,160  
; PRIOR FILING DATE: 2003-04-18  
; NUMBER OF SEQ ID NOS: 23  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 8  
; LENGTH: 21  
; TYPE: DNA  
; ORGANISM: human  
US-10-828-395-8

Query Match		1.3%;	Score 21;	DB 1;	Length 21;		
Best Local Similarity		100.0%;	Pred. No. 1.2e+02;				
Matches		21;	Conservative	0;	Mismatches 0; Indels 0; Gaps 0;		
Qy	515	TGACCGCATCGACTCCCTGCT	535				
Db	21	TGACCGCATCGACTCCCTGCT	1				
RESULT 243							
US-10-828-395-9/c							
; Sequence 9, Application US/10828395							
; Publication No. US20040224914A1							
; GENERAL INFORMATION:							
; APPLICANT: Jackson, John							
; APPLICANT: Burt, Helen							
; APPLICANT: Springate, Christopher							
; TITLE OF INVENTION: Method for Treatment of Angiogenic Disorders							
; FILE REFERENCE: UBC.P-032							
; CURRENT APPLICATION NUMBER: US/10/828,395							
; CURRENT FILING DATE: 2004-04-19							
; PRIOR APPLICATION NUMBER: US 60/464,159							
; PRIOR FILING DATE: 2003-04-18							
; PRIOR APPLICATION NUMBER: US 60/464,160							
; PRIOR FILING DATE: 2003-04-18							
; NUMBER OF SEQ ID NOS: 23							
; SOFTWARE: PatentIn version 3.2							
; SEQ ID NO 9							
; LENGTH: 21							
; TYPE: DNA							
; ORGANISM: human							
US-10-828-395-9							
Query Match		1.3%;	Score 21;	DB 1;	Length 21;		
Best Local Similarity		100.0%;	Pred. No. 1.2e+02;				
Matches		21;	Conservative	0;	Mismatches 0; Indels 0; Gaps 0;		
Qy	716	CGCATCGTCGCGACGTTGAT	736				
Db	21	CGCATCGTCGCGACGTTGAT	1				
RESULT 244							
US-10-828-395-10/c							
; Sequence 10, Application US/10828395							
; Publication No. US20040224914A1							
; GENERAL INFORMATION:							
; APPLICANT: Jackson, John							
; APPLICANT: Burt, Helen							
; APPLICANT: Springate, Christopher							
; TITLE OF INVENTION: Method for Treatment of Angiogenic Disorders							
; FILE REFERENCE: UBC.P-032							
; CURRENT APPLICATION NUMBER: US/10/828,395							
; CURRENT FILING DATE: 2004-04-19							
; PRIOR APPLICATION NUMBER: US 60/464,159							
; PRIOR FILING DATE: 2003-04-18							
; PRIOR APPLICATION NUMBER: US 60/464,160							
; PRIOR FILING DATE: 2003-04-18							
; NUMBER OF SEQ ID NOS: 23							
; SOFTWARE: PatentIn version 3.2							
; SEQ ID NO 10							
; LENGTH: 21							
; TYPE: DNA							
; ORGANISM: human							
US-10-828-395-10							
Query Match		1.3%;	Score 21;	DB 1;	Length 21;		
Best Local Similarity		100.0%;	Pred. No. 1.2e+02;				
Matches		21;	Conservative	0;	Mismatches 0; Indels 0; Gaps 0;		

Query Match		1.3%;	Score 21;	DB 1;	Length 21;		
Best Local Similarity		100.0%;	Pred. No. 1.2e+02;				
Matches		21;	Conservative	0;	Mismatches 0; Indels 0; Gaps 0;		
Qy	916	ACAACCTCCACGGGCTGCCTGC	936				
Db	21	ACAACCTCCACGGGCTGCCTGC	1				
RESULT 245							
US-10-828-395-11/c							
; Sequence 11, Application US/10828395							
; Publication No. US20040224914A1							
; GENERAL INFORMATION:							
; APPLICANT: Jackson, John							
; APPLICANT: Burt, Helen							
; APPLICANT: Springate, Christopher							
; TITLE OF INVENTION: Method for Treatment of Angiogenic Disorders							
; FILE REFERENCE: UBC.P-032							
; CURRENT APPLICATION NUMBER: US/10/828,395							
; CURRENT FILING DATE: 2004-04-19							
; PRIOR APPLICATION NUMBER: US 60/464,159							
; PRIOR FILING DATE: 2003-04-18							
; PRIOR APPLICATION NUMBER: US 60/464,160							
; PRIOR FILING DATE: 2003-04-18							
; NUMBER OF SEQ ID NOS: 23							
; SOFTWARE: PatentIn version 3.2							
; SEQ ID NO 11							
; LENGTH: 21							
; TYPE: DNA							
; ORGANISM: human							
US-10-828-395-11							
Query Match		1.3%;	Score 21;	DB 1;	Length 21;		
Best Local Similarity		100.0%;	Pred. No. 1.2e+02;				
Matches		21;	Conservative	0;	Mismatches 0; Indels 0; Gaps 0;		
Qy	1115	CTCCTTGCTGGAGCAGCTGAA	1135				
Db	21	CTCCTTGCTGGAGCAGCTGAA	1				
RESULT 246							
US-10-828-395-12/c							
; Sequence 12, Application US/10828395							
; Publication No. US20040224914A1							
; GENERAL INFORMATION:							
; APPLICANT: Jackson, John							
; APPLICANT: Burt, Helen							
; APPLICANT: Springate, Christopher							
; TITLE OF INVENTION: Method for Treatment of Angiogenic Disorders							
; FILE REFERENCE: UBC.P-032							
; CURRENT APPLICATION NUMBER: US/10/828,395							
; CURRENT FILING DATE: 2004-04-19							
; PRIOR APPLICATION NUMBER: US 60/464,159							
; PRIOR FILING DATE: 2003-04-18							
; PRIOR APPLICATION NUMBER: US 60/464,160							
; PRIOR FILING DATE: 2003-04-18							
; NUMBER OF SEQ ID NOS: 23							
; SOFTWARE: PatentIn version 3.2							
; SEQ ID NO 12							
; LENGTH: 21							
; TYPE: DNA							
; ORGANISM: human							
US-10-828-395-12							
Query Match		1.3%;	Score 21;	DB 1;	Length 21;		
Best Local Similarity		100.0%;	Pred. No. 1.2e+02;				
Matches		21;	Conservative	0;	Mismatches 0; Indels 0; Gaps 0;		
Qy	1316	CTCCAGGAGAACCCCTAAATT	1336				
Db	21	CTCCAGGAGAACCCCTAAATT	1				

```
RESULT 247
US-10-828-395-13/c
; Sequence 13, Application US/10828395
; Publication No. US20040224914A1
; GENERAL INFORMATION:
; APPLICANT: Jackson, John
; APPLICANT: Burt, Helen
; APPLICANT: Springate, Christopher
; APPLICANT: Gleave, Martin
; TITLE OF INVENTION: Method for Treatment of Angiogenic Disorders
; FILE REFERENCE: UBC-P-032
; CURRENT APPLICATION NUMBER: US/10/828,395
; CURRENT FILING DATE: 2004-04-19
; PRIOR APPLICATION NUMBER: US 60/464,159
; PRIOR FILING DATE: 2003-04-18
; PRIOR APPLICATION NUMBER: US 60/464,160
; PRIOR FILING DATE: 2003-04-18
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 13
; LENGTH: 21
; TYPE: DNA
; ORGANISM: human
US-10-828-395-13

Query Match      1.3%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1516 AGGCCCGCCCACTCGCCCGC 1536
Db      21 AGGCCCGCCCACTCGCCCGC 1

RESULT 248
US-10-719-900-695781/c
; Sequence 695781, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 695781
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-695781

Query Match      1.3%; Score 20.8; DB 1; Length 25;
Best Local Similarity 91.7%; Pred. No. 1.8e+02;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      565 TGGATGTCATCGACGACCTTCA 588
Db      25 TGCATGTCATCGACGACCTTCA 2

RESULT 249
US-10-719-900-56803
; Sequence 56803, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
```

```
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 56803
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-56803

Query Match      1.2%; Score 20.2; DB 1; Length 25;
Best Local Similarity 88.0%; Pred. No. 2e+02;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      1269 AAGCTCTTTGACTCTGATCCCATCA 1293
Db      1 AAGCTGTTTGACACTGACCCCATCA 25

RESULT 250
US-10-719-900-452919
; Sequence 452919, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 452919
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-452919

Query Match      1.2%; Score 20.2; DB 1; Length 25;
Best Local Similarity 88.0%; Pred. No. 2e+02;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      1137 GACGAGTTTAACGTGGGTGTCGCCGC 1161
Db      1 GACGAGTTCAACTGGGTGTCGCCGC 25

RESULT 251
US-10-719-900-815717
; Sequence 815717, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 815717
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-815717

Query Match      1.2%; Score 20.2; DB 1; Length 25;
Best Local Similarity 88.0%; Pred. No. 2e+02;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      1245 TCCGGTGTCACTGAGGTGTCGTGA 1269
```

```
Db 1 TCCCGTGTCTACTCAGGTGGTGTGA 25
|||||
RESULT 252
US-10-719-900-892166
; Sequence 892166, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 892166
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-892166

Query Match 1.2%; Score 20.2; DB 1; Length 25;
Best Local Similarity 88.0%; Pred. No. 2e+02;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1149 TGGGTGTCCCGCTGGCAACCTCA 1173
|||||
Db 1 TGGGTGTCCAGGTGGCTAACCTCA 25
|||||

RESULT 253
US-10-809-189-31758
; Sequence 31758, Application US/10809189
; Publication No. US20050048531A1
; GENERAL INFORMATION:
; APPLICANT: Michael Mitmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/10/809,189
; CURRENT FILING DATE: 2004-03-25
; PRIOR APPLICATION NUMBER: US/09/396,196
; PRIOR FILING DATE: 1999-09-15
; PRIOR FILING DATE: 1999-09-15
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 31758
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-809-189-31758

Query Match 1.2%; Score 20.2; DB 1; Length 25;
Best Local Similarity 88.0%; Pred. No. 2e+02;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1171 TCACGCAAGCGGAGACCACTACTA 1195
|||||
Db 1 TCACAGGGCGAGACAGTACTA 25
|||||

RESULT 254
US-10-956-157-271151
; Sequence 271151, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth

; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 271151
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-271151

Query Match 1.2%; Score 20.2; DB 1; Length 25;
Best Local Similarity 88.0%; Pred. No. 2e+02;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1588 GAAGAACAGAAATGCTCTGCATGC 1612
|||||
Db 1 GGAAGACAGAAATGCTCTGCATGC 25
|||||

RESULT 255
US-10-719-956-30750/c
; Sequence 30750, Application US/10719956
; Publication No. US20040146910A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527.1
; CURRENT APPLICATION NUMBER: US/10/719,956
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,836
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 30750
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-10-719-956-30750

Query Match 1.2%; Score 20.2; DB 1; Length 25;
Best Local Similarity 88.0%; Pred. No. 2e+02;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1120 TGCTGACGACGTGAACGAGCAGTT 1144
|||||
Db 25 TGCTGGAACAGACGAAACGACCAGTT 1
|||||

RESULT 256
US-10-719-956-70566/c
; Sequence 70566, Application US/10719956
; Publication No. US20040146910A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527.1
; CURRENT APPLICATION NUMBER: US/10/719,956
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,836
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 70566
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-10-719-956-70566

Query Match 1.2%; Score 20.2; DB 1; Length 25;
```



```
Best Local Similarity 88.0%; Pred. No. 2e+02;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 951 TGTGACAAAGTCCGGAGATCTTGT 975
      ||||| ||||| ||||| ||||| |||||
Db 25 TGTGAAAGTGCCAAAGATCTTGT 1

RESULT 257
US-10-719-956-355802/c
; Sequence 355802, Application US/10719956
; Publication No. US20040146910A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527.1
; CURRENT APPLICATION NUMBER: US/10/719,956
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,836
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 355802
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-10-719-956-355802

Query Match 1.2%; Score 20.2; DB 1; Length 25;
Best Local Similarity 88.0%; Pred. No. 2e+02;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 898 TGTGCGGAGATCGCCCAACT 922
      ||||| ||||| ||||| ||||| |||||
Db 25 TGTGCAAGGAGATCGCCCAATC 1

RESULT 258
US-10-719-956-374027/c
; Sequence 374027, Application US/10719956
; Publication No. US20040146910A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527.1
; CURRENT APPLICATION NUMBER: US/10/719,956
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,836
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 374027
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-10-719-956-374027

Query Match 1.2%; Score 20.2; DB 1; Length 25;
Best Local Similarity 88.0%; Pred. No. 2e+02;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 975 TCTGTGACTGTTCACCAAC 999
      ||||| ||||| ||||| ||||| |||||
Db 25 TCTGTGACTGTACCAACATC 1

RESULT 259
US-10-719-956-501380
; Sequence 501380, Application US/10719956
; Publication No. US20040146910A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527.1
; CURRENT APPLICATION NUMBER: US/10/719,956
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,836
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 501380
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-10-719-956-501380

Query Match 1.2%; Score 20.2; DB 1; Length 25;
Best Local Similarity 88.0%; Pred. No. 2e+02;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1266 GTGAAGCTCTTGACTCTGATCCCA 1290
      ||||| ||||| ||||| ||||| |||||
Db 1 GTGAAGCTGTTTCACTCTGACCCCA 25

RESULT 260
US-10-719-956-517912
; Sequence 517912, Application US/10719956
; Publication No. US20040146910A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527.1
; CURRENT APPLICATION NUMBER: US/10/719,956
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,836
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 517912
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-10-719-956-517912

Query Match 1.2%; Score 20.2; DB 1; Length 25;
Best Local Similarity 88.0%; Pred. No. 2e+02;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 897 GTGTGCGGAGATCCGCCCAACT 921
      ||||| ||||| ||||| ||||| |||||
Db 1 GTGTGCAAGGAGATCCGCCCAACT 25

RESULT 261
US-10-719-956-604881/c
; Sequence 604881, Application US/10719956
; Publication No. US20040146910A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527.1
; CURRENT APPLICATION NUMBER: US/10/719,956
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,836
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 604881
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-10-719-956-604881

Query Match 1.2%; Score 20.2; DB 1; Length 25;
Best Local Similarity 88.0%; Pred. No. 2e+02;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

```
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 778 TCAGCCCTTCCTTGAGATGATACA 802
      ||||| ||||| ||||| ||||| |||||
Db 25 TCAGCGCTTCCTTGAGTGGATCA 1

RESULT 262
US-10-719-956-612441/c
; Sequence 612441, Application US/10719956
; Publication No. US20040146910A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527.1
; CURRENT APPLICATION NUMBER: US/10/719,956
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,836
; PRIOR FILING DATE: 2002.11.20
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 612441
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-10-719-956-612441

Query Match 1.2%; Score 20.2; DB 1; Length 25;
Best Local Similarity 88.0%; Pred. No. 2e+02;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1149 TGGGTGTCCCGCTGGCAAACTCA 1173
      ||||| ||||| ||||| ||||| |||||
Db 25 TGGGTGTCCCGGTGGCTAACTCA 1

RESULT 263
US-10-124-14/c
; Sequence 14, Application US/10380124
; Publication No. US20040053874A1
; GENERAL INFORMATION:
; APPLICANT: Isis Pharmaceuticals, Inc.
; APPLICANT: Brett P. Monia
; APPLICANT: Susan M. Freier
; TITLE OF INVENTION: ANTISENSE MODULATION OF CLUSTERIN EXPRESSION
; FILE REFERENCE: RTS-0156
; CURRENT APPLICATION NUMBER: US/10/380,124
; CURRENT FILING DATE: 2003-03-10
; NUMBER OF SEQ ID NOS: 90
; SEQ ID NO 14
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-380-124-14

Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 13 TGACCGAGCGGTGCAAGAC 32
      ||||| ||||| ||||| ||||| |||||
Db 20 TGACCGAGCGGTGCAAGAC 1

RESULT 264
US-10-380-124-15/c
; Sequence 15, Application US/10380124
; Publication No. US20040053874A1
; GENERAL INFORMATION:
; APPLICANT: Isis Pharmaceuticals, Inc.
; APPLICANT: Brett P. Monia
; APPLICANT: Susan M. Freier
; TITLE OF INVENTION: ANTISENSE MODULATION OF CLUSTERIN EXPRESSION
; FILE REFERENCE: RTS-0156
; CURRENT APPLICATION NUMBER: US/10/380,124
; CURRENT FILING DATE: 2003-03-10
; NUMBER OF SEQ ID NOS: 90
; SEQ ID NO 17
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-380-124-15

Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 21 GCGTGCAAGACTCCAGAAT 40
      ||||| ||||| ||||| ||||| |||||
Db 20 GCGTGCAAGACTCCAGAAT 1

RESULT 265
US-10-380-124-16/c
; Sequence 16, Application US/10380124
; Publication No. US20040053874A1
; GENERAL INFORMATION:
; APPLICANT: Isis Pharmaceuticals, Inc.
; APPLICANT: Brett P. Monia
; APPLICANT: Susan M. Freier
; TITLE OF INVENTION: ANTISENSE MODULATION OF CLUSTERIN EXPRESSION
; FILE REFERENCE: RTS-0156
; CURRENT APPLICATION NUMBER: US/10/380,124
; CURRENT FILING DATE: 2003-03-10
; NUMBER OF SEQ ID NOS: 90
; SEQ ID NO 16
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-380-124-16

Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 39 ATTGGAGGCATGATGAAGAC 58
      ||||| ||||| ||||| ||||| |||||
Db 20 ATTGGAGGCATGATGAAGAC 1

RESULT 266
US-10-380-124-17/c
; Sequence 17, Application US/10380124
; Publication No. US20040053874A1
; GENERAL INFORMATION:
; APPLICANT: Isis Pharmaceuticals, Inc.
; APPLICANT: Brett P. Monia
; APPLICANT: Susan M. Freier
; TITLE OF INVENTION: ANTISENSE MODULATION OF CLUSTERIN EXPRESSION
; FILE REFERENCE: RTS-0156
; CURRENT APPLICATION NUMBER: US/10/380,124
; CURRENT FILING DATE: 2003-03-10
; NUMBER OF SEQ ID NOS: 90
; SEQ ID NO 17
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-380-124-17
```

```
Query Match      1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 77 GCTGCTGCTGACCTGGGAGA 96
    |||||
Db 20 GCTGCTGCTGACCTGGGAGA 1

RESULT 267
US-10-380-124-18/c
; Sequence 18, Application US/10380124
; Publication No. US20040053874A1
; GENERAL INFORMATION:
; APPLICANT: Isis Pharmaceuticals, Inc.
; APPLICANT: Brett P. Monia
; APPLICANT: Susan M. Freier
; TITLE OF INVENTION: ANTISENSE MODULATION OF CLUSTERIN EXPRESSION
; FILE REFERENCE: RTS-0156
; CURRENT APPLICATION NUMBER: US/10/380,124
; CURRENT FILING DATE: 2003-03-10
; NUMBER OF SEQ ID NOS: 90
; SEQ ID NO 18
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-380-124-18

Query Match      1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 101 GCAGTCTCTGGGGACCAGA 120
    |||||
Db 20 GCAGTCTCTGGGGACCAGA 1

RESULT 268
US-10-380-124-19/c
; Sequence 19, Application US/10380124
; Publication No. US20040053874A1
; GENERAL INFORMATION:
; APPLICANT: Isis Pharmaceuticals, Inc.
; APPLICANT: Brett P. Monia
; APPLICANT: Susan M. Freier
; TITLE OF INVENTION: ANTISENSE MODULATION OF CLUSTERIN EXPRESSION
; FILE REFERENCE: RTS-0156
; CURRENT APPLICATION NUMBER: US/10/380,124
; CURRENT FILING DATE: 2003-03-10
; NUMBER OF SEQ ID NOS: 90
; SEQ ID NO 19
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-380-124-19

Query Match      1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 122 GGTCTCAGACATGAGCTCC 141
    |||||
Db 20 GGTCTCAGACATGAGCTCC 1

RESULT 269
US-10-380-124-20/c
; Sequence 20, Application US/10380124
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; Publication No. US20040053874A1
; GENERAL INFORMATION:
; APPLICANT: Isis Pharmaceuticals, Inc.
; APPLICANT: Brett P. Monia
; APPLICANT: Susan M. Freier
; TITLE OF INVENTION: ANTISENSE MODULATION OF CLUSTERIN EXPRESSION
; FILE REFERENCE: RTS-0156
; CURRENT APPLICATION NUMBER: US/10/380,124
; CURRENT FILING DATE: 2003-03-10
; NUMBER OF SEQ ID NOS: 90
; SEQ ID NO 20
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-380-124-20

Query Match      1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 149 GTCCAATCAGGGAAGTAAGT 168
    |||||
Db 20 GTCCAATCAGGGAAGTAAGT 1

RESULT 270
US-10-380-124-21/c
; Sequence 21, Application US/10380124
; Publication No. US20040053874A1
; GENERAL INFORMATION:
; APPLICANT: Isis Pharmaceuticals, Inc.
; APPLICANT: Brett P. Monia
; APPLICANT: Susan M. Freier
; TITLE OF INVENTION: ANTISENSE MODULATION OF CLUSTERIN EXPRESSION
; FILE REFERENCE: RTS-0156
; CURRENT APPLICATION NUMBER: US/10/380,124
; CURRENT FILING DATE: 2003-03-10
; NUMBER OF SEQ ID NOS: 90
; SEQ ID NO 21
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-380-124-21

Query Match      1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 166 AGTACGTCATAAGGAATT 185
    |||||
Db 20 AGTACGTCATAAGGAATT 1

RESULT 271
US-10-380-124-22/c
; Sequence 22, Application US/10380124
; Publication No. US20040053874A1
; GENERAL INFORMATION:
; APPLICANT: Isis Pharmaceuticals, Inc.
; APPLICANT: Brett P. Monia
; APPLICANT: Susan M. Freier
; TITLE OF INVENTION: ANTISENSE MODULATION OF CLUSTERIN EXPRESSION
; FILE REFERENCE: RTS-0156
; CURRENT APPLICATION NUMBER: US/10/380,124
; CURRENT FILING DATE: 2003-03-10
; NUMBER OF SEQ ID NOS: 90
; SEQ ID NO 22
; LENGTH: 20
; TYPE: DNA
```

```
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-380-124-22

Query Match          1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 201 GGGGTGAACAGATAAAGAC 220
    |||||
Db 20 GGGGTGAACAGATAAAGAC 1

RESULT 272
US-10-380-124-23/c
; Sequence 23, Application US/10380124
; Publication No. US20040053874A1
; GENERAL INFORMATION:
; APPLICANT: Isis Pharmaceuticals, Inc.
; APPLICANT: Brett P. Monia
; APPLICANT: Susan M. Freier
; TITLE OF INVENTION: ANTISENSE MODULATION OF CLUSTERIN EXPRESSION
; FILE REFERENCE: RTS-0156
; CURRENT APPLICATION NUMBER: US/10/380,124
; CURRENT FILING DATE: 2003-03-10
; NUMBER OF SEQ ID NOS: 90
; SEQ ID NO 23
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-380-124-23

Query Match          1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 281 GAAGAGAAAGAGATGCC 300
    |||||
Db 20 GAAGAGAAAGAGATGCC 1

RESULT 273
US-10-380-124-24/c
; Sequence 24, Application US/10380124
; Publication No. US20040053874A1
; GENERAL INFORMATION:
; APPLICANT: Isis Pharmaceuticals, Inc.
; APPLICANT: Brett P. Monia
; APPLICANT: Susan M. Freier
; TITLE OF INVENTION: ANTISENSE MODULATION OF CLUSTERIN EXPRESSION
; FILE REFERENCE: RTS-0156
; CURRENT APPLICATION NUMBER: US/10/380,124
; CURRENT FILING DATE: 2003-03-10
; NUMBER OF SEQ ID NOS: 90
; SEQ ID NO 24
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-380-124-24

Query Match          1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 286 AGAAGAGGATGCCCTAAAT 305
    |||||
Db 20 AGAAGAGGATGCCCTAAAT 1
```

```
RESULT 274
US-10-380-124-25/c
; Sequence 25, Application US/10380124
; Publication No. US20040053874A1
; GENERAL INFORMATION:
; APPLICANT: Isis Pharmaceuticals, Inc.
; APPLICANT: Brett P. Monia
; APPLICANT: Susan M. Freier
; TITLE OF INVENTION: ANTISENSE MODULATION OF CLUSTERIN EXPRESSION
; FILE REFERENCE: RTS-0156
; CURRENT APPLICATION NUMBER: US/10/380,124
; CURRENT FILING DATE: 2003-03-10
; NUMBER OF SEQ ID NOS: 90
; SEQ ID NO 25
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-380-124-25

Query Match          1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 298 CCCTAATGAGACCGGAA 317
    |||||
Db 20 CCCTAATGAGACCGGAA 1

RESULT 275
US-10-380-124-26/c
; Sequence 26, Application US/10380124
; Publication No. US20040053874A1
; GENERAL INFORMATION:
; APPLICANT: Isis Pharmaceuticals, Inc.
; APPLICANT: Brett P. Monia
; APPLICANT: Susan M. Freier
; TITLE OF INVENTION: ANTISENSE MODULATION OF CLUSTERIN EXPRESSION
; FILE REFERENCE: RTS-0156
; CURRENT APPLICATION NUMBER: US/10/380,124
; CURRENT FILING DATE: 2003-03-10
; NUMBER OF SEQ ID NOS: 90
; SEQ ID NO 26
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-380-124-26

Query Match          1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 307 AGACCAGGGAATCAGAGACA 326
    |||||
Db 20 AGACCAGGGAATCAGAGACA 1

RESULT 276
US-10-380-124-27/c
; Sequence 27, Application US/10380124
; Publication No. US20040053874A1
; GENERAL INFORMATION:
; APPLICANT: Isis Pharmaceuticals, Inc.
; APPLICANT: Brett P. Monia
; APPLICANT: Susan M. Freier
; TITLE OF INVENTION: ANTISENSE MODULATION OF CLUSTERIN EXPRESSION
; FILE REFERENCE: RTS-0156
; CURRENT APPLICATION NUMBER: US/10/380,124
; CURRENT FILING DATE: 2003-03-10
```

<p>QY      364 TGATGGCCCTCTGGGAAGAG 383                               Db      20 TGATGGCCCTCTGGGAAGAG 1</p>	<p>US-10-380-124-30/c ; Sequence 30, Application US/10380124 ; Publication No. US20040053874A1 ; GENERAL INFORMATION: ; APPLICANT: Isis Pharmaceuticals, Inc. ; APPLICANT: Brett P. Monia ; APPLICANT: Susan M. Freier ; TITLE OF INVENTION: ANTISENSE MODULATION OF CLUSTERIN EXPRESSION ; FILE REFERENCE: RTS-0156 ; CURRENT APPLICATION NUMBER: US/10/380,124 ; CURRENT FILING DATE: 2003-03-10 ; NUMBER OF SEQ ID NOS: 90 ; SEQ ID NO 30 ; LENGTH: 20 ; TYPE: DNA ; ORGANISM: Artificial Sequence ; FEATURE: ; OTHER INFORMATION: Antisense Oligonucleotide US-10-380-124-30</p>	<p>Query Match                  1.2%; Score 20; DB 1; Length 20; Best Local Similarity      100.0%; Pred. No. 1.3e+02; Matches      20; Conservative      0; Mismatches      0; Indels      0; Gaps      0;</p>
<p>QY      380 AGAGTGTAAAGCCTGCCTGA 399                               Db      20 AGAGTGTAAAGCCTGCCTGA 1</p>	<p>US-10-380-124-31/c ; Sequence 31, Application US/10380124 ; Publication No. US20040053874A1 ; GENERAL INFORMATION: ; APPLICANT: Isis Pharmaceuticals, Inc. ; APPLICANT: Brett P. Monia ; APPLICANT: Susan M. Freier ; TITLE OF INVENTION: ANTISENSE MODULATION OF CLUSTERIN EXPRESSION ; FILE REFERENCE: RTS-0156 ; CURRENT APPLICATION NUMBER: US/10/380,124 ; CURRENT FILING DATE: 2003-03-10 ; NUMBER OF SEQ ID NOS: 90 ; SEQ ID NO 31 ; LENGTH: 20 ; TYPE: DNA ; ORGANISM: Artificial Sequence ; FEATURE: ; OTHER INFORMATION: Antisense Oligonucleotide US-10-380-124-31</p>	<p>Query Match                  1.2%; Score 20; DB 1; Length 20; Best Local Similarity      100.0%; Pred. No. 1.3e+02; Matches      20; Conservative      0; Mismatches      0; Indels      0; Gaps      0;</p>
<p>QY      407 CTGCGTGAAAGTTCTACGCAC 426                               Db      20 CTGCGTGAAAGTTCTACGCAC 1</p>	<p>US-10-380-124-32/c ; Sequence 32, Application US/10380124 ; Publication No. US20040053874A1 ; GENERAL INFORMATION: ; APPLICANT: Isis Pharmaceuticals, Inc. ; APPLICANT: Brett P. Monia ; APPLICANT: Susan M. Freier ; TITLE OF INVENTION: ANTISENSE MODULATION OF CLUSTERIN EXPRESSION ; FILE REFERENCE: RTS-0156 ; CURRENT APPLICATION NUMBER: US/10/380,124 ; CURRENT FILING DATE: 2003-03-10 ; NUMBER OF SEQ ID NOS: 90 ; SEQ ID NO 32 ; LENGTH: 20 ; TYPE: DNA ; ORGANISM: Artificial Sequence ; FEATURE: ; OTHER INFORMATION: Antisense Oligonucleotide US-10-380-124-32</p>	<p>Query Match                  1.2%; Score 20; DB 1; Length 20; Best Local Similarity      100.0%; Pred. No. 1.3e+02; Matches      20; Conservative      0; Mismatches      0; Indels      0; Gaps      0;</p>

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; TITLE OF INVENTION: ANTISENSE MODULATION OF CLUSTERIN EXPRESSION
; FILE REFERENCE: RTS-0156
; CURRENT APPLICATION NUMBER: US/10/380,124
; CURRENT FILING DATE: 2003-03-10
; NUMBER OF SEQ ID NOS: 90
; SEQ ID NO 32
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-380-124-32

Query Match      1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 443 CTCAGGCGCTGGTTGGCGGCC 462
Db 20 CTCAGGCGCTGGTTGGCGGCC 1

RESULT 282
US-10-380-124-33/c
; Sequence 33, Application US/10380124
; Publication No. US20040053874A1
; GENERAL INFORMATION:
; APPLICANT: Isis Pharmaceuticals, Inc.
; APPLICANT: Brett P. Monia
; APPLICANT: Susan M. Freier
; TITLE OF INVENTION: ANTISENSE MODULATION OF CLUSTERIN EXPRESSION
; FILE REFERENCE: RTS-0156
; CURRENT APPLICATION NUMBER: US/10/380,124
; CURRENT FILING DATE: 2003-03-10
; NUMBER OF SEQ ID NOS: 90
; SEQ ID NO 33
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-380-124-33

Query Match      1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 444 TCAGGCGCTGGTTGGCGGCCA 463
Db 20 TCAGGCGCTGGTTGGCGGCCA 1

RESULT 283
US-10-380-124-34/c
; Sequence 34, Application US/10380124
; Publication No. US20040053874A1
; GENERAL INFORMATION:
; APPLICANT: Isis Pharmaceuticals, Inc.
; APPLICANT: Brett P. Monia
; APPLICANT: Susan M. Freier
; TITLE OF INVENTION: ANTISENSE MODULATION OF CLUSTERIN EXPRESSION
; FILE REFERENCE: RTS-0156
; CURRENT APPLICATION NUMBER: US/10/380,124
; CURRENT FILING DATE: 2003-03-10
; NUMBER OF SEQ ID NOS: 90
; SEQ ID NO 34
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-380-124-34
```

```
Query Match      1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 455 TGGCCGCCAGCTTGAGGAGT 474
Db 20 TGGCCGCCAGCTTGAGGAGT 1

RESULT 284
US-10-380-124-35/c
; Sequence 35, Application US/10380124
; Publication No. US20040053874A1
; GENERAL INFORMATION:
; APPLICANT: Isis Pharmaceuticals, Inc.
; APPLICANT: Brett P. Monia
; APPLICANT: Susan M. Freier
; TITLE OF INVENTION: ANTISENSE MODULATION OF CLUSTERIN EXPRESSION
; FILE REFERENCE: RTS-0156
; CURRENT APPLICATION NUMBER: US/10/380,124
; CURRENT FILING DATE: 2003-03-10
; NUMBER OF SEQ ID NOS: 90
; SEQ ID NO 35
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-380-124-35

Query Match      1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 482 CCAGAGCTCGCCCTTCTACT 501
Db 20 CCAGAGCTCGCCCTTCTACT 1

RESULT 285
US-10-380-124-36/c
; Sequence 36, Application US/10380124
; Publication No. US20040053874A1
; GENERAL INFORMATION:
; APPLICANT: Isis Pharmaceuticals, Inc.
; APPLICANT: Brett P. Monia
; APPLICANT: Susan M. Freier
; TITLE OF INVENTION: ANTISENSE MODULATION OF CLUSTERIN EXPRESSION
; FILE REFERENCE: RTS-0156
; CURRENT APPLICATION NUMBER: US/10/380,124
; CURRENT FILING DATE: 2003-03-10
; NUMBER OF SEQ ID NOS: 90
; SEQ ID NO 36
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-380-124-36

Query Match      1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 492 CCCTTCTACTTCTGGATGAA 511
Db 20 CCCTTCTACTTCTGGATGAA 1

RESULT 286
US-10-380-124-37/c
; Sequence 37, Application US/10380124
; Publication No. US20040053874A1
```

```
; GENERAL INFORMATION:
; APPLICANT: Isis Pharmaceuticals, Inc.
; APPLICANT: Brett P. Monia
; APPLICANT: Susan M. Freier
; TITLE OF INVENTION: ANTISENSE MODULATION OF CLUSTERIN EXPRESSION
; FILE REFERENCE: RTS-0156
; CURRENT APPLICATION NUMBER: US/10/380,124
; CURRENT FILING DATE: 2003-03-10
; NUMBER OF SEQ ID NOS: 90
; SEQ ID NO 37
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-380-124-37

Query Match      1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 517 ACCGATCGACTCCCTGCTG 536
Db 20 ACCGATCGACTCCCTGCTG 1

RESULT 287
US-10-380-124-38/c
; Sequence 38, Application US/10380124
; Publication No. US20040053874A1
; GENERAL INFORMATION:
; APPLICANT: Isis Pharmaceuticals, Inc.
; APPLICANT: Brett P. Monia
; APPLICANT: Susan M. Freier
; TITLE OF INVENTION: ANTISENSE MODULATION OF CLUSTERIN EXPRESSION
; FILE REFERENCE: RTS-0156
; CURRENT APPLICATION NUMBER: US/10/380,124
; CURRENT FILING DATE: 2003-03-10
; NUMBER OF SEQ ID NOS: 90
; SEQ ID NO 38
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-380-124-38

Query Match      1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 533 GCTGGAAGACGACGGCAGC 552
Db 20 GCTGGAAGACGACGGCAGC 1

RESULT 288
US-10-380-124-39/c
; Sequence 39, Application US/10380124
; Publication No. US20040053874A1
; GENERAL INFORMATION:
; APPLICANT: Isis Pharmaceuticals, Inc.
; APPLICANT: Brett P. Monia
; APPLICANT: Susan M. Freier
; TITLE OF INVENTION: ANTISENSE MODULATION OF CLUSTERIN EXPRESSION
; FILE REFERENCE: RTS-0156
; CURRENT APPLICATION NUMBER: US/10/380,124
; CURRENT FILING DATE: 2003-03-10
; NUMBER OF SEQ ID NOS: 90
; SEQ ID NO 39
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
```

```
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-380-124-39

Query Match      1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 551 GCAGACGCACATGCTGGATG 570
Db 20 GCAGACGCACATGCTGGATG 1

RESULT 289
US-10-380-124-40/c
; Sequence 40, Application US/10380124
; Publication No. US20040053874A1
; GENERAL INFORMATION:
; APPLICANT: Isis Pharmaceuticals, Inc.
; APPLICANT: Brett P. Monia
; APPLICANT: Susan M. Freier
; TITLE OF INVENTION: ANTISENSE MODULATION OF CLUSTERIN EXPRESSION
; FILE REFERENCE: RTS-0156
; CURRENT APPLICATION NUMBER: US/10/380,124
; CURRENT FILING DATE: 2003-03-10
; NUMBER OF SEQ ID NOS: 90
; SEQ ID NO 40
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-380-124-40

Query Match      1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 553 AGACGCACATGCTGGATGTC 572
Db 20 AGACGCACATGCTGGATGTC 1

RESULT 290
US-10-380-124-41/c
; Sequence 41, Application US/10380124
; Publication No. US20040053874A1
; GENERAL INFORMATION:
; APPLICANT: Isis Pharmaceuticals, Inc.
; APPLICANT: Brett P. Monia
; APPLICANT: Susan M. Freier
; TITLE OF INVENTION: ANTISENSE MODULATION OF CLUSTERIN EXPRESSION
; FILE REFERENCE: RTS-0156
; CURRENT APPLICATION NUMBER: US/10/380,124
; CURRENT FILING DATE: 2003-03-10
; NUMBER OF SEQ ID NOS: 90
; SEQ ID NO 41
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-380-124-41

Query Match      1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 565 TGGATGTCATGCAGGACCAC 584
Db 20 TGGATGTCATGCAGGACCAC 1
```

```
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-380-124-41

Query Match      1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 565 TGGATGTCATGCAGGACCAC 584
Db 20 TGGATGTCATGCAGGACCAC 1
```

```
RESULT 291
US-10-380-124-42/c
; Sequence 42, Application US/10380124
; Publication No. US20040053874A1
; GENERAL INFORMATION:
; APPLICANT: Isis Pharmaceuticals, Inc.
; APPLICANT: Brett P. Monia
; APPLICANT: Susan M. Freier
; TITLE OF INVENTION: ANTISENSE MODULATION OF CLUSTERIN EXPRESSION
; FILE REFERENCE: RTS-0156
; CURRENT APPLICATION NUMBER: US/10/380,124
; CURRENT FILING DATE: 2003-03-10
; NUMBER OF SEQ ID NOS: 90
; SEQ ID NO 42
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-380-124-42

Query Match      1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      567 GATGTCATGCGAGCCACTT 586
Db      20 GATGTCATGCGAGCCACTT 1
|||||

RESULT 292
US-10-380-124-43/c
; Sequence 43, Application US/10380124
; Publication No. US20040053874A1
; GENERAL INFORMATION:
; APPLICANT: Isis Pharmaceuticals, Inc.
; APPLICANT: Brett P. Monia
; APPLICANT: Susan M. Freier
; TITLE OF INVENTION: ANTISENSE MODULATION OF CLUSTERIN EXPRESSION
; FILE REFERENCE: RTS-0156
; CURRENT APPLICATION NUMBER: US/10/380,124
; CURRENT FILING DATE: 2003-03-10
; NUMBER OF SEQ ID NOS: 90
; SEQ ID NO 43
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-380-124-43

Query Match      1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      604 TCATAGACGAGCTCTTCCAG 623
Db      20 TCATAGACGAGCTCTTCCAG 1
|||||

RESULT 293
US-10-380-124-44/c
; Sequence 44, Application US/10380124
; Publication No. US20040053874A1
; GENERAL INFORMATION:
; APPLICANT: Isis Pharmaceuticals, Inc.
; APPLICANT: Brett P. Monia
; APPLICANT: Susan M. Freier
; TITLE OF INVENTION: ANTISENSE MODULATION OF CLUSTERIN EXPRESSION
; FILE REFERENCE: RTS-0156
; CURRENT APPLICATION NUMBER: US/10/380,124
; CURRENT FILING DATE: 2003-03-10
; NUMBER OF SEQ ID NOS: 90
; SEQ ID NO 44
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-380-124-44

Query Match      1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      608 AGACGAGCTCTTCCAGGACA 627
Db      20 AGACGAGCTCTTCCAGGACA 1
|||||

RESULT 294
US-10-380-124-45/c
; Sequence 45, Application US/10380124
; Publication No. US20040053874A1
; GENERAL INFORMATION:
; APPLICANT: Isis Pharmaceuticals, Inc.
; APPLICANT: Brett P. Monia
; APPLICANT: Susan M. Freier
; TITLE OF INVENTION: ANTISENSE MODULATION OF CLUSTERIN EXPRESSION
; FILE REFERENCE: RTS-0156
; CURRENT APPLICATION NUMBER: US/10/380,124
; CURRENT FILING DATE: 2003-03-10
; NUMBER OF SEQ ID NOS: 90
; SEQ ID NO 45
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-380-124-45

Query Match      1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      613 AGCTCTTCCAGGACAGGTTTC 632
Db      20 AGCTCTTCCAGGACAGGTTTC 1
|||||

RESULT 295
US-10-380-124-46/c
; Sequence 46, Application US/10380124
; Publication No. US20040053874A1
; GENERAL INFORMATION:
; APPLICANT: Isis Pharmaceuticals, Inc.
; APPLICANT: Brett P. Monia
; APPLICANT: Susan M. Freier
; TITLE OF INVENTION: ANTISENSE MODULATION OF CLUSTERIN EXPRESSION
; FILE REFERENCE: RTS-0156
; CURRENT APPLICATION NUMBER: US/10/380,124
; CURRENT FILING DATE: 2003-03-10
; NUMBER OF SEQ ID NOS: 90
; SEQ ID NO 46
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-380-124-46

Query Match      1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      690 AGGCTCACTTCTTCTTCC 709
```



```
Db      20 AGGCTCACTTCTTCTTCC 1
|||||
; FILE REFERENCE: RTS-0156
; CURRENT APPLICATION NUMBER: US/10/380,124
; CURRENT FILING DATE: 2003-03-10
; NUMBER OF SEQ ID NOS: 90
; SEQ ID NO 47
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-380-124-47/c
Query Match      1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      721 TCGTCCGAGCTTGATGCC 740
|||||
Db      20 TCGTCCGAGCTTGATGCC 1
|||||

RESULT 297
US-10-380-124-48/c
; Sequence 48, Application US/10380124
; Publication No. US20040053874A1
; GENERAL INFORMATION:
; APPLICANT: Isis Pharmaceuticals, Inc.
; APPLICANT: Brett P. Monia
; APPLICANT: Susan M. Freier
; TITLE OF INVENTION: ANTISENSE MODULATION OF CLUSTERIN EXPRESSION
; FILE REFERENCE: RTS-0156
; CURRENT APPLICATION NUMBER: US/10/380,124
; CURRENT FILING DATE: 2003-03-10
; NUMBER OF SEQ ID NOS: 90
; SEQ ID NO 48
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-380-124-48
Query Match      1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      775 TGTTCAGCCCTTCTTGAG 794
|||||
Db      20 TGTTCAGCCCTTCTTGAG 1
|||||

RESULT 298
US-10-380-124-49/c
; Sequence 49, Application US/10380124
; Publication No. US20040053874A1
; GENERAL INFORMATION:
; APPLICANT: Isis Pharmaceuticals, Inc.
; APPLICANT: Brett P. Monia
; APPLICANT: Susan M. Freier
; TITLE OF INVENTION: ANTISENSE MODULATION OF CLUSTERIN EXPRESSION
```

```
; FILE REFERENCE: RTS-0156
; CURRENT APPLICATION NUMBER: US/10/380,124
; CURRENT FILING DATE: 2003-03-10
; NUMBER OF SEQ ID NOS: 90
; SEQ ID NO 49
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-380-124-49
Query Match      1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      776 GTTCCAGCCCTTCTTGAGA 795
|||||
Db      20 GTTCCAGCCCTTCTTGAGA 1
|||||

RESULT 299
US-10-380-124-50/c
; Sequence 50, Application US/10380124
; Publication No. US20040053874A1
; GENERAL INFORMATION:
; APPLICANT: Isis Pharmaceuticals, Inc.
; APPLICANT: Brett P. Monia
; APPLICANT: Susan M. Freier
; TITLE OF INVENTION: ANTISENSE MODULATION OF CLUSTERIN EXPRESSION
; FILE REFERENCE: RTS-0156
; CURRENT APPLICATION NUMBER: US/10/380,124
; CURRENT FILING DATE: 2003-03-10
; NUMBER OF SEQ ID NOS: 90
; SEQ ID NO 50
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-380-124-50
Query Match      1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      783 CCCTTCCTTGAGATGATACA 802
|||||
Db      20 CCCTTCCTTGAGATGATACA 1
|||||

RESULT 300
US-10-380-124-51/c
; Sequence 51, Application US/10380124
; Publication No. US20040053874A1
; GENERAL INFORMATION:
; APPLICANT: Isis Pharmaceuticals, Inc.
; APPLICANT: Brett P. Monia
; APPLICANT: Susan M. Freier
; TITLE OF INVENTION: ANTISENSE MODULATION OF CLUSTERIN EXPRESSION
; FILE REFERENCE: RTS-0156
; CURRENT APPLICATION NUMBER: US/10/380,124
; CURRENT FILING DATE: 2003-03-10
; NUMBER OF SEQ ID NOS: 90
; SEQ ID NO 51
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-380-124-51
Query Match      1.2%; Score 20; DB 1; Length 20;
```

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```
Best Local Similarity 100.0%; Pred. No. 1.3e+02; Mismatches 0; Indels 0; Gaps 0;
Matches 20; Conservative 0;

QY 820 TGGACATCCACTCCACAGC 839
    |||||
Db 20 TGGACATCCACTCCACAGC 1

RESULT 301
US-10-380-124-52/c
; Sequence 52, Application US/10380124
; Publication No. US20040053874A1
; GENERAL INFORMATION:
; APPLICANT: Isis Pharmaceuticals, Inc.
; APPLICANT: Brett P. Monia
; TITLE OF INVENTION: ANTISENSE MODULATION OF CLUSTERIN EXPRESSION
; FILE REFERENCE: RTS-0156
; CURRENT APPLICATION NUMBER: US/10/380,124
; CURRENT FILING DATE: 2003-03-10
; NUMBER OF SEQ ID NOS: 90
; SEQ ID NO 52
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-380-124-52

Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.3e+02; Mismatches 0; Indels 0; Gaps 0;
Matches 20; Conservative 0;

QY 893 GACTGTGTGCGGAGATCC 912
    |||||
Db 20 GACTGTGTGCGGAGATCC 1

RESULT 304
US-10-380-124-55/c
; Sequence 55, Application US/10380124
; Publication No. US20040053874A1
; GENERAL INFORMATION:
; APPLICANT: Isis Pharmaceuticals, Inc.
; APPLICANT: Brett P. Monia
; APPLICANT: Susan M. Freier
; TITLE OF INVENTION: ANTISENSE MODULATION OF CLUSTERIN EXPRESSION
; FILE REFERENCE: RTS-0156
; CURRENT APPLICATION NUMBER: US/10/380,124
; CURRENT FILING DATE: 2003-03-10
; NUMBER OF SEQ ID NOS: 90
; SEQ ID NO 55
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-380-124-55

Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.3e+02; Mismatches 0; Indels 0; Gaps 0;
Matches 20; Conservative 0;

QY 894 ACTGTGTGCGGAGATCCG 913
    |||||
Db 20 ACTGTGTGCGGAGATCCG 1

RESULT 305
US-10-380-124-56/c
; Sequence 56, Application US/10380124
; Publication No. US20040053874A1
; GENERAL INFORMATION:
; APPLICANT: Isis Pharmaceuticals, Inc.
; APPLICANT: Brett P. Monia
; APPLICANT: Susan M. Freier
; TITLE OF INVENTION: ANTISENSE MODULATION OF CLUSTERIN EXPRESSION
; FILE REFERENCE: RTS-0156
; CURRENT APPLICATION NUMBER: US/10/380,124
; CURRENT FILING DATE: 2003-03-10
; NUMBER OF SEQ ID NOS: 90
; SEQ ID NO 56
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-380-124-56
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```
Best Local Similarity 100.0%; Pred. No. 1.3e+02; Mismatches 0; Indels 0; Gaps 0;
Matches 20; Conservative 0;

QY 820 TGGACATCCACTCCACAGC 839
    |||||
Db 20 TGGACATCCACTCCACAGC 1

RESULT 301
US-10-380-124-52/c
; Sequence 52, Application US/10380124
; Publication No. US20040053874A1
; GENERAL INFORMATION:
; APPLICANT: Isis Pharmaceuticals, Inc.
; APPLICANT: Brett P. Monia
; TITLE OF INVENTION: ANTISENSE MODULATION OF CLUSTERIN EXPRESSION
; FILE REFERENCE: RTS-0156
; CURRENT APPLICATION NUMBER: US/10/380,124
; CURRENT FILING DATE: 2003-03-10
; NUMBER OF SEQ ID NOS: 90
; SEQ ID NO 52
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-380-124-52

Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.3e+02; Mismatches 0; Indels 0; Gaps 0;
Matches 20; Conservative 0;

QY 848 CCAGCACCCGCCACAGAAT 867
    |||||
Db 20 CCAGCACCCGCCACAGAAT 1

RESULT 302
US-10-380-124-53/c
; Sequence 53, Application US/10380124
; Publication No. US20040053874A1
; GENERAL INFORMATION:
; APPLICANT: Isis Pharmaceuticals, Inc.
; APPLICANT: Brett P. Monia
; APPLICANT: Susan M. Freier
; TITLE OF INVENTION: ANTISENSE MODULATION OF CLUSTERIN EXPRESSION
; FILE REFERENCE: RTS-0156
; CURRENT APPLICATION NUMBER: US/10/380,124
; CURRENT FILING DATE: 2003-03-10
; NUMBER OF SEQ ID NOS: 90
; SEQ ID NO 53
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-380-124-53

Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.3e+02; Mismatches 0; Indels 0; Gaps 0;
Matches 20; Conservative 0;

QY 853 ACCCGCCACAGAAATTCATA 872
    |||||
Db 20 ACCCGCCACAGAAATTCATA 1

RESULT 303
US-10-380-124-54/c
; Sequence 54, Application US/10380124
; Publication No. US20040053874A1
; GENERAL INFORMATION:
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; OTHER INFORMATION: Antisense Oligonucleotide
US-10-380-124-56

Query Match      1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 906 GAGATCCGCCCAACTCCAC 925
      |||||
Db 20 GAGATCCGCCCAACTCCAC 1

RESULT 306
US-10-380-124-57/c
; Sequence 57, Application US/10380124
; Publication No. US20040053874A1
; GENERAL INFORMATION:
; APPLICANT: Isis Pharmaceuticals, Inc.
; APPLICANT: Brett P. Monia
; APPLICANT: Susan M. Freier
; TITLE OF INVENTION: ANTISENSE MODULATION OF CLUSTERIN EXPRESSION
; FILE REFERENCE: RTS-0156
; CURRENT APPLICATION NUMBER: US/10/380,124
; CURRENT FILING DATE: 2003-03-10
; NUMBER OF SEQ ID NOS: 90
; SEQ ID NO 57
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-380-124-57

Query Match      1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 928 GCTGCTCGCATGAAGAC 947
      |||||
Db 20 GCTGCTCGCATGAAGAC 1

RESULT 307
US-10-380-124-58/c
; Sequence 58, Application US/10380124
; Publication No. US20040053874A1
; GENERAL INFORMATION:
; APPLICANT: Isis Pharmaceuticals, Inc.
; APPLICANT: Brett P. Monia
; APPLICANT: Susan M. Freier
; TITLE OF INVENTION: ANTISENSE MODULATION OF CLUSTERIN EXPRESSION
; FILE REFERENCE: RTS-0156
; CURRENT APPLICATION NUMBER: US/10/380,124
; CURRENT FILING DATE: 2003-03-10
; NUMBER OF SEQ ID NOS: 90
; SEQ ID NO 58
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-380-124-58

Query Match      1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 967 AGATCTTGCTGTGACTGT 986
      |||||
Db 20 AGATCTTGCTGTGACTGT 1

RESULT 308
US-10-380-124-59/c
; Sequence 59, Application US/10380124
; Publication No. US20040053874A1
; GENERAL INFORMATION:
; APPLICANT: Isis Pharmaceuticals, Inc.
; APPLICANT: Brett P. Monia
; APPLICANT: Susan M. Freier
; TITLE OF INVENTION: ANTISENSE MODULATION OF CLUSTERIN EXPRESSION
; FILE REFERENCE: RTS-0156
; CURRENT APPLICATION NUMBER: US/10/380,124
; CURRENT FILING DATE: 2003-03-10
; NUMBER OF SEQ ID NOS: 90
; SEQ ID NO 59
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-380-124-59

Query Match      1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1009 CTAAGCTGCGCGGAGCTC 1028
      |||||
Db 20 CTAAGCTGCGCGGAGCTC 1

RESULT 309
US-10-380-124-60/c
; Sequence 60, Application US/10380124
; Publication No. US20040053874A1
; GENERAL INFORMATION:
; APPLICANT: Isis Pharmaceuticals, Inc.
; APPLICANT: Brett P. Monia
; APPLICANT: Susan M. Freier
; TITLE OF INVENTION: ANTISENSE MODULATION OF CLUSTERIN EXPRESSION
; FILE REFERENCE: RTS-0156
; CURRENT APPLICATION NUMBER: US/10/380,124
; CURRENT FILING DATE: 2003-03-10
; NUMBER OF SEQ ID NOS: 90
; SEQ ID NO 60
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-380-124-60

Query Match      1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1022 GGAGCTCGAGCAATCCCTCC 1041
      |||||
Db 20 GGAGCTCGAGCAATCCCTCC 1

RESULT 310
US-10-380-124-61/c
; Sequence 61, Application US/10380124
; Publication No. US20040053874A1
; GENERAL INFORMATION:
; APPLICANT: Isis Pharmaceuticals, Inc.
; APPLICANT: Brett P. Monia
; APPLICANT: Susan M. Freier
; TITLE OF INVENTION: ANTISENSE MODULATION OF CLUSTERIN EXPRESSION
; FILE REFERENCE: RTS-0156
; CURRENT APPLICATION NUMBER: US/10/380,124
; CURRENT FILING DATE: 2003-03-10
; NUMBER OF SEQ ID NOS: 90
; SEQ ID NO 61
```

```
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-380-124-61

Query Match      1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1083 AAGTCCTACCAAGTGAAGAT 1102
|||||
Db 20 AAGTCCTACCAAGTGAAGAT 1

RESULT 311
US-10-380-124-62/c
; Sequence 62, Application US/10380124
; Publication No. US20040053874A1
; GENERAL INFORMATION:
; APPLICANT: Isis Pharmaceuticals, Inc.
; APPLICANT: Brett P. Monia
; APPLICANT: Susan M. Freier
; TITLE OF INVENTION: ANTISENSE MODULATION OF CLUSTERIN EXPRESSION
; FILE REFERENCE: RTS-0156
; CURRENT APPLICATION NUMBER: US/10/380,124
; CURRENT FILING DATE: 2003-03-10
; NUMBER OF SEQ ID NOS: 90
; SEQ ID NO 62
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-380-124-62

Query Match      1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1091 CCAGTGGAGAGATGCTCAACA 1110
|||||
Db 20 CCAGTGGAGAGATGCTCAACA 1

RESULT 312
US-10-380-124-63/c
; Sequence 63, Application US/10380124
; Publication No. US20040053874A1
; GENERAL INFORMATION:
; APPLICANT: Isis Pharmaceuticals, Inc.
; APPLICANT: Brett P. Monia
; APPLICANT: Susan M. Freier
; TITLE OF INVENTION: ANTISENSE MODULATION OF CLUSTERIN EXPRESSION
; FILE REFERENCE: RTS-0156
; CURRENT APPLICATION NUMBER: US/10/380,124
; CURRENT FILING DATE: 2003-03-10
; NUMBER OF SEQ ID NOS: 90
; SEQ ID NO 63
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-380-124-63

Query Match      1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1113 TCCTCCTTGTGGAGCAGCT 1132
|||||
```

```
Db 20 TCCTCCTTGTGGAGCAGCT 1

RESULT 313
US-10-380-124-64/c
; Sequence 64, Application US/10380124
; Publication No. US20040053874A1
; GENERAL INFORMATION:
; APPLICANT: Isis Pharmaceuticals, Inc.
; APPLICANT: Brett P. Monia
; APPLICANT: Susan M. Freier
; TITLE OF INVENTION: ANTISENSE MODULATION OF CLUSTERIN EXPRESSION
; FILE REFERENCE: RTS-0156
; CURRENT APPLICATION NUMBER: US/10/380,124
; CURRENT FILING DATE: 2003-03-10
; NUMBER OF SEQ ID NOS: 90
; SEQ ID NO 64
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-380-124-64

Query Match      1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1121 GCTGGAGCAGCTGAACGAGC 1140
|||||
Db 20 GCTGGAGCAGCTGAACGAGC 1

RESULT 314
US-10-380-124-65/c
; Sequence 65, Application US/10380124
; Publication No. US20040053874A1
; GENERAL INFORMATION:
; APPLICANT: Isis Pharmaceuticals, Inc.
; APPLICANT: Brett P. Monia
; APPLICANT: Susan M. Freier
; TITLE OF INVENTION: ANTISENSE MODULATION OF CLUSTERIN EXPRESSION
; FILE REFERENCE: RTS-0156
; CURRENT APPLICATION NUMBER: US/10/380,124
; CURRENT FILING DATE: 2003-03-10
; NUMBER OF SEQ ID NOS: 90
; SEQ ID NO 65
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-380-124-65

Query Match      1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1148 CTGGGTGTCCCGCTGGCAA 1167
|||||
Db 20 CTGGGTGTCCCGCTGGCAA 1

RESULT 315
US-10-380-124-66/c
; Sequence 66, Application US/10380124
; Publication No. US20040053874A1
; GENERAL INFORMATION:
; APPLICANT: Isis Pharmaceuticals, Inc.
; APPLICANT: Brett P. Monia
; APPLICANT: Susan M. Freier
; TITLE OF INVENTION: ANTISENSE MODULATION OF CLUSTERIN EXPRESSION
; FILE REFERENCE: RTS-0156
```

```
; CURRENT APPLICATION NUMBER: US/10/380,124
; CURRENT FILING DATE: 2003-03-10
; NUMBER OF SEQ ID NOS: 90
; SEQ ID NO 66
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-380-124-66

Query Match      1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1182 GAAGACCACTACTATCTGCG 1201
Db 20 GAAGACCACTACTATCTGCG 1

RESULT 316
US-10-380-124-67/c
; Sequence 67, Application US/10380124
; Publication No. US20040053874A1
; GENERAL INFORMATION:
; APPLICANT: Isis Pharmaceuticals, Inc.
; APPLICANT: Brett P. Monia
; APPLICANT: Susan M. Freier
; TITLE OF INVENTION: ANTISENSE MODULATION OF CLUSTERIN EXPRESSION
; FILE REFERENCE: RTS-0156
; CURRENT APPLICATION NUMBER: US/10/380,124
; CURRENT FILING DATE: 2003-03-10
; NUMBER OF SEQ ID NOS: 90
; SEQ ID NO 67
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-380-124-67

Query Match      1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1194 TATCTGCGGGTCACACGGT 1213
Db 20 TATCTGCGGGTCACACGGT 1

RESULT 317
US-10-380-124-68/c
; Sequence 68, Application US/10380124
; Publication No. US20040053874A1
; GENERAL INFORMATION:
; APPLICANT: Isis Pharmaceuticals, Inc.
; APPLICANT: Brett P. Monia
; APPLICANT: Susan M. Freier
; TITLE OF INVENTION: ANTISENSE MODULATION OF CLUSTERIN EXPRESSION
; FILE REFERENCE: RTS-0156
; CURRENT APPLICATION NUMBER: US/10/380,124
; CURRENT FILING DATE: 2003-03-10
; NUMBER OF SEQ ID NOS: 90
; SEQ ID NO 68
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-380-124-68

Query Match      1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1216 CTTCCACACTTCTGACTCG 1235
Db 20 CTTCCACACTTCTGACTCG 1

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1216 CTTCCACACTTCTGACTCG 1235
Db 20 CTTCCACACTTCTGACTCG 1

RESULT 318
US-10-380-124-69/c
; Sequence 69, Application US/10380124
; Publication No. US20040053874A1
; GENERAL INFORMATION:
; APPLICANT: Isis Pharmaceuticals, Inc.
; APPLICANT: Brett P. Monia
; APPLICANT: Susan M. Freier
; TITLE OF INVENTION: ANTISENSE MODULATION OF CLUSTERIN EXPRESSION
; FILE REFERENCE: RTS-0156
; CURRENT APPLICATION NUMBER: US/10/380,124
; CURRENT FILING DATE: 2003-03-10
; NUMBER OF SEQ ID NOS: 90
; SEQ ID NO 69
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-380-124-69

Query Match      1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1275 TTTGACTCTGATCCCATCAC 1294
Db 20 TTTGACTCTGATCCCATCAC 1

RESULT 319
US-10-380-124-70/c
; Sequence 70, Application US/10380124
; Publication No. US20040053874A1
; GENERAL INFORMATION:
; APPLICANT: Isis Pharmaceuticals, Inc.
; APPLICANT: Brett P. Monia
; APPLICANT: Susan M. Freier
; TITLE OF INVENTION: ANTISENSE MODULATION OF CLUSTERIN EXPRESSION
; FILE REFERENCE: RTS-0156
; CURRENT APPLICATION NUMBER: US/10/380,124
; CURRENT FILING DATE: 2003-03-10
; NUMBER OF SEQ ID NOS: 90
; SEQ ID NO 70
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-380-124-70

Query Match      1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1300 CGGTCCCTGTAGAAGTCTCC 1319
Db 20 CGGTCCCTGTAGAAGTCTCC 1

RESULT 320
US-10-380-124-71/c
; Sequence 71, Application US/10380124
; Publication No. US20040053874A1
; GENERAL INFORMATION:
; APPLICANT: Isis Pharmaceuticals, Inc.
```

US-10-380-124-73					
Query Match 1.2%; Score 20; DB 1; Length 20;					
Best Local Similarity 100.0%; Pred. No. 1.3e+02;					
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;					
QY	1545	GCTCTGGATCCTGCACCTCTA	1564		
DB	20	GCTCTGGATCCTGCACCTCTA	1		
RESULT 323					
US-10-380-124-74/c					
Sequence 74, Application US/10380124					
Publication No. US20040053874A1					
GENERAL INFORMATION:					
APPLICANT: Isis Pharmaceuticals, Inc.					
APPLICANT: Brett P. Monia					
APPLICANT: Susan M. Freier					
TITLE OF INVENTION: ANTISENSE MODULATION OF CLUSTERIN EXPRESSION					
FILE REFERENCE: RTS-0156					
CURRENT APPLICATION NUMBER: US/10/380,124					
CURRENT FILING DATE: 2003-03-10					
NUMBER OF SEQ ID NOS: 90					
SEQ ID NO 74					
LENGTH: 20					
TYPE: DNA					
ORGANISM: Artificial Sequence					
FEATURE:					
OTHER INFORMATION: Antisense Oligonucleotide					
US-10-380-124-74					
Query Match 1.2%; Score 20; DB 1; Length 20;					
Best Local Similarity 100.0%; Pred. No. 1.3e+02;					
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;					
QY	1600	TGCTCCTGCATGCCAACTAAT	1619		
DB	20	TGCTCCTGCATGCCAACTAAT	1		
RESULT 324					
US-10-380-124-75/c					
Sequence 75, Application US/10380124					
Publication No. US20040053874A1					
GENERAL INFORMATION:					
APPLICANT: Isis Pharmaceuticals, Inc.					
APPLICANT: Brett P. Monia					
APPLICANT: Susan M. Freier					
TITLE OF INVENTION: ANTISENSE MODULATION OF CLUSTERIN EXPRESSION					
FILE REFERENCE: RTS-0156					
CURRENT APPLICATION NUMBER: US/10/380,124					
CURRENT FILING DATE: 2003-03-10					
NUMBER OF SEQ ID NOS: 90					
SEQ ID NO 75					
LENGTH: 20					
TYPE: DNA					
ORGANISM: Artificial Sequence					
FEATURE:					
OTHER INFORMATION: Antisense Oligonucleotide					
US-10-380-124-75					
Query Match 1.2%; Score 20; DB 1; Length 20;					
Best Local Similarity 100.0%; Pred. No. 1.3e+02;					
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;					
QY	1615	CTAATTCAATAAAAAGTGTCT	1634		
DB	20	CTAATTCAATAAAAAGTGTCT	1		
RESULT 325					
US-10-380-124-78/c					

US-10-380-124-73					
APPLICANT: Brett P. Monia					
APPLICANT: Susan M. Freier					
TITLE OF INVENTION: ANTISENSE MODULATION OF CLUSTERIN EXPRESSION					
FILE REFERENCE: RTS-0156					
CURRENT APPLICATION NUMBER: US/10/380,124					
CURRENT FILING DATE: 2003-03-10					
NUMBER OF SEQ ID NOS: 90					
SEQ ID NO 71					
LENGTH: 20					
TYPE: DNA					
ORGANISM: Artificial Sequence					
FEATURE:					
OTHER INFORMATION: Antisense Oligonucleotide					
US-10-380-124-71					
Query Match 1.2%; Score 20; DB 1; Length 20;					
Best Local Similarity 100.0%; Pred. No. 1.3e+02;					
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;					
QY	1332	AAATTATGAGACCGTGCC	1351		
DB	20	AAATTATGAGACCGTGCC	1		
RESULT 321					
US-10-380-124-72/c					
Sequence 72, Application US/10380124					
Publication No. US20040053874A1					
GENERAL INFORMATION:					
APPLICANT: Isis Pharmaceuticals, Inc.					
APPLICANT: Brett P. Monia					
APPLICANT: Susan M. Freier					
TITLE OF INVENTION: ANTISENSE MODULATION OF CLUSTERIN EXPRESSION					
FILE REFERENCE: RTS-0156					
CURRENT APPLICATION NUMBER: US/10/380,124					
CURRENT FILING DATE: 2003-03-10					
NUMBER OF SEQ ID NOS: 90					
SEQ ID NO 72					
LENGTH: 20					
TYPE: DNA					
ORGANISM: Artificial Sequence					
FEATURE:					
OTHER INFORMATION: Antisense Oligonucleotide					
US-10-380-124-72					
Query Match 1.2%; Score 20; DB 1; Length 20;					
Best Local Similarity 100.0%; Pred. No. 1.3e+02;					
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;					
QY	1398	GATGTGATTTGCTTTTC	1417		
DB	20	GATGTGATTTGCTTTTC	1		
RESULT 322					
US-10-380-124-73/c					
Sequence 73, Application US/10380124					
Publication No. US20040053874A1					
GENERAL INFORMATION:					
APPLICANT: Isis Pharmaceuticals, Inc.					
APPLICANT: Brett P. Monia					
APPLICANT: Susan M. Freier					
TITLE OF INVENTION: ANTISENSE MODULATION OF CLUSTERIN EXPRESSION					
FILE REFERENCE: RTS-0156					
CURRENT APPLICATION NUMBER: US/10/380,124					
CURRENT FILING DATE: 2003-03-10					
NUMBER OF SEQ ID NOS: 90					
SEQ ID NO 73					
LENGTH: 20					
TYPE: DNA					
ORGANISM: Artificial Sequence					
FEATURE:					
OTHER INFORMATION: Antisense Oligonucleotide					

```
; Sequence 78, Application US/10380124
; Publication No. US20040053874A1
; GENERAL INFORMATION:
; APPLICANT: Isis Pharmaceuticals, Inc.
; APPLICANT: Brett P. Monia
; APPLICANT: Susan M. Freier
; TITLE OF INVENTION: ANTISENSE MODULATION OF CLUSTERIN EXPRESSION
; FILE REFERENCE: RTS-0156
; CURRENT APPLICATION NUMBER: US/10/380,124
; CURRENT FILING DATE: 2003-03-10
; NUMBER OF SEQ ID NOS: 90
; SEQ ID NO 78
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-380-124-78

Query Match      1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      979 TGGACTGTTCCACCAACAAC 998
Db      20 TGGACTGTTCCACCAACAAC 1

RESULT 326
US-10-380-124-80/c
; Sequence 80, Application US/10380124
; Publication No. US20040053874A1
; GENERAL INFORMATION:
; APPLICANT: Isis Pharmaceuticals, Inc.
; APPLICANT: Brett P. Monia
; APPLICANT: Susan M. Freier
; TITLE OF INVENTION: ANTISENSE MODULATION OF CLUSTERIN EXPRESSION
; FILE REFERENCE: RTS-0156
; CURRENT APPLICATION NUMBER: US/10/380,124
; CURRENT FILING DATE: 2003-03-10
; NUMBER OF SEQ ID NOS: 90
; SEQ ID NO 80
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-380-124-80

Query Match      1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1383 CACCGGAGGAGTGAGATGT 1402
Db      20 CACCGGAGGAGTGAGATGT 1

RESULT 327
US-10-980-850-17
; Sequence 17, Application US/10980850
; Publication No. US20050152908A1
; GENERAL INFORMATION:
; APPLICANT: Liew, Choong-Chin
; TITLE OF INVENTION: LIVER CANCER BIOMARKERS
; FILE REFERENCE: 4231/2072
; CURRENT APPLICATION NUMBER: US/10/980,850
; CURRENT FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/516,853
; PRIOR FILING DATE: 2003-11-03
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 17
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Forward Primer for OAS1
US-10-980-850-33

Query Match      1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      870 ATACGAGAGCGGACGATGA 889
Db      20 ATACGAGAGCGGACGATGA 1

RESULT 329
US-10-980-850-33
; Sequence 33, Application US/10980850
; Publication No. US20050152908A1
; GENERAL INFORMATION:
; APPLICANT: Liew, Choong-Chin
; TITLE OF INVENTION: LIVER CANCER BIOMARKERS
; FILE REFERENCE: 4231/2072
; CURRENT APPLICATION NUMBER: US/10/980,850
; CURRENT FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/516,853
; PRIOR FILING DATE: 2003-11-03
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 33
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Forward Primer for OAS1
US-10-980-850-33

Query Match      1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      762 AACTTCCAGCCCATGTTCCA 781
Db      1 AACTTCCAGCCCATGTTCCA 20

RESULT 328
US-10-980-850-18/c
; Sequence 18, Application US/10980850
; Publication No. US20050152908A1
; GENERAL INFORMATION:
; APPLICANT: Liew, Choong-Chin
; TITLE OF INVENTION: LIVER CANCER BIOMARKERS
; FILE REFERENCE: 4231/2072
; CURRENT APPLICATION NUMBER: US/10/980,850
; CURRENT FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/516,853
; PRIOR FILING DATE: 2003-11-03
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 18
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Reverse Primer for CLU
US-10-980-850-18

Query Match      1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      870 ATACGAGAGCGGACGATGA 889
Db      20 ATACGAGAGCGGACGATGA 1

RESULT 329
US-10-980-850-33
; Sequence 33, Application US/10980850
; Publication No. US20050152908A1
; GENERAL INFORMATION:
; APPLICANT: Liew, Choong-Chin
; TITLE OF INVENTION: LIVER CANCER BIOMARKERS
; FILE REFERENCE: 4231/2072
; CURRENT APPLICATION NUMBER: US/10/980,850
; CURRENT FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/516,853
; PRIOR FILING DATE: 2003-11-03
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 33
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Forward Primer for OAS1
US-10-980-850-33

Query Match      1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 977 TGTGGACTGTTCCACCAACA 996
      |||||
      1 TGTGGACTGTTCCACCAACA 20
      |||||

RESULT 330
US-10-646-391A-28
; Sequence 28, Application US/10646391A
; Publication No. US20040082534A1
; GENERAL INFORMATION:
; APPLICANT: Gleave, Martin
; APPLICANT: Jansen, Burkhard
; TITLE OF INVENTION: Treatment of Melanoma by Reduction in Clusterin Levels
; FILE REFERENCE: UBC-P-035
; CURRENT APPLICATION NUMBER: US/10/646,391A
; CURRENT FILING DATE: 2003-08-21
; PRIOR APPLICATION NUMBER: US 60/405,193
; PRIOR FILING DATE: 2002-08-21
; PRIOR APPLICATION NUMBER: US 60/319,748
; PRIOR FILING DATE: 2002-12-02
; PRIOR APPLICATION NUMBER: US 60/408,152
; PRIOR FILING DATE: 2002-09-03
; PRIOR APPLICATION NUMBER: US 60/473,387
; PRIOR FILING DATE: 2003-05-20
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 28
; LENGTH: 21
; TYPE: DNA
; ORGANISM: artificial
; FEATURE:
; OTHER INFORMATION: RNAi for human clusterin
US-10-646-391A-28

Query Match 1.2%; Score 20; DB 1; Length 21;
Best Local Similarity 75.0%; Pred. No. 1.4e+02;
Matches 15; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 48 ATGATGAAGACTCTGCTGCT 67
      |||||
      1 AUGAUGAAGACUCUGCUGCT 20
      |||||

RESULT 331
US-10-646-436-9
; Sequence 9, Application US/10646436
; Publication No. US20040096882A1
; GENERAL INFORMATION:
; APPLICANT: Jansen, Burkhard
; APPLICANT: Gleave, Martin
; APPLICANT: Signaevsky, Maxim
; APPLICANT: Beraldi, Eliana
; APPLICANT: Trougakos, Ioannis
; APPLICANT: Gonos, Efsthios
; TITLE OF INVENTION: RNAi Probes Targeting Cancer-Related Proteins
; FILE REFERENCE: UBC-P-030
; CURRENT APPLICATION NUMBER: US/10/646,436
; CURRENT FILING DATE: 2003-08-21
; PRIOR APPLICATION NUMBER: US 60/405,193
; PRIOR FILING DATE: 2002-08-21
; PRIOR APPLICATION NUMBER: US 60/408,152
; PRIOR FILING DATE: 2002-09-03
; PRIOR APPLICATION NUMBER: US 60/473,387
; PRIOR FILING DATE: 2003-05-20
; NUMBER OF SEQ ID NOS: 68
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 9
; LENGTH: 21
; TYPE: DNA
; ORGANISM: artificial
; FEATURE:
; OTHER INFORMATION: RNAi for human clusterin
US-10-646-436-9

Query Match 1.2%; Score 20; DB 1; Length 21;
Best Local Similarity 75.0%; Pred. No. 1.4e+02;
Matches 15; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 48 ATGATGAAGACTCTGCTGCT 67
      |||||
      1 AUGAUGAAGACUCUGCUGCT 20
      |||||

RESULT 332
US-10-270-871-13
; Sequence 13, Application US/10270871
; Publication No. US20030162702A1
; GENERAL INFORMATION:
; APPLICANT: Millis, Albert J. T.
; TITLE OF INVENTION: Compositions and Methods For Altering Cell Migration
; FILE REFERENCE: 0794.016A
; CURRENT APPLICATION NUMBER: US/10/270,871
; CURRENT FILING DATE: 2002-10-15
; PRIOR APPLICATION NUMBER: US/09/459,749D
; PRIOR FILING DATE: 1999-12-10
; PRIOR APPLICATION NUMBER: 60/111,856
; PRIOR FILING DATE: 1998-12-11
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 13
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:primer_bind
; OTHER INFORMATION: synthetic antisense primer based on murine clusterin
US-10-270-871-13

Query Match 1.2%; Score 19.4; DB 1; Length 21;
Best Local Similarity 95.2%; Pred. No. 1.6e+02;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 271 AAGAAGCCCAAGAGAAGAAAG 291
      |||||
      1 AGGAAGCCCAAGAGAAGAAAG 21
      |||||

RESULT 333
US-10-270-871-13
; Sequence 13, Application US/10270871
; Publication No. US20030162702A1
; GENERAL INFORMATION:
; APPLICANT: Millis, Albert J. T.
; TITLE OF INVENTION: Compositions and Methods For Altering Cell Migration
; FILE REFERENCE: 0794.016A
; CURRENT APPLICATION NUMBER: US/10/270,871
; CURRENT FILING DATE: 2002-10-15
; PRIOR APPLICATION NUMBER: US/09/459,749D
; PRIOR FILING DATE: 1999-12-10
; PRIOR APPLICATION NUMBER: 60/111,856
; PRIOR FILING DATE: 1998-12-11
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 13
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:primer_bind
; OTHER INFORMATION: synthetic antisense primer based on murine clusterin
US-10-270-871-13

Query Match 1.2%; Score 19.4; DB 1; Length 21;
Best Local Similarity 95.2%; Pred. No. 1.6e+02;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 271 AAGAAGCCCAAGAGAAGAAAG 291
      |||||
      1 AGGAAGCCCAAGAGAAGAAAG 21
      |||||
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; ORGANISM: artificial
; FEATURE:
; OTHER INFORMATION: RNAi fo rhuman clusterin
US-10-646-436-68

Query Match      1.2%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 48 ATGATGAAGACTCTGCTGC 66
Db 19 ATGATGAAGACTCTGCTGC 1

RESULT 338
US-10-828-394-16
; Sequence 16, Application US/10828394
; Publication No. US20040220131A1
; GENERAL INFORMATION:
; APPLICANT: Jackson, John
; APPLICANT: Burt, Helen
; APPLICANT: Springate, Christopher
; TITLE OF INVENTION: Method for Treatment of Cancerous Angiogenic Disorders
; CURRENT APPLICATION NUMBER: US/10/828,394
; PRIOR FILING DATE: 2004-04-19
; PRIOR APPLICATION NUMBER: US 60/464,159
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 16
; LENGTH: 19
; TYPE: DNA
; ORGANISM: human
US-10-828-394-16

Query Match      1.2%; Score 19; DB 1; Length 19;
Best Local Similarity 78.9%; Pred. No. 1.4e+02;
Matches 15; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy 482 CCAGAGCTCGCCCTTCTAC 500
Db 1 CCAGAGCTCGCCCUUCUAC 19

RESULT 339
US-10-828-394-17
; Sequence 17, Application US/10828394
; Publication No. US20040220131A1
; GENERAL INFORMATION:
; APPLICANT: Jackson, John
; APPLICANT: Burt, Helen
; APPLICANT: Springate, Christopher
; APPLICANT: Gleave, Martin
; TITLE OF INVENTION: Method for Treatment of Cancerous Angiogenic Disorders
; CURRENT APPLICATION NUMBER: US/10/828,394
; PRIOR FILING DATE: 2004-04-19
; PRIOR APPLICATION NUMBER: US 60/464,159
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 17
; LENGTH: 19
; TYPE: RNA
; ORGANISM: human
US-10-828-394-17

Query Match      1.2%; Score 19; DB 1; Length 19;
Best Local Similarity 78.9%; Pred. No. 1.4e+02;
Matches 15; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy 482 CCAGAGCTCGCCCTTCTAC 500
Db 1 CCAGAGCTCGCCCUUCUAC 19

RESULT 340
US-10-828-394-18
; Sequence 18, Application US/10828394
; Publication No. US20040220131A1
; GENERAL INFORMATION:
; APPLICANT: Jackson, John
; APPLICANT: Burt, Helen
; APPLICANT: Springate, Christopher
; APPLICANT: Gleave, Martin
; TITLE OF INVENTION: Method for Treatment of Cancerous Angiogenic Disorders
; CURRENT APPLICATION NUMBER: US/10/828,394
; PRIOR FILING DATE: 2004-04-19
; PRIOR APPLICATION NUMBER: US 60/464,159
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 18
; LENGTH: 19
; TYPE: RNA
; ORGANISM: human
US-10-828-394-18

Query Match      1.2%; Score 19; DB 1; Length 19;
Best Local Similarity 68.4%; Pred. No. 1.4e+02;
Matches 13; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

Qy 1615 CTAATTCAATAAACTGTC 1633
Db 1 CUNAUUCAUAAACUGUC 19

RESULT 341
US-10-828-395-16
; Sequence 16, Application US/10828395
; Publication No. US20040224914A1
; GENERAL INFORMATION:
; APPLICANT: Jackson, John
; APPLICANT: Burt, Helen
; APPLICANT: Springate, Christopher
; APPLICANT: Gleave, Martin
; TITLE OF INVENTION: Method for Treatment of Angiogenic Disorders
; CURRENT APPLICATION NUMBER: US/10/828,395
; PRIOR FILING DATE: 2004-04-19
; PRIOR APPLICATION NUMBER: US 60/464,159
; PRIOR FILING DATE: 2003-04-18
; PRIOR APPLICATION NUMBER: US 60/464,160
; PRIOR FILING DATE: 2003-04-18
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 16
; LENGTH: 19
; TYPE: DNA
; ORGANISM: human
US-10-828-395-16

Query Match      1.2%; Score 19; DB 1; Length 19;
Best Local Similarity 78.9%; Pred. No. 1.4e+02;
Matches 15; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy 482 CCAGAGCTCGCCCTTCTAC 500
Db 1 CCAGAGCTCGCCCUUCUAC 19

RESULT 342
US-10-828-395-17
```

; Sequence 17, Application US/10828395  
; Publication No. US20040224914A1  
; GENERAL INFORMATION:  
; APPLICANT: Jackson, John  
; APPLICANT: Burt, Helen  
; APPLICANT: Springate, Christopher  
; APPLICANT: Gleave, Martin  
; TITLE OF INVENTION: Method for Treatment of Angiogenic Disorders  
; FILE REFERENCE: UBC.P-032  
; CURRENT APPLICATION NUMBER: US/10/828,395  
; CURRENT FILING DATE: 2004-04-19  
; PRIOR APPLICATION NUMBER: US 60/464,159  
; PRIOR FILING DATE: 2003-04-18  
; PRIOR APPLICATION NUMBER: US 60/464,160  
; PRIOR FILING DATE: 2003-04-18  
; NUMBER OF SEQ ID NOS: 23  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 17  
; LENGTH: 19  
; TYPE: RNA  
; ORGANISM: human  
US-10-828-395-17

Query Match 1.2%; Score 19; DB 1; Length 19;  
Best Local Similarity 78.9%; Pred. No. 1.4e+02;  
Matches 15; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy 1100 GATGCTCAACACCTCTCC 1118  
||:|||||:|:|  
Db 1 GAUGCUCACACCUCC 19

RESULT 343  
US-10-828-395-18  
; Sequence 18, Application US/10828395  
; Publication No. US20040224914A1  
; GENERAL INFORMATION:  
; APPLICANT: Jackson, John  
; APPLICANT: Burt, Helen  
; APPLICANT: Springate, Christopher  
; APPLICANT: Gleave, Martin  
; TITLE OF INVENTION: Method for Treatment of Angiogenic Disorders  
; FILE REFERENCE: UBC.P-032  
; CURRENT APPLICATION NUMBER: US/10/828,395  
; CURRENT FILING DATE: 2004-04-19  
; PRIOR APPLICATION NUMBER: US 60/464,159  
; PRIOR FILING DATE: 2003-04-18  
; PRIOR APPLICATION NUMBER: US 60/464,160  
; PRIOR FILING DATE: 2003-04-18  
; NUMBER OF SEQ ID NOS: 23  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 18  
; LENGTH: 19  
; TYPE: RNA  
; ORGANISM: human  
US-10-828-395-18

Query Match 1.2%; Score 19; DB 1; Length 19;  
Best Local Similarity 68.4%; Pred. No. 1.4e+02;  
Matches 13; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

Qy 1615 CTAATTCATAAAACTGTC 1633  
|:|:|:|:|:|:|:|  
Db 1 CUNAUCAUAAACUGUC 19

RESULT 344  
US-10-646-391A-29/c  
; Sequence 29, Application US/10646391A  
; Publication No. US20040082534A1  
; GENERAL INFORMATION:  
; APPLICANT: Gleave, Martin  
; APPLICANT: Jansen, Burkhard

; TITLE OF INVENTION: Treatment of Melanoma by Reduction in Clusterin Levels  
; FILE REFERENCE: UBC.P-035  
; CURRENT APPLICATION NUMBER: US/10/646,391A  
; CURRENT FILING DATE: 2003-08-21  
; PRIOR APPLICATION NUMBER: US 60/405,193  
; PRIOR FILING DATE: 2002-08-21  
; PRIOR APPLICATION NUMBER: US 60/319,748  
; PRIOR FILING DATE: 2002-12-02  
; PRIOR APPLICATION NUMBER: US 60/408,152  
; PRIOR FILING DATE: 2002-09-03  
; PRIOR APPLICATION NUMBER: US 60/473,387  
; PRIOR FILING DATE: 2003-05-20  
; NUMBER OF SEQ ID NOS: 43  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 29  
; LENGTH: 21  
; TYPE: DNA  
; ORGANISM: artificial  
; FEATURE:  
; OTHER INFORMATION: RNAi for human clusterin  
US-10-646-391A-29

Query Match 1.2%; Score 19; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 1.8e+02;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 48 ATGATGAAGACTCTGCTGC 66  
|||||:|:|:|:|:|:|  
Db 19 ATGATGAAGACTCTGCTGC 1

RESULT 345  
US-10-646-436-10/c  
; Sequence 10, Application US/10646436  
; Publication No. US20040096882A1  
; GENERAL INFORMATION:  
; APPLICANT: Jansen, Burkhard  
; APPLICANT: Gleave, Martin  
; APPLICANT: Signaevsky, Maxim  
; APPLICANT: Beraldi, Eliana  
; APPLICANT: Trougakos, Ioannis  
; APPLICANT: Gonos, Elestathios  
; TITLE OF INVENTION: RNAi Probes Targeting Cancer-Related Proteins  
; FILE REFERENCE: UBC.P-030  
; CURRENT APPLICATION NUMBER: US/10/646,436  
; CURRENT FILING DATE: 2003-08-21  
; PRIOR APPLICATION NUMBER: US 60/405,193  
; PRIOR FILING DATE: 2002-08-21  
; PRIOR APPLICATION NUMBER: US 60/408,152  
; PRIOR FILING DATE: 2002-09-03  
; PRIOR APPLICATION NUMBER: US 60/473,387  
; PRIOR FILING DATE: 2003-05-20  
; NUMBER OF SEQ ID NOS: 68  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 10  
; LENGTH: 21  
; TYPE: DNA  
; ORGANISM: artificial  
; FEATURE:  
; OTHER INFORMATION: RNAi for human clusterin  
US-10-646-436-10

Query Match 1.2%; Score 19; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 1.8e+02;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 48 ATGATGAAGACTCTGCTGC 66  
|||||:|:|:|:|:|:|  
Db 19 ATGATGAAGACTCTGCTGC 1

RESULT 346  
US-10-380-124-4

; Sequence 4, Application US/10380124  
; Publication No. US20040053874A1  
; GENERAL INFORMATION:  
; APPLICANT: Isis Pharmaceuticals, Inc.  
; APPLICANT: Brett P. Monia  
; APPLICANT: Susan M. Freier  
; TITLE OF INVENTION: ANTISENSE MODULATION OF CLUSTERIN EXPRESSION  
; FILE REFERENCE: RTS-0156  
; CURRENT APPLICATION NUMBER: US/10/380,124  
; CURRENT FILING DATE: 2003-03-10  
; NUMBER OF SEQ ID NOS: 90  
; SEQ ID NO 4  
; LENGTH: 18  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: PCR Primer  
US-10-380-124-4

Query Match 1.1%; Score 18; DB 1; Length 18;  
Best Local Similarity 100.0%; Pred. No. 1.6e+02;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 746 TCCGTACGAGCCCTGAA 763  
|||||  
Db 1 TCCGTACGAGCCCTGAA 18

## RESULT 347

US-09-967-726A-15/c  
; Sequence 15, Application US/09967726A  
; Publication No. US20030158130A1  
; GENERAL INFORMATION:  
; APPLICANT: Gleave, Martin  
; APPLICANT: Rennie, Paul S.  
; APPLICANT: Miyake, Hideaki  
; APPLICANT: Neilson, Colleen  
; APPLICANT: Zellweger, Tobias  
; TITLE OF INVENTION: Chemo- and Radiation-Sensitization of Cancer by Antisense TRPM-2  
; FILE REFERENCE: Oligonucleotides  
; FILE REFERENCE: UBC.P-022  
; CURRENT APPLICATION NUMBER: US/09/967,726A  
; CURRENT FILING DATE: 2001-09-28  
; NUMBER OF SEQ ID NOS: 15  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 15  
; LENGTH: 21  
; TYPE: DNA  
; ORGANISM: Artificial  
; FEATURE:  
; OTHER INFORMATION: 2 base mismatch primer from human TRPM-2  
US-09-967-726A-15

Query Match 1.1%; Score 17.8; DB 1; Length 21;  
Best Local Similarity 90.5%; Pred. No. 2.3e+02;  
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 48 ATGATGAAGACTCTGCTGCTG 68  
|||||  
Db 21 ATGATAAATACTCTGCTGCTG 1

## RESULT 348

US-10-080-794-15/c  
; Sequence 15, Application US/10080794  
; Publication No. US20030166591A1  
; GENERAL INFORMATION:  
; APPLICANT: Gleave, Martin  
; APPLICANT: Rennie, Paul S.  
; APPLICANT: Miyake, Hideaki  
; APPLICANT: Neilson, Colleen  
; APPLICANT: Monia, Brett P.  
; TITLE OF INVENTION: TRPM-2 ANTISENSE THERAPY USING AN OLIGONUCLEOTIDE

; TITLE OF INVENTION: HAVING 2'-O-(2-METHOXY)ETHYL MODIFICATIONS  
; FILE REFERENCE: UBC.P-020-3  
; CURRENT APPLICATION NUMBER: US/10/080,794  
; CURRENT FILING DATE: 2002-02-22  
; PRIOR APPLICATION NUMBER: 60/121,726  
; PRIOR FILING DATE: 1999-02-26  
; PRIOR APPLICATION NUMBER: 09/913,325  
; PRIOR FILING DATE: 2001-08-10  
; PRIOR APPLICATION NUMBER: 09/944,326  
; PRIOR FILING DATE: 2001-08-30  
; NUMBER OF SEQ ID NOS: 19  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 15  
; LENGTH: 21  
; TYPE: DNA  
; ORGANISM: HUMAN  
US-10-080-794-15

Query Match 1.1%; Score 17.8; DB 1; Length 21;  
Best Local Similarity 90.5%; Pred. No. 2.3e+02;  
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 48 ATGATGAAGACTCTGCTGCTG 68  
|||||  
Db 21 ATGATAAATACTCTGCTGCTG 1

## RESULT 349

US-10-751-736-11047  
; Sequence 11047, Application US/10751736  
; Publication No. US20040265230A1  
; GENERAL INFORMATION:  
; APPLICANT: Wyeth  
; APPLICANT: Martinez, Robert  
; APPLICANT: Brown, Eugene  
; APPLICANT: Liu, Wei  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING AND TREATING COLON  
; FILE REFERENCE: AM100927 (031896-002000)  
; CURRENT APPLICATION NUMBER: US/10/751,736  
; CURRENT FILING DATE: 2003-01-06  
; PRIOR APPLICATION NUMBER: US Provisional Application 60/438,000  
; PRIOR FILING DATE: 2003-01-06  
; NUMBER OF SEQ ID NOS: 54873  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 11047  
; LENGTH: 21  
; TYPE: DNA  
; ORGANISM: homo sapiens  
US-10-751-736-11047

Query Match 1.1%; Score 17.8; DB 1; Length 21;  
Best Local Similarity 90.5%; Pred. No. 2.3e+02;  
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 35 CAGAAATGGAGGCATGATGAA 55  
|||||  
Db 1 CAGTATTGGAGCATGATGAA 21

## RESULT 350

US-10-921-868A-37/c  
; Sequence 37, Application US/10921868A  
; Publication No. US20050118251A1  
; GENERAL INFORMATION:  
; APPLICANT: Nagata, Leslie P.  
; APPLICANT: Wong, Jonathan P.  
; TITLE OF INVENTION: NOVEL DNA-BASED VACCINE AGAINST THE ENCEPHALITIS ALPHAVIRUSES  
; FILE REFERENCE: NEL-0001/DIV1  
; CURRENT APPLICATION NUMBER: US/10/921,868A  
; CURRENT FILING DATE: 2004-08-20  
; PRIOR APPLICATION NUMBER: 10/023,649  
; PRIOR FILING DATE: 2001-12-21

; PRIOR APPLICATION NUMBER: 60/256,948  
; PRIOR FILING DATE: 2000-12-21  
; NUMBER OF SEQ ID NOS: 49  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 37  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: DNA Primer  
US-10-921-868A-37

Query Match 1.0%; Score 16.8; DB 1; Length 20;  
Best Local Similarity 90.0%; Pred. No. 2.5e+02;  
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 524 CGACTCCCTGCTGGAGACG 543  
Db 20 CGACACGCTGCTGGAGAACG 1

## RESULT 351

US-10-786-720-3371/c  
; Sequence 3371, Application US/10786720  
; Publication No. US20040191818A1  
; GENERAL INFORMATION:  
; APPLICANT: Wyeth  
; APPLICANT: O'Toole, Margot  
; APPLICANT: Liu, Wei

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING AND TREATING AUTOIMMUNE  
; FILE REFERENCE: 031896-023000 (AM101331L)  
; CURRENT APPLICATION NUMBER: US/10/786,720  
; CURRENT FILING DATE: 2004-02-26  
; NUMBER OF SEQ ID NOS: 21135  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 3371  
; LENGTH: 21  
; TYPE: RNA  
; ORGANISM: RNAi-sense strand  
US-10-786-720-3371

Query Match 1.0%; Score 16.8; DB 1; Length 21;  
Best Local Similarity 90.0%; Pred. No. 2.8e+02;  
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 583 ACTTCAGCCGCGCTCCAGC 602  
Db 20 ACTTCAGCCGCTCCCTCCAGC 1

## RESULT 352

US-10-786-720-4073/c  
; Sequence 4073, Application US/10786720  
; Publication No. US20040191818A1  
; GENERAL INFORMATION:  
; APPLICANT: Wyeth  
; APPLICANT: O'Toole, Margot  
; APPLICANT: Liu, Wei

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING AND TREATING AUTOIMMUNE  
; FILE REFERENCE: 031896-023000 (AM101331L)  
; CURRENT APPLICATION NUMBER: US/10/786,720  
; CURRENT FILING DATE: 2004-02-26  
; NUMBER OF SEQ ID NOS: 21135  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 4073  
; LENGTH: 21  
; TYPE: RNA  
; ORGANISM: RNAi-sense strand  
US-10-786-720-4073

Query Match 1.0%; Score 16.8; DB 1; Length 21;

Best Local Similarity 90.0%; Pred. No. 2.8e+02;  
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
Qy 583 ACTTCAGCCGCGCTCCAGC 602  
Db 20 ACTTCAGCCGCTCCCTCCAGC 1

## RESULT 353

US-10-786-720-4811/c  
; Sequence 4811, Application US/10786720  
; Publication No. US20040191818A1  
; GENERAL INFORMATION:  
; APPLICANT: Wyeth  
; APPLICANT: O'Toole, Margot  
; APPLICANT: Liu, Wei

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING AND TREATING AUTOIMMUNE  
; FILE REFERENCE: 031896-023000 (AM101331L)  
; CURRENT APPLICATION NUMBER: US/10/786,720  
; CURRENT FILING DATE: 2004-02-26  
; NUMBER OF SEQ ID NOS: 21135  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 4811  
; LENGTH: 21  
; TYPE: RNA  
; ORGANISM: RNAi-sense strand  
US-10-786-720-4811

Query Match 1.0%; Score 16.8; DB 1; Length 21;  
Best Local Similarity 90.0%; Pred. No. 2.8e+02;  
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 583 ACTTCAGCCGCGCTCCAGC 602  
Db 20 ACTTCAGCCGCTCCCTCCAGC 1

## RESULT 354

US-10-751-736-24026/c  
; Sequence 24026, Application US/10751736  
; Publication No. US20040265230A1  
; GENERAL INFORMATION:  
; APPLICANT: Wyeth  
; APPLICANT: Martinez, Robert  
; APPLICANT: Brown, Eugene  
; APPLICANT: Liu, Wei

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING AND TREATING COLON  
; FILE REFERENCE: AM100927 (031896-002000)  
; CURRENT APPLICATION NUMBER: US/10/751,736  
; CURRENT FILING DATE: 2003-01-06  
; PRIOR APPLICATION NUMBER: US Provisional Application 60/438,000  
; PRIOR FILING DATE: 2003-01-06  
; NUMBER OF SEQ ID NOS: 54873  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 24026  
; LENGTH: 21  
; TYPE: RNA  
; ORGANISM: RNAi  
US-10-751-736-24026

Query Match 1.0%; Score 16.8; DB 1; Length 21;  
Best Local Similarity 90.0%; Pred. No. 2.8e+02;  
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 136 AGCTCCAGGAAATCTCCAAT 155  
Db 20 AGCTCCAGGAAATCTCCAAT 1

## RESULT 355

US-10-911-318-81/c

; Sequence 81, Application US/10911318  
; Publication No. US20050130186A1  
; GENERAL INFORMATION:  
; APPLICANT: We Gene Technologies, Inc.  
; TITLE OF INVENTION: MENINGITIS DETECTION CHIP AND FABRICATION METHOD THEREOF AND  
; TITLE OF INVENTION: METHOD OF DETECTING MENINGITIS AND PRIMER SET FOR MENINGITIS  
; TITLE OF INVENTION: DETECTION  
; FILE REFERENCE: 12333-US-PA  
; CURRENT APPLICATION NUMBER: US/10/911,318  
; CURRENT FILING DATE: 2004-08-03  
; PRIOR APPLICATION NUMBER: TW 92135134  
; PRIOR FILING DATE: 2003-12-12  
; NUMBER OF SEQ ID NOS: 134  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 81  
; LENGTH: 21  
; TYPE: DNA  
; ORGANISM: artificial sequence  
; FEATURE:  
; OTHER INFORMATION: Primer  
US-10-911-318-81

Query Match 1.0%; Score 16.8; DB 1; Length 21;  
Best Local Similarity 90.0%; Pred. No. 2.8e+02;  
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1281 TCTGATCCCATCACTGTGAC 1300  
||||| |||||||  
Db 21 TCTGGTCCCATCACTGTGAC 2

RESULT 356  
US-09-294-121A-97/c  
; Sequence 97, Application US/09294121A  
; Patent No. US20020069422A1  
; GENERAL INFORMATION:  
; APPLICANT: MAERTENS, GEERT; STUYVER, LIEVEN;  
; APPLICANT: ROSSAU, RUDI; VAN HEUVERSWYN, HUGO  
; TITLE OF INVENTION: PROCESS FOR TYPING OF HCV  
; TITLE OF INVENTION: ISOLATES  
; NUMBER OF SEQUENCES: 97  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BIERMAN & MUSERLIAN  
; STREET: 600 THIRD AVENUE  
; CITY: NEW YORK  
; STATE: NEW YORK  
; COUNTRY: USA  
; ZIP: 10016  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: ASCII  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/294,121A  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/256,568  
; FILING DATE: 18-JUL-1994  
; APPLICATION NUMBER: PCT/EP93/03325  
; FILING DATE: 26-NOV-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: EP/93/402,129.6  
; FILING DATE: 31-AUG-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: EP/92/403,222.0  
; FILING DATE: 27-NOV-1992  
; NAME: CHARLES A. MUSERLIAN  
; REGISTRATION NUMBER: 19,683  
; REFERENCE/DOCKET NUMBER: 410.004  
; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (212) 661-8000  
; TELEFAX: (212) 661-8002  
; INFORMATION FOR SEQ ID NO: 97:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 16 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; HYPOTHETICAL: NO  
; ANTI-SENSE: YES  
US-09-294-121A-97

Query Match 1.0%; Score 16; DB 1; Length 16;  
Best Local Similarity 100.0%; Pred. No. 1.9e+02;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1508 CAGCCTCCAGGCCCC 1523  
||||| |||||||  
Db 16 CAGCCTCCAGGCCCC 1

RESULT 357  
US-09-899-082A-97/c  
; Sequence 97, Application US/09899082A  
; Patent No. US20020106638A1  
; GENERAL INFORMATION:  
; APPLICANT: MAERTENS, GEERT; STUYVER, LIEVEN;  
; APPLICANT: ROSSAU, RUDI; VAN HEUVERSWYN, HUGO  
; TITLE OF INVENTION: PROCESS FOR TYPING OF HCV  
; TITLE OF INVENTION: ISOLATES  
; NUMBER OF SEQUENCES: 97  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BIERMAN & MUSERLIAN  
; STREET: 600 THIRD AVENUE  
; CITY: NEW YORK  
; STATE: NEW YORK  
; COUNTRY: USA  
; ZIP: 10016  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: ASCII  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/899,082A  
; FILING DATE: 06-Jul-2001  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/09/378,900  
; FILING DATE: <Unknown>  
; APPLICATION NUMBER: 08/256,568  
; FILING DATE: 18-JUL-1994  
; APPLICATION NUMBER: PCT/EP93/03325  
; FILING DATE: 26-NOV-1993  
; APPLICATION NUMBER: EP/93/402,129.6  
; FILING DATE: 31-AUG-1993  
; APPLICATION NUMBER: EP/92/403,222.0  
; FILING DATE: 27-NOV-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: CHARLES A. MUSERLIAN  
; REGISTRATION NUMBER: 19,683  
; REFERENCE/DOCKET NUMBER: 410.004  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 661-8000  
; TELEFAX: (212) 661-8002  
; INFORMATION FOR SEQ ID NO: 97:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 16 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA

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;
; HYPOTHETICAL: NO
; ANTI-SENSE: YES
; SEQUENCE DESCRIPTION: SEQ ID NO: 97:
US-09-899-082A-97

Query Match 1.0%; Score 16; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1508 CAGCCTCCAGGCCCCC 1523
Db 16 CAGCCTCCAGGCCCCC 1

RESULT 358
US-09-899-302-97/c
; Sequence 97, Application US/09899302
; Patent No. US20020168626A1
; GENERAL INFORMATION:
; APPLICANT: MAERTENS, GEERT; STUYVER, LIEVEN;
; APPLICANT: ROSSAU, RUDI; VAN HEUVERSWEYN, HUGO
; TITLE OF INVENTION: PROCESS FOR TYPING OF HCV
; TITLE OF INVENTION: ISOLATES
; NUMBER OF SEQUENCES: 97
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BIERMAN & MUSERLIAN
; STREET: 600 THIRD AVENUE
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: USA
; ZIP: 10016
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/899,302
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/378,900
; FILING DATE:
; APPLICATION NUMBER: 08/256,568
; FILING DATE: 18-JUL-1994
; APPLICATION NUMBER: PCT/EP93/03325
; FILING DATE: 26-NOV-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP/93/402,129.6
; FILING DATE: 31-AUG-1993
; APPLICATION NUMBER: EP/92/403,222.0
; FILING DATE: 27-NOV-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: CHARLES A. MUSERLIAN
; REGISTRATION NUMBER: 19,683
; REFERENCE/DOCKET NUMBER: 410.004
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 661-8000
; TELEFAX: (212) 661-8002
; INFORMATION FOR SEQ ID NO: 97:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
; HYPOTHETICAL: NO
; ANTI-SENSE: YES
; SEQUENCE DESCRIPTION: SEQ ID NO: 97:
US-09-899-302-97

Query Match 1.0%; Score 16; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1508 CAGCCTCCAGGCCCCC 1523
Db 16 CAGCCTCCAGGCCCCC 1

RESULT 360
US-10-822-711-97/c
; Sequence 97, Application US/10822711
```

```
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1508 CAGCCTCCAGGCCCCC 1523
Db 16 CAGCCTCCAGGCCCCC 1

RESULT 359
US-09-899-044-97/c
; Sequence 97, Application US/09899044
; Publication No. US20030036053A1
; GENERAL INFORMATION:
; APPLICANT: MAERTENS, GEERT; STUYVER, LIEVEN;
; APPLICANT: ROSSAU, RUDI; VAN HEUVERSWEYN, HUGO
; TITLE OF INVENTION: PROCESS FOR TYPING OF HCV
; TITLE OF INVENTION: ISOLATES
; NUMBER OF SEQUENCES: 97
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BIERMAN & MUSERLIAN
; STREET: 600 THIRD AVENUE
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: USA
; ZIP: 10016
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/899,044
; FILING DATE: 06-Jul-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/378,900
; FILING DATE: <Unknown>
; APPLICATION NUMBER: PCT/EP93/03325
; FILING DATE: 26-NOV-1993
; APPLICATION NUMBER: EP/93/402,129.6
; FILING DATE: 31-AUG-1993
; APPLICATION NUMBER: EP/92/403,222.0
; FILING DATE: 27-NOV-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: CHARLES A. MUSERLIAN
; REGISTRATION NUMBER: 19,683
; REFERENCE/DOCKET NUMBER: 410.004
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 661-8000
; TELEFAX: (212) 661-8002
; INFORMATION FOR SEQ ID NO: 97:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
; HYPOTHETICAL: NO
; ANTI-SENSE: YES
; SEQUENCE DESCRIPTION: SEQ ID NO: 97:
US-09-899-044-97

Query Match 1.0%; Score 16; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1508 CAGCCTCCAGGCCCCC 1523
Db 16 CAGCCTCCAGGCCCCC 1

RESULT 360
US-10-822-711-97/c
; Sequence 97, Application US/10822711
```

Publication No. US20040191768A1  
GENERAL INFORMATION:  
APPLICANT: ROSSAU, RUDI; VAN HEUVERSWYN, HUGO  
TITLE OF INVENTION: PROCESS FOR TYPING OF HCV ISOLATES  
NUMBER OF SEQUENCES: 97  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BIERMAN & MUSERLIAN  
STREET: 600 THIRD AVENUE  
CITY: NEW YORK  
STATE: NEW YORK  
COUNTRY: USA  
ZIP: 10016  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: ASCII  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/822.711  
FILING DATE: 13-Apr-2004  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/09/899,082A  
FILING DATE: 06-Jul-2001  
APPLICATION NUMBER: US/09/378,900  
FILING DATE: <Unknown>  
APPLICATION NUMBER: 08/256,568  
FILING DATE: 18-JUL-1994  
APPLICATION NUMBER: PCT/EP93/03325  
FILING DATE: 26-NOV-1993  
APPLICATION NUMBER: EP/93/402,129.6  
FILING DATE: 31-AUG-1993  
APPLICATION NUMBER: EP/92/403,222.0  
FILING DATE: 27-NOV-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: CHARLES A. MUSERLIAN  
REGISTRATION NUMBER: 19,683  
REFERENCE/DOCKET NUMBER: 410,004  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 661-8000  
TELEFAX: (212) 661-8002  
INFORMATION FOR SEQ ID NO: 97:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 16 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
HYPOTHETICAL: NO  
ANTI-SENSE: YES  
SEQUENCE DESCRIPTION: SEQ ID NO: 97:  
US-10-822-711-97  
Query Match 1.0%; Score 16; DB 1; Length 16;  
Best Local Similarity 100.0%; Pred. No. 1.9e+02;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1508 CAGCCTCCAGGCCCCC 1523  
Db 16 CAGCCTCCAGGCCCCC 1  
RESULT 361  
US-10-160-787-84/c  
Sequence 84, Application US/10160787  
Publication No. US20030225256A1  
GENERAL INFORMATION:  
APPLICANT: Andrew T. Watt  
TITLE OF INVENTION: ANTISENSE MODULATION OF PCTAIRE PROTEIN KINASE 2 EXPRESSION  
FILE REFERENCE: RTS-0204  
CURRENT APPLICATION NUMBER: US/10/160,787

CURRENT FILING DATE: 2002-05-31  
NUMBER OF SEQ ID NOS: 141  
SEQ ID NO 84  
LENGTH: 20  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Antisense Oligonucleotide  
US-10-160-787-84  
Query Match 1.0%; Score 16; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 3e+02;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1583 CATGGGAAGACAGAA 1598  
Db 17 CATGGGAAGACAGAA 2  
RESULT 362  
US-10-160-787-137  
Sequence 137, Application US/10160787  
Publication No. US20030225256A1  
GENERAL INFORMATION:  
APPLICANT: Andrew T. Watt  
TITLE OF INVENTION: ANTISENSE MODULATION OF PCTAIRE PROTEIN KINASE 2 EXPRESSION  
FILE REFERENCE: RTS-0204  
CURRENT APPLICATION NUMBER: US/10/160,787  
CURRENT FILING DATE: 2002-05-31  
NUMBER OF SEQ ID NOS: 141  
SEQ ID NO 137  
LENGTH: 20  
TYPE: DNA  
ORGANISM: H. sapiens  
FEATURE:  
US-10-160-787-137  
Query Match 1.0%; Score 16; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 3e+02;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1583 CATGGGAAGACAGAA 1598  
Db 4 CATGGGAAGACAGAA 19  
RESULT 363  
US-10-646-391A-24  
Sequence 24, Application US/10646391A  
Publication No. US20040082534A1  
GENERAL INFORMATION:  
APPLICANT: Gleave, Martin  
APPLICANT: Jansen, Burkhard  
TITLE OF INVENTION: Treatment of Melanoma by Reduction in Clusterin Levels  
FILE REFERENCE: UBC.P-035  
CURRENT APPLICATION NUMBER: US/10/646,391A  
CURRENT FILING DATE: 2003-08-21  
PRIOR APPLICATION NUMBER: US 60/405,193  
PRIOR FILING DATE: 2002-08-21  
PRIOR APPLICATION NUMBER: US 60/319,748  
PRIOR FILING DATE: 2002-12-02  
PRIOR APPLICATION NUMBER: US 60/408,152  
PRIOR FILING DATE: 2002-09-03  
PRIOR APPLICATION NUMBER: US 60/473,387  
PRIOR FILING DATE: 2003-05-20  
NUMBER OF SEQ ID NOS: 43  
SOFTWARE: PatentIn version 3.2  
SEQ ID NO 24  
LENGTH: 19  
TYPE: DNA  
ORGANISM: artificial  
FEATURE:  
OTHER INFORMATION: RNAi for human clusterin



## US-10-646-391A-24

Query Match 1.0%; Score 15.8; DB 1; Length 19;  
Best Local Similarity 63.2%; Pred. No. 2.8e+02;  
Matches 12; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

Qy 1616 TAATTCAATATAAACTGTCT 1634  
:||||| |||||:|  
Db 1 UAAUUCACAAACACUGUTT 19

## RESULT 364

US-10-646-391A-26  
; Sequence 26, Application US/10646391A  
; Publication No. US20040082534A1  
; GENERAL INFORMATION:  
; APPLICANT: Gleave, Martin  
; APPLICANT: Jansen, Burkhard  
; TITLE OF INVENTION: Treatment of Melanoma by Reduction in Clusterin Levels  
; FILE REFERENCE: UBC.P-035  
; CURRENT APPLICATION NUMBER: US/10/646,391A  
; CURRENT FILING DATE: 2003-08-21  
; PRIOR APPLICATION NUMBER: US 60/405,193  
; PRIOR FILING DATE: 2002-08-21  
; PRIOR APPLICATION NUMBER: US 60/319,748  
; PRIOR FILING DATE: 2002-12-02  
; PRIOR APPLICATION NUMBER: US 60/408,152  
; PRIOR FILING DATE: 2002-09-03  
; PRIOR APPLICATION NUMBER: US 60/473,387  
; PRIOR FILING DATE: 2003-05-20  
; NUMBER OF SEQ ID NOS: 43  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 26  
; LENGTH: 19  
; TYPE: DNA  
; ORGANISM: artificial  
; FEATURE:  
; OTHER INFORMATION: RNAi for human clusterin  
US-10-646-391A-26

Query Match 1.0%; Score 15.8; DB 1; Length 19;  
Best Local Similarity 63.2%; Pred. No. 2.8e+02;  
Matches 12; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

Qy 1616 TAATTCAATATAAACTGTCT 1634  
:||||| |||||:|  
Db 1 UAAUUCACAAACACUGUTT 19

## RESULT 365

US-10-646-391A-27/c  
; Sequence 27, Application US/10646391A  
; Publication No. US20040082534A1  
; GENERAL INFORMATION:  
; APPLICANT: Gleave, Martin  
; APPLICANT: Jansen, Burkhard  
; TITLE OF INVENTION: Treatment of Melanoma by Reduction in Clusterin Levels  
; FILE REFERENCE: UBC.P-035  
; CURRENT APPLICATION NUMBER: US/10/646,391A  
; CURRENT FILING DATE: 2003-08-21  
; PRIOR APPLICATION NUMBER: US 60/405,193  
; PRIOR FILING DATE: 2002-08-21  
; PRIOR APPLICATION NUMBER: US 60/319,748  
; PRIOR FILING DATE: 2002-12-02  
; PRIOR APPLICATION NUMBER: US 60/408,152  
; PRIOR FILING DATE: 2002-09-03  
; PRIOR APPLICATION NUMBER: US 60/473,387  
; PRIOR FILING DATE: 2003-05-20  
; NUMBER OF SEQ ID NOS: 43  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 27  
; LENGTH: 19  
; TYPE: DNA

## ; ORGANISM: artificial

; FEATURE:  
; OTHER INFORMATION: RNAi for human clusterin  
US-10-646-391A-27

Query Match 1.0%; Score 15.8; DB 1; Length 19;  
Best Local Similarity 89.5%; Pred. No. 2.8e+02;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1614 ACTAATTCATATAAACTGT 1632  
:||||| |||||:|  
Db 19 AATAATTCACAAACTGT 1

## RESULT 366

US-10-646-436-7  
; Sequence 7, Application US/10646436  
; Publication No. US20040096882A1  
; GENERAL INFORMATION:  
; APPLICANT: Jansen, Burkhard  
; APPLICANT: Gleave, Martin  
; APPLICANT: Signaevsky, Maxim  
; APPLICANT: Beraldi, Eliana  
; APPLICANT: Trougakos, Ioannis  
; APPLICANT: Gonos, Efethios  
; TITLE OF INVENTION: RNAi Probes Targeting Cancer-Related Proteins  
; FILE REFERENCE: UBC.P-030  
; CURRENT APPLICATION NUMBER: US/10/646,436  
; CURRENT FILING DATE: 2003-08-21  
; PRIOR APPLICATION NUMBER: US 60/405,193  
; PRIOR FILING DATE: 2002-08-21  
; PRIOR APPLICATION NUMBER: US 60/408,152  
; PRIOR FILING DATE: 2002-09-03  
; PRIOR APPLICATION NUMBER: US 60/473,387  
; PRIOR FILING DATE: 2003-05-20  
; NUMBER OF SEQ ID NOS: 68  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 7  
; LENGTH: 19  
; TYPE: DNA  
; ORGANISM: artificial  
; FEATURE:  
; OTHER INFORMATION: RNAi for human clusterin  
US-10-646-436-7

Query Match 1.0%; Score 15.8; DB 1; Length 19;  
Best Local Similarity 63.2%; Pred. No. 2.8e+02;  
Matches 12; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

Qy 1616 TAATTCAATATAAACTGTCT 1634  
:||||| |||||:|  
Db 1 UAAUUCACAAACACUGUTT 19

## RESULT 367

US-10-646-436-8/c  
; Sequence 8, Application US/10646436  
; Publication No. US20040096882A1  
; GENERAL INFORMATION:  
; APPLICANT: Jansen, Burkhard  
; APPLICANT: Gleave, Martin  
; APPLICANT: Signaevsky, Maxim  
; APPLICANT: Beraldi, Eliana  
; APPLICANT: Trougakos, Ioannis  
; APPLICANT: Gonos, Efethios  
; TITLE OF INVENTION: RNAi Probes Targeting Cancer-Related Proteins  
; FILE REFERENCE: UBC.P-030  
; CURRENT APPLICATION NUMBER: US/10/646,436  
; CURRENT FILING DATE: 2003-08-21  
; PRIOR APPLICATION NUMBER: US 60/405,193  
; PRIOR FILING DATE: 2002-08-21  
; PRIOR APPLICATION NUMBER: US 60/408,152  
; PRIOR FILING DATE: 2002-09-03

QY 222 CTCATAGAAAAACAACG 240

Query Match 0.9%; Score 15.4; DB 1; Length 17;  
Best Local Similarity 94.1%; Pred. No. 2.4e+02;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 273 GAAGCCAGAGAGAGAA 289  
Db 1 GAAGCCAGAGAGAGAA 17

RESULT 371  
US-09-780-533A-170/c  
; Sequence 170, Application US/09780533A  
; Publication No. US20030060611A1  
; GENERAL INFORMATION:  
; APPLICANT: Ribozyme Pharmaceuticals, Inc.  
; APPLICANT: Blatt, Larry  
; APPLICANT: McSwigen, Jim  
; APPLICANT: Chowrira, Bharat  
; APPLICANT: Haeblerli, Pete  
; TITLE OF INVENTION: Method and Reagent for the Inhibition of NOGO Gene  
; FILE REFERENCE: MBH00,878-A (400/011)  
; CURRENT APPLICATION NUMBER: US/09/780,533A  
; CURRENT FILING DATE: 2001-02-09  
; PRIOR APPLICATION NUMBER: US 60/181,797  
; PRIOR FILING DATE: 2000-02-11  
; NUMBER OF SEQ ID NOS: 6679  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 170  
; LENGTH: 17  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-09-780-533A-170

Query Match 0.9%; Score 15.4; DB 1; Length 17;

Best Local Similarity 94.1%; Pred. No. 2.4e+02;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 273 GAAGCCAGAGAGAGAA 289  
Db 1 GAAGCCAGAGAGAGAA 17

RESULT 371  
US-09-780-533A-170/c  
; Sequence 170, Application US/09780533A  
; Publication No. US20030060611A1  
; GENERAL INFORMATION:  
; APPLICANT: Ribozyme Pharmaceuticals, Inc.  
; APPLICANT: Blatt, Larry  
; APPLICANT: McSwigen, Jim  
; APPLICANT: Chowrira, Bharat  
; APPLICANT: Haeblerli, Pete  
; TITLE OF INVENTION: Method and Reagent for the Inhibition of NOGO Gene  
; FILE REFERENCE: MBH00,878-A (400/011)  
; CURRENT APPLICATION NUMBER: US/09/780,533A  
; CURRENT FILING DATE: 2001-02-09  
; PRIOR APPLICATION NUMBER: US 60/181,797  
; PRIOR FILING DATE: 2000-02-11  
; NUMBER OF SEQ ID NOS: 6679  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 170  
; LENGTH: 17  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-09-780-533A-170

Best Local Similarity 94.1%; Pred. No. 2.4e+02;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1619 TTCAATAAACTGCTT 1635  
Db 17 TTCAATAAACTGCTT 1

RESULT 372  
US-09-740-332-1542  
; Sequence 1542, Application US/09740332  
; Publication No. US20030125270A1  
; GENERAL INFORMATION:  
; APPLICANT: Ribozyme Pharmaceuticals Inc.  
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related  
; TITLE OF INVENTION: Hepatitis C Virus Infection  
; FILE REFERENCE: RPI 400/003  
; CURRENT APPLICATION NUMBER: US/09/740,332  
; CURRENT FILING DATE: 2001-03-26  
; NUMBER OF SEQ ID NOS: 9704  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 1542  
; LENGTH: 17  
; TYPE: RNA  
; ORGANISM: artificial sequence  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION:  
; OTHER INFORMATION: oligonucleotide substrate  
US-09-740-332-1542

Query Match 0.9%; Score 15.4; DB 1; Length 17;  
Best Local Similarity 94.1%; Pred. No. 2.4e+02;  
Matches 12; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 766 TCCAGCCCATGTTCCAG 782  
Db 1 UCCAGCCCAUGUCCGG 17

RESULT 373  
US-09-740-332-3013/c  
; Sequence 3013, Application US/09740332  
; Publication No. US20030125270A1  
; GENERAL INFORMATION:  
; APPLICANT: Ribozyme Pharmaceuticals Inc.  
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related  
; FILE REFERENCE: RPI 400/003  
; CURRENT APPLICATION NUMBER: US/09/740,332  
; CURRENT FILING DATE: 2001-03-26  
; NUMBER OF SEQ ID NOS: 9704  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 3013  
; LENGTH: 17  
; TYPE: RNA  
; ORGANISM: artificial sequence  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION:  
; OTHER INFORMATION: oligonucleotide substrate  
US-09-740-332-3013

Query Match 0.9%; Score 15.4; DB 1; Length 17;  
Best Local Similarity 94.1%; Pred. No. 2.4e+02;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 767 CCAGCCCATGTTCCAGC 783  
Db 17 CCAGCCCATGTTCCGGC 1

RESULT 374

```
US-09-817-879-1542
; Sequence 1542, Application US/09817879
; Publication No. US20030171311A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals Inc.
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related to Hepatitis C Virus Infection
; FILE REFERENCE: MBH00-801-F
; CURRENT APPLICATION NUMBER: US/09/817,879
; CURRENT FILING DATE: 2001-03-26
; NUMBER OF SEQ ID NOS: 9703
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1542
; LENGTH: 17
; TYPE: RNA
; ORGANISM: artificial sequence
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION:
; OTHER INFORMATION: oligonucleotide substrate
US-09-817-879-1542
Query Match 0.9%; Score 15.4; DB 1; Length 17;
Best Local Similarity 70.6%; Pred. No. 2.4e+02;
Matches 12; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 766 TCCACGCCCATGTTCCAG 782
Db 1 UCCACGCCCAUGUCCGG 17

RESULT 375
US-09-817-879-3013/c
; Sequence 3013, Application US/09817879
; Publication No. US20030171311A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals Inc.
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related to Hepatitis C Virus Infection
; FILE REFERENCE: MBH00-801-F
; CURRENT APPLICATION NUMBER: US/09/817,879
; CURRENT FILING DATE: 2001-03-26
; NUMBER OF SEQ ID NOS: 9703
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3013
; LENGTH: 17
; TYPE: RNA
; ORGANISM: artificial sequence
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION:
; OTHER INFORMATION: oligonucleotide substrate
US-09-817-879-3013
Query Match 0.9%; Score 15.4; DB 1; Length 17;
Best Local Similarity 94.1%; Pred. No. 2.4e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 767 CCACGCCCATGTTCCAGC 783
Db 17 CCACGCCCATGTTCCGGC 1

RESULT 376
US-10-669-841-4135
; Sequence 4135, Application US/10669841
; Publication No. US20040127446A1
; GENERAL INFORMATION:
; APPLICANT: Sirna Therapeutics, Inc.
; APPLICANT: Lawrence, Blatt
; APPLICANT: Dennis, Macejak
; APPLICANT: James, McSwiggen
; APPLICANT: David, Morrissey
; APPLICANT: Pamela, Pavco
; APPLICANT: Kenneth, Draper
; APPLICANT: Elisabeth, Roberts
; TITLE OF INVENTION: OLIGONUCLEOTIDE MEDIATED INHIBITION OF HEPATITIS B VIRUS AND HEPATITIS C VIRUS
; FILE REFERENCE: 400/042US (MBH02-249-E)
; CURRENT APPLICATION NUMBER: US/10/669,841
; CURRENT FILING DATE: 2003-09-23
; PRIOR APPLICATION NUMBER: PCT/US02/09187
```

```
; APPLICANT: Pamela, Pavco
; APPLICANT: Patrice, Lee
; APPLICANT: Kenneth, Draper
; APPLICANT: Elisabeth, Roberts
; TITLE OF INVENTION: OLIGONUCLEOTIDE MEDIATED INHIBITION OF HEPATITIS B VIRUS AND HEPATITIS C VIRUS
; FILE REFERENCE: 400/042US (MBH02-249-E)
; CURRENT APPLICATION NUMBER: US/10/669,841
; CURRENT FILING DATE: 2003-09-23
; PRIOR APPLICATION NUMBER: PCT/US02/09187
; PRIOR FILING DATE: 2002-03-26
; PRIOR APPLICATION NUMBER: US 60/296,876
; PRIOR FILING DATE: 2001-06-08
; PRIOR APPLICATION NUMBER: US 60/335,059
; PRIOR FILING DATE: 2001-10-24
; PRIOR APPLICATION NUMBER: US 60/337,055
; PRIOR FILING DATE: 2001-12-05
; PRIOR APPLICATION NUMBER: US 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/363,124
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: US 09/817,879
; PRIOR FILING DATE: 2001-03-26
; PRIOR APPLICATION NUMBER: US 09/740,332
; PRIOR FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: US 09/611,931
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: US 09/504,321
; PRIOR FILING DATE: 2000-02-15
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 16207
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4135
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION:
; OTHER INFORMATION: oligonucleotide substrate
US-10-669-841-4135
Query Match 0.9%; Score 15.4; DB 1; Length 17;
Best Local Similarity 70.6%; Pred. No. 2.4e+02;
Matches 12; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 766 TCCACGCCCATGTTCCAG 782
Db 1 UCCACGCCCAUGUCCGG 17

RESULT 377
US-10-669-841-5606/c
; Sequence 5606, Application US/10669841
; Publication No. US20040127446A1
; GENERAL INFORMATION:
; APPLICANT: Sirna Therapeutics, Inc.
; APPLICANT: Lawrence, Blatt
; APPLICANT: Dennis, Macejak
; APPLICANT: James, McSwiggen
; APPLICANT: David, Morrissey
; APPLICANT: Pamela, Pavco
; APPLICANT: Patrice, Lee
; APPLICANT: Kenneth, Draper
; APPLICANT: Elisabeth, Roberts
; TITLE OF INVENTION: OLIGONUCLEOTIDE MEDIATED INHIBITION OF HEPATITIS B VIRUS AND HEPATITIS C VIRUS
; FILE REFERENCE: 400/042US (MBH02-249-E)
; CURRENT APPLICATION NUMBER: US/10/669,841
; CURRENT FILING DATE: 2003-09-23
; PRIOR APPLICATION NUMBER: PCT/US02/09187
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; PRIOR FILING DATE: 2002-03-26
; PRIOR APPLICATION NUMBER: US 60/296,876
; PRIOR FILING DATE: 2001-06-08
; PRIOR APPLICATION NUMBER: US 60/335,059
; PRIOR FILING DATE: 2001-10-24
; PRIOR APPLICATION NUMBER: US 60/337,055
; PRIOR FILING DATE: 2001-12-05
; PRIOR APPLICATION NUMBER: US 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/363,124
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: US 09/817,879
; PRIOR FILING DATE: 2001-03-26
; PRIOR APPLICATION NUMBER: US 09/740,332
; PRIOR FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: US 09/611,931
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: US 09/504,321
; PRIOR FILING DATE: 2000-02-15
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 16207
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5606
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid
; NAME/KEY: misc_feature
; LOCATION:
; OTHER INFORMATION: oligonucleotide substrate
US-10-669-841-5606

Query Match          0.9%; Score 15.4; DB 1; Length 17;
Best Local Similarity 94.1%; Pred. No. 2.4e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 767 CCACGCCATGTTCCAGC 783
Db 17 CCACGCCATGTTCCGC 1

RESULT 378
US-10-723-361-8666
; Sequence 8666, Application US/10723361
; Publication No. US20040137589A1
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharon G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: HUMAN MYOSIN-LIKE POLYPEPTIDE EXPRESSED PREDOMINANTLY IN HEART AN
; FILE REFERENCE: PB0105
; CURRENT APPLICATION NUMBER: US/10723,361
; CURRENT FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: US 09/866,108
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
```

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; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 8666
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-723-361-8666

Query Match          0.9%; Score 15.4; DB 1; Length 17;
Best Local Similarity 94.1%; Pred. No. 2.4e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 273 GAAGCCCAAGGAAGAA 289
Db 1 GAAGCCCAAGGAAGAA 17

RESULT 379
US-10-828-394-19/c
; Sequence 19, Application US/10828394
; Publication No. US20040220131A1
; GENERAL INFORMATION:
; APPLICANT: Jackson, John
; APPLICANT: Burt, Helen
; APPLICANT: Springate, Christopher
; APPLICANT: Gleave, Martin
; TITLE OF INVENTION: Method for Treatment of Cancerous Angiogenic Disorders
; FILE REFERENCE: UBC-P-033
; CURRENT APPLICATION NUMBER: US/10/828,394
; CURRENT FILING DATE: 2004-04-19
; PRIOR APPLICATION NUMBER: US 60/464,159
; PRIOR FILING DATE: 2003-04-18
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 19
; LENGTH: 17
; TYPE: RNA
; ORGANISM: artificial
; FEATURE:
; OTHER INFORMATION: clusterin targeted sirna
US-10-828-394-19
```

```
Query Match          0.9%; Score 15.4; DB 1; Length 17;
Best Local Similarity 94.1%; Pred. No. 2.4e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1616 TAATTCAATAAACTGT 1632
Db 17 TAATTCAACAAACTGT 1

RESULT 380
US-10-828-395-19/c
; Sequence 19, Application US/10828395
; Publication No. US20040224914A1
; GENERAL INFORMATION:
; APPLICANT: Jackson, John
; APPLICANT: Burt, Helen
; APPLICANT: Springate, Christopher
; APPLICANT: Gleave, Martin
; TITLE OF INVENTION: Method for Treatment of Angiogenic Disorders
; FILE REFERENCE: UBC-P-032
; CURRENT APPLICATION NUMBER: US/10/828,395
; CURRENT FILING DATE: 2004-04-19
; PRIOR APPLICATION NUMBER: US 60/464,159
; PRIOR FILING DATE: 2003-04-18
```

US-10-828-395-19

PRIOR APPLICATION NUMBER: US 60/464,160

PRIOR FILING DATE: 2003-04-18

NUMBER OF SEQ ID NOS: 23

SOFTWARE: PatentIn version 3.2

SEQ ID NO 15

LENGTH: 17

TYPE: RNA

ORGANISM: artificial

FEATURE:

OTHER INFORMATION: clusterin targeted siRNA sequence

Query Match

Best Local Similarity 0.9%; Score 15.4; DB 1; Length 17;

Mismatches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1616 TAATTCATTAATAACTGT 1632

Db 17 TAATTCACAAACTGT 1

RESULT 381

US-10-758-451-883/c

Sequence 883, Application US/10758451

Publication No. US20050014711A1

GENERAL INFORMATION:

APPLICANT: East Carolina University

TITLE OF INVENTION: COMPOSITION, FORMULATION & METHOD FOR PREVENTION & TREATMENT OF

TITLE OF INVENTION: AND CONDITIONS ASSOCIATED WITH BRONCHOCONSTRICTION, ALLERGY (IES)

TITLE OF INVENTION: INFLAMMATION

FILE REFERENCE: 30775-705.301

CURRENT APPLICATION NUMBER: US/10/758,451

CURRENT FILING DATE: 2004-01-14

PRIOR APPLICATION NUMBER: 09/093,972

PRIOR FILING DATE: 1998-06-09

NUMBER OF SEQ ID NOS: 996

SOFTWARE: PatentIn version 3.1

SEQ ID NO 883

LENGTH: 15

TYPE: DNA

ORGANISM: Homo sapiens

US-10-758-451-883

Query Match

Best Local Similarity 0.9%; Score 15; DB 1; Length 15;

Mismatches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1531 CCCAGCCTCTCCCG 1545

Db 15 CCCAGCCTCTCCCG 1

RESULT 382

US-09-740-332-3014/c

Sequence 3014, Application US/09740332

Publication No. US20030125270A1

GENERAL INFORMATION:

APPLICANT: Ribozyme Pharmaceuticals, Inc.

TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Relate

TITLE OF INVENTION: Hepatitis C Virus Infection

FILE REFERENCE: RPI 400/003

CURRENT APPLICATION NUMBER: US/09/740,332

CURRENT FILING DATE: 2001-03-26

NUMBER OF SEQ ID NOS: 9704

SOFTWARE: PatentIn version 3.0

SEQ ID NO 3014

LENGTH: 17

TYPE: RNA

ORGANISM: artificial sequence

FEATURE:

NAME/KEY: misc\_feature

LOCATION:

OTHER INFORMATION: oligonucleotide substrate

US-09-740-332-3014

Query Match

Best Local Similarity 0.9%; Score 15; DB 1; Length 17;

Mismatches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 766 TCCACGCCCATGTTC 780

Db 15 TCCACGCCCATGTTC 1

RESULT 383

US-09-817-879-3014/c

Sequence 3014, Application US/09817879

Publication No. US20030171311A1

GENERAL INFORMATION:

APPLICANT: Ribozyme Pharmaceuticals Inc.

TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Relate

TITLE OF INVENTION: Hepatitis C Virus Infection

FILE REFERENCE: MBHB00-801-F

CURRENT APPLICATION NUMBER: US/09/817,879

CURRENT FILING DATE: 2001-03-26

NUMBER OF SEQ ID NOS: 9703

SOFTWARE: PatentIn version 3.0

SEQ ID NO 3014

LENGTH: 17

TYPE: RNA

ORGANISM: artificial sequence

FEATURE:

NAME/KEY: misc\_feature

LOCATION:

OTHER INFORMATION: oligonucleotide substrate

US-09-817-879-3014

Query Match

Best Local Similarity 0.9%; Score 15; DB 1; Length 17;

Mismatches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 766 TCCACGCCCATGTTC 780

Db 15 TCCACGCCCATGTTC 1

RESULT 384

US-10-669-841-5607/c

Sequence 5607, Application US/10669841

Publication No. US20040127446A1

GENERAL INFORMATION:

APPLICANT: Sirna Therapeutics, Inc.

APPLICANT: Lawrence, Blatt

APPLICANT: Dennis, Macejak

APPLICANT: James, McSwiggen

APPLICANT: David, Morrissey

APPLICANT: Pamela, Pavco

APPLICANT: Patrice, Lee

APPLICANT: Kenneth, Draper

APPLICANT: Elisabeth, Roberts

TITLE OF INVENTION: OLIGONUCLEOTIDE MEDIATED INHIBITION OF HEPATITIS B VIRUS AND HEPAT

TITLE OF INVENTION: VIRUS REPLICATION

FILE REFERENCE: 400/042US (MBHB02-249-E)

CURRENT APPLICATION NUMBER: US/10/669,841

CURRENT FILING DATE: 2003-09-23

PRIOR APPLICATION NUMBER: PCT/US02/09187

PRIOR FILING DATE: 2002-03-26

PRIOR APPLICATION NUMBER: US 60/296,876

PRIOR FILING DATE: 2001-06-08

PRIOR APPLICATION NUMBER: US 60/335,059

PRIOR FILING DATE: 2001-10-24

PRIOR APPLICATION NUMBER: US 60/337,055

PRIOR FILING DATE: 2001-12-05

PRIOR APPLICATION NUMBER: US 60/358,580

PRIOR FILING DATE: 2002-02-20

PRIOR APPLICATION NUMBER: US 60/363,124

; PRIOR FILING DATE: 2002-03-11  
; PRIOR APPLICATION NUMBER: US 09/817,879  
; PRIOR FILING DATE: 2001-03-26  
; PRIOR APPLICATION NUMBER: US 09/740,332  
; PRIOR FILING DATE: 2000-12-18  
; PRIOR APPLICATION NUMBER: US 09/611,931  
; PRIOR FILING DATE: 2000-07-07  
; PRIOR APPLICATION NUMBER: US 09/504,321  
; PRIOR FILING DATE: 2000-02-15  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 16207  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 5607  
; LENGTH: 17  
; TYPE: RNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION:  
; OTHER INFORMATION: oligonucleotide substrate  
US-10-669-841-5607

Query Match 0.9%; Score 15; DB 1; Length 17;  
Best Local Similarity 100.0%; Pred. No. 2.6e+02;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 766 TCCACGCCCATGTTCC 780  
|||||  
Db 15 TCCACGCCCATGTTCC 1

## RESULT 385

US-10-497-692-11  
; Sequence 11, Application US/10497692  
; Publication No. US2005004056A1  
; GENERAL INFORMATION:  
; APPLICANT: Meise, Martin  
; APPLICANT: Eulenberg, Karsten  
; APPLICANT: Fritsch, Rudiger  
; APPLICANT: Hader, Thomas  
; APPLICANT: Bronner, Gunter  
; APPLICANT: Stueternagel, Arnd  
; TITLE OF INVENTION: PTP10D, Tec protein tyrosine kinase and EDP homologous proteins  
; TITLE OF INVENTION: involved in the regulation of energy homeostasis  
; FILE REFERENCE: 2923-632  
; CURRENT APPLICATION NUMBER: US/10/497,692  
; CURRENT FILING DATE: 2004-06-04  
; PRIOR APPLICATION NUMBER: PCT/EP02/13744  
; PRIOR FILING DATE: 2002-12-04  
; PRIOR APPLICATION NUMBER: EP 01 000 010.5  
; PRIOR FILING DATE: 2002-01-02  
; PRIOR APPLICATION NUMBER: EP 01 129 138.2  
; PRIOR FILING DATE: 2001-12-07  
; PRIOR APPLICATION NUMBER: EP 01 128 844.6  
; PRIOR FILING DATE: 2001-12-04  
; NUMBER OF SEQ ID NOS: 20  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 11  
; LENGTH: 18  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: mouse PTPRB reverse primer  
US-10-497-692-11

Query Match 0.9%; Score 14.8; DB 1; Length 18;  
Best Local Similarity 88.9%; Pred. No. 3.1e+02;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 764 CTTCCACGCCCATGTTCCA 781  
|||||

Db 1 CTCCACGCCCATCTTCCA 18

## RESULT 386

US-09-866-108-8352/c  
; Sequence 8352, Application US/09866108  
; Patent No. US20020048800A1  
; GENERAL INFORMATION:  
; APPLICANT: GU, Yizhong  
; APPLICANT: JI, Yonggang  
; APPLICANT: PENN, Sharron G.  
; APPLICANT: HANZEL, David K.  
; APPLICANT: RANK, David R.  
; APPLICANT: SHEN, Wensheng  
; APPLICANT: SHANNON, Mark  
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE  
; CURRENT APPLICATION NUMBER: US/09/866,108  
; CURRENT FILING DATE: 2001-05-25  
; PRIOR APPLICATION NUMBER: US 60/207,456  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: GB 24263.6  
; PRIOR FILING DATE: 2000-10-04  
; PRIOR APPLICATION NUMBER: US 60/236,359  
; PRIOR FILING DATE: 2000-09-27  
; PRIOR APPLICATION NUMBER: PCT/US01/00666  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00667  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00664  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00669  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00665  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00668  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00663  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00662  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00661  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00670  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: US 60/234,687  
; PRIOR FILING DATE: 2000-09-21  
; PRIOR APPLICATION NUMBER: US 60/266,860  
; PRIOR FILING DATE: 2001-02-05  
; NUMBER OF SEQ ID NOS: 15752  
; SOFTWARE: Aecomica Sequence Listing Engine  
; SEQ ID NO 8352  
; LENGTH: 17  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-866-108-8352

Query Match 0.9%; Score 14.4; DB 1; Length 17;  
Best Local Similarity 93.8%; Pred. No. 3e+02;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1109 CACCTCCTCTTGTG 1124  
|||  
Db 17 CAGCTCCTCTTGTG 2

## RESULT 387

US-09-866-108-8353/c  
; Sequence 8353, Application US/09866108  
; Patent No. US20020048800A1  
; GENERAL INFORMATION:  
; APPLICANT: GU, Yizhong  
; APPLICANT: JI, Yonggang

```

1  APPLICANT: PENN, Sharron G.
2  APPLICANT: HANZEL, David K.
3  APPLICANT: RANK, David R.
4  APPLICANT: CHEN, Wensheng
5  APPLICANT: SHANNON, Mark
6  TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
7  FILE REFERENCE: AEOMICA-7
8  CURRENT APPLICATION NUMBER: US/09/866,108
9  CURRENT FILING DATE: 2001-05-25
10 PRIOR APPLICATION NUMBER: US 60/207,456
11 PRIOR FILING DATE: 2000-05-26
12 PRIOR APPLICATION NUMBER: GB 24263.6
13 PRIOR FILING DATE: 2000-10-04
14 PRIOR APPLICATION NUMBER: US 60/236,359
15 PRIOR FILING DATE: 2000-09-27
16 PRIOR APPLICATION NUMBER: PCT/US01/006666
17 PRIOR FILING DATE: 2001-01-30
18 PRIOR APPLICATION NUMBER: PCT/US01/006667
19 PRIOR FILING DATE: 2001-01-30
20 PRIOR APPLICATION NUMBER: PCT/US01/006664
21 PRIOR FILING DATE: 2001-01-30
22 PRIOR APPLICATION NUMBER: PCT/US01/006669
23 PRIOR FILING DATE: 2001-01-30
24 PRIOR APPLICATION NUMBER: PCT/US01/006665
25 PRIOR FILING DATE: 2001-01-30
26 PRIOR APPLICATION NUMBER: PCT/US01/006668
27 PRIOR FILING DATE: 2001-01-30
28 PRIOR APPLICATION NUMBER: PCT/US01/006663
29 PRIOR FILING DATE: 2001-01-30
30 PRIOR APPLICATION NUMBER: PCT/US01/006662
31 PRIOR FILING DATE: 2001-01-30
32 PRIOR APPLICATION NUMBER: PCT/US01/006661
33 PRIOR FILING DATE: 2001-01-30
34 PRIOR APPLICATION NUMBER: PCT/US01/006670
35 PRIOR FILING DATE: 2001-01-30
36 PRIOR APPLICATION NUMBER: US 60/234,687
37 PRIOR FILING DATE: 2000-09-21
38 PRIOR APPLICATION NUMBER: US 60/266,860
39 PRIOR FILING DATE: 2001-02-05
40 NUMBER OF SEQ ID NOS: 15752
41 SOFTWARE: Aecomica Sequence Listing Engine
42 SEQ ID NO 8353
43 LENGTH: 17
44 TYPE: DNA
45 ORGANISM: Homo sapiens
46 US-09-866-108-8353
47
48 Query Match 0.9%; Score 14.4; DB 1; Length 17;
49 Best Local Similarity 93.8%; Pred. No. 3a+02;
50 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps
51
52 Qy 1109 CACCTCTCTCTGCTG 1124
53 Db 16 CAGCTCTCTCTGCTG 1
54
55 RESULT 388
56 US-09-866-108-8665
57 Sequence 8665, Application US/09866108
58 Patent No. US20020048800A1
59 GENERAL INFORMATION:
60 APPLICANT: GU, Yizhong
61 APPLICANT: JI, Yonggang
62 APPLICANT: PENN, Sharron G.
63 APPLICANT: HANZEL, David K.
64 APPLICANT: RANK, David R.
65 APPLICANT: CHEN, Wensheng
66 APPLICANT: SHANNON, Mark
67 TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
68 FILE REFERENCE: AEOMICA-7
69 CURRENT APPLICATION NUMBER: US/09/866,108
70 CURRENT FILING DATE: 2001-05-25
71 PRIOR APPLICATION NUMBER: US 60/207,456

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; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00669  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00665  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00668  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00663  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00662  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00661  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00670  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: US 60/234,687  
; PRIOR FILING DATE: 2000-09-21  
; PRIOR APPLICATION NUMBER: US 60/266,860  
; NUMBER OF SEQ ID NOS: 15752  
; SOFTWARE: Aecomica Sequence Listing Engine  
; SEQ ID NO 8667  
; LENGTH: 17  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-866-108-8667

Query Match 0.9%; Score 14.4; DB 1; Length 17;  
Best Local Similarity 93.8%; Pred. No. 3e+02; Mismatches 0; Indels 1; Gaps 0;  
Matches 15; Conservative 0;

Qy 274 AAGCCAGAGAGAGAA 289  
Db 1 AAGCCAGAGAGAGAA 16  
|||||

RESULT 390  
US-09-866-108-10037/c  
; Sequence 10037, Application US/09866108  
; Patent No. US20020048800A1  
; GENERAL INFORMATION:  
; APPLICANT: GU, Yizhong  
; APPLICANT: JI, Yonggang  
; APPLICANT: PENN, Sharron G.  
; APPLICANT: HANZEL, David K.  
; APPLICANT: RANK, David R.  
; APPLICANT: CHEN, Wensheng  
; APPLICANT: SHANNON, Mark  
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE  
; FILE REFERENCE: AEOMICA-7  
; CURRENT APPLICATION NUMBER: US/09/866,108  
; CURRENT FILING DATE: 2001-05-25  
; PRIOR APPLICATION NUMBER: US 60/207,456  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: GB 24263.6  
; PRIOR FILING DATE: 2000-10-04  
; PRIOR APPLICATION NUMBER: US 60/236,359  
; PRIOR FILING DATE: 2000-09-27  
; PRIOR APPLICATION NUMBER: PCT/US01/00666  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00667  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00664  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00669  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00665  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00668  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00663  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00662

; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00661  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00670  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: US 60/234,687  
; PRIOR FILING DATE: 2000-09-21  
; PRIOR APPLICATION NUMBER: US 60/266,860  
; NUMBER OF SEQ ID NOS: 15752  
; SOFTWARE: Aecomica Sequence Listing Engine  
; SEQ ID NO 10037  
; LENGTH: 17  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-866-108-10037

Query Match 0.9%; Score 14.4; DB 1; Length 17;  
Best Local Similarity 93.8%; Pred. No. 3e+02; Mismatches 0; Indels 1; Gaps 0;  
Matches 15; Conservative 0;

Qy 715 CCCGATCGTCCGACG 730  
Db 17 CCCGATCGTCCACG 2  
|||||

RESULT 391  
US-09-866-108-10038/c  
; Sequence 10038, Application US/09866108  
; Patent No. US20020048800A1  
; GENERAL INFORMATION:  
; APPLICANT: GU, Yizhong  
; APPLICANT: JI, Yonggang  
; APPLICANT: PENN, Sharron G.  
; APPLICANT: HANZEL, David K.  
; APPLICANT: RANK, David R.  
; APPLICANT: CHEN, Wensheng  
; APPLICANT: SHANNON, Mark  
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE  
; FILE REFERENCE: AEOMICA-7  
; CURRENT APPLICATION NUMBER: US/09/866,108  
; CURRENT FILING DATE: 2001-05-25  
; PRIOR APPLICATION NUMBER: US 60/207,456  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: GB 24263.6  
; PRIOR FILING DATE: 2000-10-04  
; PRIOR APPLICATION NUMBER: US 60/236,359  
; PRIOR FILING DATE: 2000-09-27  
; PRIOR APPLICATION NUMBER: PCT/US01/00666  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00667  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00664  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00669  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00665  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00668  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00661  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00670  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: US 60/234,687  
; PRIOR FILING DATE: 2000-09-21  
; PRIOR APPLICATION NUMBER: US 60/266,860  
; PRIOR FILING DATE: 2001-02-05  
; NUMBER OF SEQ ID NOS: 15752

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; SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 10038
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108-10038

Query Match      0.9%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 3e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 715 CCCGCATCGTCGCAG 730
Db 16 CCCGCATCGTCACAG 1

RESULT 392
US-09-928-412-7
; Sequence 7, Application US/09928412
; Patent No. US20020123623A1
; GENERAL INFORMATION:
; APPLICANT: KAWAOKA, Akiyoshi
; APPLICANT: EBINUMA, Hiroyasu
; TITLE OF INVENTION: TRANSCRIPTION FACTOR CONTROLLING PHENYLPROPANOID
; FILE REFERENCE: BIOSYNTHESIS PATHWAY
; CURRENT FILING DATE: 2001-12-31
; PRIOR APPLICATION NUMBER: US/09/928,412
; CURRENT FILING DATE: 2001-08-14
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/282,146
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-03-31
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: JP 10-125171
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-03-31
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic DNA
US-09-928-412-7

Query Match      0.9%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 3e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1104 CTCACACCTCTCTCT 1119
Db 2 CTCACACCTCTCTCTCT 17

RESULT 393
US-09-780-533A-171/c
; Sequence 171, Application US/09780533A
; Publication No. US20030060611A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Blatt, Larry
; APPLICANT: McSwiggen, Jim
; APPLICANT: Chowrira, Bharat
; APPLICANT: Haeblerli, Pete
; TITLE OF INVENTION: Method and Reagent for the Inhibition of NOGO Gene
; FILE REFERENCE: MBH00.878-A (400/011)
; CURRENT APPLICATION NUMBER: US/09/780,533A
; CURRENT FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: US 60/181,797
; PRIOR FILING DATE: 2000-02-11
; NUMBER OF SEQ ID NOS: 6679
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 171
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
```

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US-09-780-533A-171

Query Match      0.9%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 3e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1619 TTCAATAAAACTGTCT 1634
Db 16 TTCAATAAACTGTCT 1

RESULT 394
US-09-877-478-1745/c
; Sequence 1745, Application US/09877478
; Publication No. US20030068301A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Draper, Kenneth
; APPLICANT: Blatt, Larry
; APPLICANT: McSwiggen, Jim
; APPLICANT: Morrissey, Dave
; TITLE OF INVENTION: Method and Reagent for Inhibiting Hepatitis B Virus Replication
; FILE REFERENCE: MBH00-845-H (400/029)
; CURRENT APPLICATION NUMBER: US/09/877,478
; CURRENT FILING DATE: 2001-12-31
; PRIOR APPLICATION NUMBER: US 07/882,712
; PRIOR FILING DATE: 1992-05-14
; PRIOR APPLICATION NUMBER: US 09/531,025
; PRIOR FILING DATE: 2000-03-20
; PRIOR APPLICATION NUMBER: US 09/636,385
; PRIOR FILING DATE: 2000-08-09
; PRIOR APPLICATION NUMBER: US 09/696,347
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 08/193,627
; PRIOR FILING DATE: 1994-02-07
; PRIOR APPLICATION NUMBER: US 08/433,993
; PRIOR FILING DATE: 1995-05-04
; PRIOR APPLICATION NUMBER: US 08/434,504
; PRIOR FILING DATE: 1995-05-04
; PRIOR APPLICATION NUMBER: US 09/436,430
; PRIOR FILING DATE: 1999-11-08
; NUMBER OF SEQ ID NOS: 6586
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1745
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Hepatitis B virus
US-09-877-478-1745

Query Match      0.9%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 3e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1519 CCCCCAACTCCGCCCA 1534
Db 16 CCCCCAACTCCTCCCA 1

RESULT 395
US-09-740-332-1543
; Sequence 1543, Application US/09740332
; Publication No. US20030125270A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals Inc.
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related
; FILE REFERENCE: RPI 400/003
; CURRENT APPLICATION NUMBER: US/09/740,332
; CURRENT FILING DATE: 2001-03-26
; NUMBER OF SEQ ID NOS: 9704
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1543
; LENGTH: 17
```

; TYPE: RNA  
; ORGANISM: artificial sequence  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION:  
; OTHER INFORMATION: oligonucleotide substrate  
US-09-740-332-1543

Query Match 0.9%; Score 14.4; DB 1; Length 17;  
Best Local Similarity 75.0%; Pred. No. 3e+02;  
Matches 12; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 768 CAGCCATGTTCCAGC 783  
Db 1 CAGCGCAUGUCCGCG 16  
|||||:|:|

## RESULT 396

US-09-817-879-1543  
; Sequence 1543, Application US/09817879  
; Publication No. US20030171311A1  
; GENERAL INFORMATION:  
; APPLICANT: Ribozyme Pharmaceuticals, Inc.  
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related to Level  
; FILE REFERENCE: MBH00-801-F  
; CURRENT APPLICATION NUMBER: US/09/817,879  
; CURRENT FILING DATE: 2001-03-26  
; NUMBER OF SEQ ID NOS: 9703  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 1543  
; LENGTH: 17  
; TYPE: RNA  
; ORGANISM: artificial sequence  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION:  
; OTHER INFORMATION: oligonucleotide substrate  
US-09-817-879-1543

Query Match 0.9%; Score 14.4; DB 1; Length 17;  
Best Local Similarity 75.0%; Pred. No. 3e+02;  
Matches 12; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 768 CAGCCATGTTCCAGC 783  
Db 1 CAGCGCAUGUCCGCG 16  
|||||:|:|

## RESULT 397

US-10-298-255-4  
; Sequence 4, Application US/10298255  
; Publication No. US20030134312A1  
; GENERAL INFORMATION:  
; APPLICANT: BURGOYNE, LEIGH A.  
; TITLE OF INVENTION: METHODS AND MATERIALS FOR DETECTING GENETIC MATERIAL  
; FILE REFERENCE: 45858-56064  
; CURRENT APPLICATION NUMBER: US/10/298,255  
; CURRENT FILING DATE: 2002-11-15  
; PRIOR APPLICATION NUMBER: 60/336,005  
; PRIOR FILING DATE: 2001-11-15  
; NUMBER OF SEQ ID NOS: 7  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 4  
; LENGTH: 17  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Primer  
US-10-298-255-4

Query Match 0.9%; Score 14.4; DB 1; Length 17;  
Best Local Similarity 93.8%; Pred. No. 3e+02;

Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
Qy 1508 CAGCCTCCAGGCCCCC 1523  
Db 1 CAGCCTCCAGGCCCCC 16  
|||||:|:|

## RESULT 398

US-10-238-700-2912/c  
; Sequence 2912, Application US/10238700  
; Publication No. US20030153521A1  
; GENERAL INFORMATION:  
; APPLICANT: Ribozyme Pharmaceuticals, Inc.  
; APPLICANT: McSwigen, James  
; TITLE OF INVENTION: Nucleic Acid Treatment of Diseases or Conditions Related to Level  
; FILE REFERENCE: 400/057 (MBHB01-1158-A)  
; CURRENT APPLICATION NUMBER: US/10/238,700  
; CURRENT FILING DATE: 2002-09-18  
; PRIOR APPLICATION NUMBER: PCT/US 02/16940  
; PRIOR FILING DATE: 2002-05-29  
; PRIOR APPLICATION NUMBER: US 60/318,471  
; PRIOR FILING DATE: 2001-09-10  
; NUMBER OF SEQ ID NOS: 4666  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 2912  
; LENGTH: 17  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-10-238-700-2912

Query Match 0.9%; Score 14.4; DB 1; Length 17;  
Best Local Similarity 93.8%; Pred. No. 3e+02;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1507 CCAGCCTCCAGGCCCCC 1522  
Db 17 CCAGCCTGCAGGCCCCC 2  
|||||:|:|

## RESULT 399

US-10-339-793-366  
; Sequence 366, Application US/10339793  
; Publication No. US20030180764A1  
; GENERAL INFORMATION:  
; APPLICANT: Lynx Therapeutics, Inc.  
; APPLICANT: Shang, Jin  
; APPLICANT: Bowen, Benjamin  
; TITLE OF INVENTION: GENES AFFECTED BY CHOLESTEROL TREATMENT AND DURING ADIPOGENESIS  
; FILE REFERENCE: 37-00031005  
; CURRENT APPLICATION NUMBER: US/10/339,793  
; CURRENT FILING DATE: 2003-01-08  
; NUMBER OF SEQ ID NOS: 443  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 366  
; LENGTH: 17  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-339-793-366

Query Match 0.9%; Score 14.4; DB 1; Length 17;  
Best Local Similarity 93.8%; Pred. No. 3e+02;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 990 ACCAACCAACCCCTCCC 1005  
Db 2 ATCAACAACCCCTCCC 17  
|||||:|:|

## RESULT 400

US-10-342-902-1745/c  
; Sequence 1745, Application US/10342902  
; Publication No. US20040054156A1  
; GENERAL INFORMATION:

```

; APPLICANT: Sirna Therapeutics, Inc.
; APPLICANT: Draper, Kenneth
; APPLICANT: Blatt, Larry
; APPLICANT: McSwiggen, Jim
; APPLICANT: Morrissey, Dave
; TITLE OF INVENTION: Method and Reagent for Inhibiting Hepatitis B Virus Replication
; FILE REFERENCE: 400/075 (MBHB00-845-1)
; CURRENT APPLICATION NUMBER: US/10/342,902
; CURRENT FILING DATE: 2003-01-15
; PRIOR APPLICATION NUMBER: US 09/877,478
; PRIOR FILING DATE: 2001-06-08
; PRIOR APPLICATION NUMBER: US 09/531,025
; PRIOR FILING DATE: 2000-03-20
; PRIOR APPLICATION NUMBER: US 09/636,385
; PRIOR FILING DATE: 2000-08-09
; PRIOR APPLICATION NUMBER: US 09/696,347
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 08/193,627
; PRIOR FILING DATE: 1994-02-07
; PRIOR APPLICATION NUMBER: US 07/882,712
; PRIOR FILING DATE: 1992-05-14
; PRIOR APPLICATION NUMBER: US 09/436,430
; PRIOR FILING DATE: 1999-11-08
; NUMBER OF SEQ ID NOS: 6592
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1745
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Hepatitis B virus
; US-10-342-902-1745

Query Match      0.9%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 3e+02; 1; Indels 0; Gaps 0;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1519 CCCCAACTCCGCCA 1534
Db 16 CCCCAACTCCGCCA 1

RESULT 401
US-10-138-674-8431/c
; Sequence 8431, Application US/10138674
; Publication No. US20040077565A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; FILE REFERENCE: MBHB00-876-N (400/049)
; CURRENT APPLICATION NUMBER: US/10/138,674
; CURRENT FILING DATE: 2002-05-03
; NUMBER OF SEQ ID NOS: 20822
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 8431
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-138-674-8431

Query Match      0.9%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 3e+02; 1; Indels 0; Gaps 0;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1545 GCTCTGGATCCTGCAC 1560
Db 17 GCTCTGCATCCTGCAC 2

RESULT 402
US-10-138-674-8431/c
; Sequence 8431, Application US/10138674
; Publication No. US20040077565A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; FILE REFERENCE: MBHB00-876-N (400/049)
; CURRENT APPLICATION NUMBER: US/10/138,674
; CURRENT FILING DATE: 2002-05-03
; NUMBER OF SEQ ID NOS: 20822
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 8431
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-138-674-8431

Query Match      0.9%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 3e+02; 1; Indels 0; Gaps 0;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1545 GCTCTGGATCCTGCAC 1560
Db 17 GCTCTGCATCCTGCAC 2

RESULT 402
US-10-138-674-8431/c
; Sequence 8431, Application US/10287949A
; Publication No. US20040102389A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; FILE REFERENCE: MBHB00-876-N (400/049)
; CURRENT APPLICATION NUMBER: US/10/287,949A
; CURRENT FILING DATE: 2003-04-11
; NUMBER OF SEQ ID NOS: 20822
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 8431
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-287-949A-8431/c

Query Match      0.9%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 3e+02; 1; Indels 0; Gaps 0;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1545 GCTCTGGATCCTGCAC 1560
Db 17 GCTCTGCATCCTGCAC 2

RESULT 403
US-10-669-841-1745/c
; Sequence 1745, Application US/10669841
; Publication No. US20040127446A1
; GENERAL INFORMATION:
; APPLICANT: Sirna Therapeutics, Inc.
; APPLICANT: Lawrence, Blatt
; APPLICANT: Dennis, Macejak
; APPLICANT: James, McSwiggen
; APPLICANT: David, Morrissey
; APPLICANT: Pamela, Pavco
; APPLICANT: Patricia, Lee
; APPLICANT: Kenneth, Draper
; APPLICANT: Elisabeth, Roberts
; TITLE OF INVENTION: OLIGONUCLEOTIDE MEDIATED INHIBITION OF HEPATITIS B VIRUS AND HEPAT
; FILE REFERENCE: 400/042US (MBHB02-249-B)
; CURRENT APPLICATION NUMBER: US/10/669,841
; CURRENT FILING DATE: 2003-09-23
; PRIOR APPLICATION NUMBER: PCT/US02/09187
; PRIOR FILING DATE: 2002-03-26
; PRIOR APPLICATION NUMBER: US 60/296,876
; PRIOR FILING DATE: 2001-06-08
; PRIOR APPLICATION NUMBER: US 60/335,059
; PRIOR FILING DATE: 2001-10-24
; PRIOR APPLICATION NUMBER: US 60/337,055
; PRIOR FILING DATE: 2001-12-05
; PRIOR APPLICATION NUMBER: US 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/363,124
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: US 09/817,879
; PRIOR FILING DATE: 2001-03-26
; PRIOR APPLICATION NUMBER: US 09/740,332
; PRIOR FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: US 09/611,931
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: US 09/504,321
; PRIOR FILING DATE: 2000-02-15
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 16207
; SOFTWARE: PatentIn version 3.0
; US-10-669-841-1745
```

; SEQ ID NO 1745  
; LENGTH: 17  
; TYPE: RNA  
; ORGANISM: Hepatitis B Virus  
US-10-669-841-1745

Query Match 0.9%; Score 14.4; DB 1; Length 17;  
Best Local Similarity 93.8%; Pred. No. 3e+02;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1519 CCCCCCACTCCGCCA 1534  
Db 16 CCCCCCACTCTCCCA 1

## RESULT 404

US-10-669-841-4136  
; Sequence 4136, Application US/10669841  
; Publication No. US20040127446A1  
; GENERAL INFORMATION:  
; APPLICANT: Lawrence, Blatt  
; APPLICANT: Dennis, Macejak  
; APPLICANT: James, McSwiggen  
; APPLICANT: David, Morrissey  
; APPLICANT: Pamela, Pavco  
; APPLICANT: Patricia, Lee  
; APPLICANT: Kenneth, Draper  
; APPLICANT: Elisabeth, Roberts  
; TITLE OF INVENTION: OLIGONUCLEOTIDE MEDIATED INHIBITION OF HEPATITIS B VIRUS AND HEPATITIS B VIRUS REPLICATION  
; FILE REFERENCE: 400/042US (MBH02-249-E)  
; CURRENT APPLICATION NUMBER: US/10/669,841  
; CURRENT FILING DATE: 2003-09-23  
; PRIOR APPLICATION NUMBER: PCT/US02/09187  
; PRIOR FILING DATE: 2002-03-26  
; PRIOR APPLICATION NUMBER: US 60/296,876  
; PRIOR FILING DATE: 2001-06-08  
; PRIOR APPLICATION NUMBER: US 60/335,059  
; PRIOR FILING DATE: 2001-10-24  
; PRIOR APPLICATION NUMBER: US 60/337,055  
; PRIOR FILING DATE: 2001-12-05  
; PRIOR APPLICATION NUMBER: US 60/358,580  
; PRIOR FILING DATE: 2002-02-20  
; PRIOR APPLICATION NUMBER: US 60/363,124  
; PRIOR FILING DATE: 2002-03-11  
; PRIOR APPLICATION NUMBER: US 09/817,879  
; PRIOR FILING DATE: 2001-03-26  
; PRIOR APPLICATION NUMBER: US 09/740,332  
; PRIOR FILING DATE: 2000-12-18  
; PRIOR APPLICATION NUMBER: US 09/611,931  
; PRIOR FILING DATE: 2000-07-07  
; PRIOR APPLICATION NUMBER: US 09/504,321  
; PRIOR FILING DATE: 2000-02-15  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 16207  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 4136  
; LENGTH: 17  
; TYPE: RNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION:  
; OTHER INFORMATION: oligonucleotide substrate  
US-10-669-841-4136

Query Match 0.9%; Score 14.4; DB 1; Length 17;  
Best Local Similarity 75.0%; Pred. No. 3e+02;  
Matches 12; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 768 CACCCATGTTCCAGC 783  
Db 1 CACGCCAUGUCCGCGC 16

## RESULT 405

US-10-723-361-8352/c  
; Sequence 8352, Application US/10723361  
; Publication No. US20040137589A1  
; GENERAL INFORMATION:  
; APPLICANT: GU, Yizhong  
; APPLICANT: JI, Yonggang  
; APPLICANT: PENN, Sharron G.  
; APPLICANT: HANZEL, David K.  
; APPLICANT: RANK, David R.  
; APPLICANT: CHEN, Wensheng  
; APPLICANT: SHANNON, Mark  
; TITLE OF INVENTION: HUMAN MYOSIN-LIKE POLYPEPTIDE EXPRESSED PREDOMINANTLY IN HEART AN  
; FILE REFERENCE: PB0105  
; CURRENT APPLICATION NUMBER: US/10/723,361  
; CURRENT FILING DATE: 2003-11-26  
; PRIOR APPLICATION NUMBER: US 09/866,108  
; PRIOR FILING DATE: 2001-05-25  
; PRIOR APPLICATION NUMBER: US 60/207,456  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: GB 24263.6  
; PRIOR FILING DATE: 2000-10-04  
; PRIOR APPLICATION NUMBER: US 60/236,359  
; PRIOR FILING DATE: 2000-09-27  
; PRIOR APPLICATION NUMBER: PCT/US01/00666  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00667  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00664  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00669  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00665  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00668  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 15755  
; SOFTWARE: Aeomica Sequence Listing Engine  
; SEQ ID NO 8352  
; LENGTH: 17  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-723-361-8352

Query Match 0.9%; Score 14.4; DB 1; Length 17;  
Best Local Similarity 93.8%; Pred. No. 3e+02;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1109 CACCTCTCTCTGCTG 1124  
Db 17 CAGCTCTCTCTGCTG 2

## RESULT 406

US-10-723-361-8353/c  
; Sequence 8353, Application US/10723361  
; Publication No. US20040137589A1  
; GENERAL INFORMATION:  
; APPLICANT: GU, Yizhong  
; APPLICANT: JI, Yonggang  
; APPLICANT: PENN, Sharron G.  
; APPLICANT: HANZEL, David K.  
; APPLICANT: RANK, David R.  
; APPLICANT: CHEN, Wensheng  
; APPLICANT: SHANNON, Mark  
; TITLE OF INVENTION: HUMAN MYOSIN-LIKE POLYPEPTIDE EXPRESSED PREDOMINANTLY IN HEART AN  
; FILE REFERENCE: PB0105

```
; CURRENT APPLICATION NUMBER: US/10/723,361
; CURRENT FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: US 09/866,108
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aecomica Sequence Listing Engine
; SEQ ID NO 8353
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-723-361-8353

Query Match          0.9%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 3e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1109 CACTCTCTCTTGCTG 1124
Db 16 CAGCTCTCTCTTGCTG 1

RESULT 407
US-10-723-361-8665
; Sequence 8665, Application US/10/723361
; Publication No. US20040137589A1
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: HUMAN MYOSIN-LIKE POLYPEPTIDE EXPRESSED PREDOMINANTLY IN HEART AN
; FILE REFERENCE: PB0105
; CURRENT APPLICATION NUMBER: US/10/723,361
; CURRENT FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: US 09/866,108
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aecomica Sequence Listing Engine
; SEQ ID NO 8667
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-723-361-8667

Query Match          0.9%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 3e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1109 CACTCTCTCTTGCTG 1124
Db 16 CAGCTCTCTCTTGCTG 1

RESULT 407
US-10-723-361-8665
; Sequence 8665, Application US/10/723361
; Publication No. US20040137589A1
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: HUMAN MYOSIN-LIKE POLYPEPTIDE EXPRESSED PREDOMINANTLY IN HEART AN
; FILE REFERENCE: PB0105
; CURRENT APPLICATION NUMBER: US/10/723,361
; CURRENT FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: US 09/866,108
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aecomica Sequence Listing Engine
; SEQ ID NO 8667
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-723-361-8667

Query Match          0.9%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 3e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 274 RAGCCCAAGAGAGAA 289
Db 1 AAGCCCAAGAGAGAA 16

RESULT 408
US-10-723-361-8667
; Sequence 8667, Application US/10/723361
; Publication No. US20040137589A1
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: HUMAN MYOSIN-LIKE POLYPEPTIDE EXPRESSED PREDOMINANTLY IN HEART AN
; FILE REFERENCE: PB0105
; CURRENT APPLICATION NUMBER: US/10/723,361
; CURRENT FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: US 09/866,108
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aecomica Sequence Listing Engine
; SEQ ID NO 8667
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-723-361-8667

Query Match          0.9%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 3e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 274 RAGCCCAAGAGAGAA 289
Db 1 AAGCCCAAGAGAGAA 16
```

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; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aecomica Sequence Listing Engine
; SEQ ID NO 8665
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-723-361-8665

Query Match          0.9%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 3e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 273 GAAGCCCAAGAGAGAA 288
Db 2 GAAGCCCAAGAGAGAA 17

RESULT 408
US-10-723-361-8667
; Sequence 8667, Application US/10/723361
; Publication No. US20040137589A1
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: HUMAN MYOSIN-LIKE POLYPEPTIDE EXPRESSED PREDOMINANTLY IN HEART AN
; FILE REFERENCE: PB0105
; CURRENT APPLICATION NUMBER: US/10/723,361
; CURRENT FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: US 09/866,108
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aecomica Sequence Listing Engine
; SEQ ID NO 8667
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-723-361-8667

Query Match          0.9%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 3e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 274 RAGCCCAAGAGAGAA 289
Db 1 AAGCCCAAGAGAGAA 16
```

## RESULT 409

US-10-723-361-10037/c  
; Sequence 10037, Application US/10723361  
; Publication No. US20040137589A1  
; GENERAL INFORMATION:  
; APPLICANT: GU, Yizhong  
; APPLICANT: JI, Yonggang  
; APPLICANT: PENN, Sharon G.  
; APPLICANT: HANZEL, David K.  
; APPLICANT: RANK, David R.  
; APPLICANT: CHEN, Wensheng  
; APPLICANT: SHANNON, Mark  
; TITLE OF INVENTION: HUMAN MYOSIN-LIKE POLYPEPTIDE EXPRESSED PREDOMINANTLY IN HEART AN  
; FILE REFERENCE: PB0105  
; CURRENT APPLICATION NUMBER: US/10/723,361  
; CURRENT FILING DATE: 2003-11-26  
; PRIOR APPLICATION NUMBER: US 09/866,108  
; PRIOR FILING DATE: 2001-05-25  
; PRIOR APPLICATION NUMBER: US 60/207,456  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: GB 24263.6  
; PRIOR FILING DATE: 2000-10-04  
; PRIOR APPLICATION NUMBER: US 60/236,359  
; PRIOR FILING DATE: 2000-09-27  
; PRIOR APPLICATION NUMBER: PCT/US01/00666  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00667  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00665  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00668  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00669  
; PRIOR FILING DATE: 2001-01-30  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 15755  
; SOFTWARE: Acomica Sequence Listing Engine  
; SEQ ID NO 10037  
; LENGTH: 17  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-723-361-10037

Query Match 0.9%; Score 14.4; DB 1; Length 17;  
Best Local Similarity 93.8%; Pred. No. 3e+02;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 715 CCCGCATCGTCCGCAG 730  
Db 17 CCCGCATCGTCCACAG 2

## RESULT 410

US-10-723-361-10038/c  
; Sequence 10038, Application US/10723361  
; Publication No. US20040137589A1  
; GENERAL INFORMATION:  
; APPLICANT: GU, Yizhong  
; APPLICANT: JI, Yonggang  
; APPLICANT: PENN, Sharon G.  
; APPLICANT: HANZEL, David K.  
; APPLICANT: RANK, David R.  
; APPLICANT: CHEN, Wensheng  
; APPLICANT: SHANNON, Mark  
; TITLE OF INVENTION: HUMAN MYOSIN-LIKE POLYPEPTIDE EXPRESSED PREDOMINANTLY IN HEART AN  
; FILE REFERENCE: PB0105  
; CURRENT APPLICATION NUMBER: US/10/723,361  
; CURRENT FILING DATE: 2003-11-26  
; PRIOR APPLICATION NUMBER: US 09/866,108

; PRIOR FILING DATE: 2001-05-25  
; PRIOR APPLICATION NUMBER: US 60/207,456  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: GB 24263.6  
; PRIOR FILING DATE: 2000-10-04  
; PRIOR APPLICATION NUMBER: US 60/236,359  
; PRIOR FILING DATE: 2000-09-27  
; PRIOR APPLICATION NUMBER: PCT/US01/00666  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00667  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00664  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00669  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00665  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00668  
; PRIOR FILING DATE: 2001-01-30  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 15755  
; SOFTWARE: Acomica Sequence Listing Engine  
; SEQ ID NO 10038  
; LENGTH: 17  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-723-361-10038

Query Match 0.9%; Score 14.4; DB 1; Length 17;  
Best Local Similarity 93.8%; Pred. No. 3e+02;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 715 CCCGCATCGTCCGCAG 730  
Db 16 CCCGCATCGTCCACAG 1

## RESULT 411

US-10-712-633-3472/c  
; Sequence 3472, Application US/10712633  
; Publication No. US20040220128A1  
; GENERAL INFORMATION:  
; APPLICANT: Ribozyne Pharmaceuticals, Inc.  
; APPLICANT: Pavco, Pamela  
; APPLICANT: Sandberg, Jennifer  
; APPLICANT: Gordon, Gilad  
; APPLICANT: McSwigen, James  
; APPLICANT: Stinchcomb, Dan  
; TITLE OF INVENTION: NUCLEIC ACID BASED MODULATION OF VASCULAR ENDOTHELIAL GROWTH FACT  
; FILE OF INVENTION: RECEPTOR FOR THE TREATMENT OF ANGIOGENESIS RELATED DISEASES AND  
; FILE REFERENCE: MBHB02-325PCT (400/047)  
; CURRENT APPLICATION NUMBER: US/10/712,633  
; CURRENT FILING DATE: 2003-11-13  
; PRIOR APPLICATION NUMBER: US 60/005,974  
; PRIOR FILING DATE: 1995-10-26  
; PRIOR APPLICATION NUMBER: US 08/584,040  
; PRIOR FILING DATE: 1996-01-08  
; PRIOR APPLICATION NUMBER: US 09/371,772  
; PRIOR FILING DATE: 1999-08-10  
; PRIOR APPLICATION NUMBER: US 09/708,690  
; PRIOR FILING DATE: 2000-11-07  
; PRIOR APPLICATION NUMBER: US 09/870,161  
; PRIOR FILING DATE: 2001-05-29  
; PRIOR APPLICATION NUMBER: US 60/334,461  
; PRIOR FILING DATE: 2001-11-30  
; PRIOR APPLICATION NUMBER: US 10/138,674  
; PRIOR FILING DATE: 2002-05-03  
; NUMBER OF SEQ ID NOS: 5989  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 3472  
; LENGTH: 17  
; TYPE: RNA  
; ORGANISM: Homo Sapiens

US-10-712-633-3472

Query Match 0.9%; Score 14.4; DB 1; Length 17;  
Best Local Similarity 93.8%; Pred. No. 3e+02;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1545 GCTCTGATCTCTGCAC 1560  
|||||  
Db 17 GCTCTGATCTCTGCAC 2

RESULT 412

US-10-724-270-1591/c  
; Sequence 1591, Application US/10724270  
; Publication No. US20050080031A1  
; GENERAL INFORMATION:  
; APPLICANT: Sirna Therapeutics, Inc.  
; APPLICANT: McSwiggen, James  
; TITLE OF INVENTION: Nucleic Acid Treatment of Diseases or Conditions Related to Leve  
; FILE REFERENCE: 400/046-US (WBH02-326-A)  
; CURRENT APPLICATION NUMBER: US/10/724,270  
; CURRENT FILING DATE: 2003-11-26  
; PRIOR APPLICATION NUMBER: PCT/US02/16840  
; PRIOR FILING DATE: 2002-05-29  
; PRIOR APPLICATION NUMBER: US 60/318,471  
; PRIOR FILING DATE: 2001-09-10  
; PRIOR APPLICATION NUMBER: US 60/296,249  
; PRIOR FILING DATE: 2001-06-06  
; PRIOR APPLICATION NUMBER: US 60/294,140  
; PRIOR FILING DATE: 2001-05-29  
; PRIOR APPLICATION NUMBER: US 10/238,700  
; PRIOR FILING DATE: 2002-09-10  
; PRIOR APPLICATION NUMBER: US 10/163,552  
; PRIOR FILING DATE: 2002-06-06  
; PRIOR APPLICATION NUMBER: US 10/157,580  
; PRIOR FILING DATE: 2002-05-29  
; PRIOR APPLICATION NUMBER: US 10/693,059  
; PRIOR FILING DATE: 2002-10-23  
; PRIOR APPLICATION NUMBER: US 10/444,853  
; PRIOR FILING DATE: 2003-05-23  
; PRIOR APPLICATION NUMBER: US 10/417,012  
; PRIOR FILING DATE: 2003-04-16  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 6810  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 1591  
; LENGTH: 17  
; TYPE: RNA  
; ORGANISM: Homo sapiens

US-10-724-270-1591

Query Match 0.9%; Score 14.4; DB 1; Length 17;  
Best Local Similarity 93.8%; Pred. No. 3e+02;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1507 CCAGCCTCAGGCCCC 1522  
|||||  
Db 17 CCAGCCTCAGGCCCC 2

RESULT 413

US-11-016-291-4  
; Sequence 4, Application US/11016291  
; Publication No. US20050095641A1  
; GENERAL INFORMATION:  
; APPLICANT: BURGOYNE, LEIGH A.  
; TITLE OF INVENTION: METHODS AND MATERIALS FOR DETECTING GENETIC MATERIAL  
; FILE REFERENCE: 45859-56064  
; CURRENT APPLICATION NUMBER: US/11/016,291  
; CURRENT FILING DATE: 2004-12-17  
; PRIOR APPLICATION NUMBER: 60/336,005  
; PRIOR FILING DATE: 2001-11-15

; NUMBER OF SEQ ID NOS: 7  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 4  
; LENGTH: 17  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Primer  
US-11-016-291-4

Query Match 0.9%; Score 14.4; DB 1; Length 17;  
Best Local Similarity 93.8%; Pred. No. 3e+02;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1508 CAGCCTCAGGCCCC 1523  
|||||  
Db 1 CAGCCTCAGGCCCC 16

RESULT 414

US-09-263-959-1251/c  
; Sequence 1251, Application US/09263959  
; Patent No. US20020150891A1  
; GENERAL INFORMATION:  
; APPLICANT: Hood, Leroy E.  
; APPLICANT: Rowen, Lee  
; APPLICANT: Koop, Ben F.  
; TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC COMPOSITIONS AND METHODS WHICH UTI  
; NUMBER OF SEQUENCES: 1279  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Seed and Berry LLP  
; STREET: 6300 Columbia Center, 701 Fifth Avenue  
; CITY: Seattle  
; STATE: Washington  
; COUNTRY: US  
; ZIP: 98104-7092  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA: US/09/263,959  
; APPLICATION NUMBER: US/09/263,959  
; FILING DATE: 05-MAR-1999  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: McMasters, David D.  
; REGISTRATION NUMBER: 33,963  
; REFERENCE/DOCKET NUMBER: 920010.426C2  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (206) 622-4900  
; TELEFAX: (206) 682-6031  
; INFORMATION FOR SEQ ID NO: 1251:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 18 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
US-09-263-959-1251

Query Match 0.9%; Score 14.4; DB 1; Length 18;  
Best Local Similarity 93.8%; Pred. No. 3.3e+02;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 634 TCACCCGGGAGCCCA 649  
|||||  
Db 17 TCACCCGGGAGCCCA 2

RESULT 415

US-10-108-260A-5102  
; Sequence 5102, Application US/10108260A  
; Publication No. US2004000560A1



```
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: NO. US20040005560A1e1 full length cDNA
; FILE REFERENCE: H1-A0106
; CURRENT APPLICATION NUMBER: US/10/108,260A
; CURRENT FILING DATE: 2002-03-27
; NUMBER OF SEQ ID NOS: 5458
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5102
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: an artificially synthesized R
US-10-108-260A-5102

Query Match          0.9%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 3.3e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1094 GTGGAAGATGCTCAAC 1109
Db 1 GTGGAAGATGCTCGAC 16

RESULT 416
US-10-758-451-884/c
; Sequence 884, Application US/10758451
; Publication No. US20050014711A1
; GENERAL INFORMATION:
; APPLICANT: East Carolina University
; TITLE OF INVENTION: COMPOSITION, FORMULATION & METHOD FOR PREVENTION & TREATMENT OF D
; TITLE OF INVENTION: AND CONDITIONS ASSOCIATED WITH BRONCHOCONSTRICTION, ALLERGY (IES)
; TITLE OF INVENTION: INFLAMMATION
; FILE REFERENCE: 30775-706.301
; CURRENT APPLICATION NUMBER: US/10/758,451
; CURRENT FILING DATE: 2004-01-14
; PRIOR APPLICATION NUMBER: 09/093,972
; PRIOR FILING DATE: 1998-06-09
; NUMBER OF SEQ ID NOS: 996
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 884
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-758-451-884

Query Match          0.9%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1532 CCAGCCTCTCCCG 1545
Db 14 CCAGCCTCTCCCG 1

RESULT 417
US-09-930-423-9
; Sequence 9, Application US/09930423
; Publication No. US20030092003A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Blatt, Larry
; APPLICANT: McSwiggen, Jim
; TITLE OF INVENTION: Method and Reagent for the Treatment of Alzheimer's Disease
; FILE REFERENCE: MBH00,918-A 400/027
; CURRENT APPLICATION NUMBER: US/09/930,423
; CURRENT FILING DATE: 2001-08-15
; NUMBER OF SEQ ID NOS: 4553
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 9
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo Sapiens
US-09-930-423-360
; Sequence 360, Application US/09930423
; Publication No. US20030092003A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Blatt, Larry
; APPLICANT: McSwiggen, Jim
; TITLE OF INVENTION: Method and Reagent for the Treatment of Alzheimer's Disease
; FILE REFERENCE: MBH00,918-A 400/027
; CURRENT APPLICATION NUMBER: US/09/930,423
; CURRENT FILING DATE: 2001-08-15
; NUMBER OF SEQ ID NOS: 4553
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 360
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo Sapiens
US-09-930-423-359
; Sequence 359, Application US/09930423
; Publication No. US20030092003A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Blatt, Larry
; APPLICANT: McSwiggen, Jim
; TITLE OF INVENTION: Method and Reagent for the Treatment of Alzheimer's Disease
; FILE REFERENCE: MBH00,918-A 400/027
; CURRENT APPLICATION NUMBER: US/09/930,423
; CURRENT FILING DATE: 2001-08-15
; NUMBER OF SEQ ID NOS: 4553
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 359
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo Sapiens
US-09-930-423-359

Query Match          0.9%; Score 14; DB 1; Length 17;
Best Local Similarity 85.7%; Pred. No. 3.2e+02;
Matches 12; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1531 CCAGCCTCTCCCG 1544
Db 1 CCAGCCUCUCCCC 14

RESULT 418
US-09-930-423-359
; Sequence 359, Application US/09930423
; Publication No. US20030092003A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Blatt, Larry
; APPLICANT: McSwiggen, Jim
; TITLE OF INVENTION: Method and Reagent for the Treatment of Alzheimer's Disease
; FILE REFERENCE: MBH00,918-A 400/027
; CURRENT APPLICATION NUMBER: US/09/930,423
; CURRENT FILING DATE: 2001-08-15
; NUMBER OF SEQ ID NOS: 4553
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 359
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo Sapiens
US-09-930-423-359

Query Match          0.9%; Score 14; DB 1; Length 17;
Best Local Similarity 85.7%; Pred. No. 3.2e+02;
Matches 12; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1531 CCAGCCTCTCCCG 1544
Db 3 CCAGCCUCUCCCC 16

RESULT 419
US-09-930-423-360
; Sequence 360, Application US/09930423
; Publication No. US20030092003A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Blatt, Larry
; APPLICANT: McSwiggen, Jim
; TITLE OF INVENTION: Method and Reagent for the Treatment of Alzheimer's Disease
; FILE REFERENCE: MBH00,918-A 400/027
; CURRENT APPLICATION NUMBER: US/09/930,423
; CURRENT FILING DATE: 2001-08-15
; NUMBER OF SEQ ID NOS: 4553
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 360
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo Sapiens
US-09-930-423-360

Query Match          0.9%; Score 14; DB 1; Length 17;
Best Local Similarity 85.7%; Pred. No. 3.2e+02;
Matches 12; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1531 CCAGCCTCTCCCG 1544
Db 2 CCAGCCUCUCCCC 15

RESULT 420
US-09-740-332-1541
; Sequence 1541, Application US/09740332
```

```

; Publication No. US20030125270A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals Inc.
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related to
; FILE REFERENCE: RPI 400/003
; CURRENT APPLICATION NUMBER: US/09/740,332
; CURRENT FILING DATE: 2001-03-26
; NUMBER OF SEQ ID NOS: 9704
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1541
; LENGTH: 17
; TYPE: RNA
; ORGANISM: artificial sequence
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION:
; OTHER INFORMATION: oligonucleotide substrate
;
US-09-740-332-1541

Query Match          0.9%; Score 14; DB 1; Length 17;
Best Local Similarity 71.4%; Pred.No.3.2e+02;
Matches 10; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy      766   TCCACGCCATGTTTC 779
Db      4      UCCACGCCAUGUUC 17

RESULT 421
US-09-745-237A-9
; Sequence 9, Application US/09745237A
; Publication No. US20030143708A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Blatt, Larry
; APPLICANT: McSwiggen, Jim
; TITLE OF INVENTION: Method and Reagent for the Treatment of Alzheimer's Disease
; FILE REFERENCE: 400/007 (MEHB00-918-A)
; CURRENT APPLICATION NUMBER: US/09/745,237A
; CURRENT FILING DATE: 2002-04-15
; NUMBER OF SEQ ID NOS: 4550
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 9
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
;
US-09-745-237A-9

Query Match          0.9%; Score 14; DB 1; Length 17;
Best Local Similarity 85.7%; Pred.No.3.2e+02;
Matches 12; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy      1531  CCCAGCCTCTCCCC 1544
Db      1      CCCAGCCUCCUCCCC 14

RESULT 422
US-09-745-237A-359
; Sequence 359, Application US/09745237A
; Publication No. US20030143708A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Blatt, Larry
; APPLICANT: McSwiggen, Jim
; TITLE OF INVENTION: Method and Reagent for the Treatment of Alzheimer's Disease
; FILE REFERENCE: 400/007 (MEHB00-918-A)
; CURRENT APPLICATION NUMBER: US/09/745,237A
; CURRENT FILING DATE: 2002-04-15
; NUMBER OF SEQ ID NOS: 4550
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 359
;

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RESULT 425  
US-10-307-005-955/c  
; Sequence 955, Application US/10307005  
; Publication No. US20030236208A1  
; GENERAL INFORMATION:  
; APPLICANT: University of Delaware  
; APPLICANT: Eric B. Kniel  
; APPLICANT: Howard B. Gamper  
; APPLICANT: Michael C. Rice  
; APPLICANT: Jungsup Kim  
; TITLE OF INVENTION: Targeted Chromosomal Genomic Alterations in Plants  
; FILE REFERENCE: Napro/009 PCT  
; CURRENT APPLICATION NUMBER: US/10/307,005  
; PRIOR APPLICATION NUMBER: PCT/US01/17672  
; PRIOR FILING DATE: 2002-11-26  
; PRIOR FILING DATE: 2001-06-01  
; PRIOR APPLICATION NUMBER: US 60/208,538  
; PRIOR FILING DATE: 2000-06-01  
; PRIOR APPLICATION NUMBER: US 60/244,989  
; PRIOR FILING DATE: 2000-10-30  
; PRIOR APPLICATION NUMBER: US 09/818,875  
; PRIOR FILING DATE: 2001-03-27  
; NUMBER OF SEQ ID NOS: 2717  
; SOFTWARE: Friedman macro Napro4  
; SEQ ID NO 955  
; LENGTH: 17  
; TYPE: DNA  
; ORGANISM: Eucalyptus camaldulensis  
US-10-307-005-955

Query Match 0.9%; Score 14; DB 1; Length 17;  
Best Local Similarity 100.0%; Pred. No. 3.2e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1202 GGTCCACCACGGTGG 1215  
Db 14 GGTCCACCACGGTGG 1

RESULT 426  
US-10-307-005-956  
; Sequence 956, Application US/10307005  
; Publication No. US20030236208A1  
; GENERAL INFORMATION:  
; APPLICANT: University of Delaware  
; APPLICANT: Eric B. Kniel  
; APPLICANT: Howard B. Gamper  
; APPLICANT: Michael C. Rice  
; APPLICANT: Jungsup Kim  
; TITLE OF INVENTION: Targeted Chromosomal Genomic Alterations in Plants  
; FILE REFERENCE: Napro/009 PCT  
; CURRENT APPLICATION NUMBER: US/10/307,005  
; PRIOR APPLICATION NUMBER: PCT/US01/17672  
; PRIOR FILING DATE: 2002-11-26  
; PRIOR FILING DATE: 2001-06-01  
; PRIOR APPLICATION NUMBER: US 60/208,538  
; PRIOR FILING DATE: 2000-06-01  
; PRIOR APPLICATION NUMBER: US 60/244,989  
; PRIOR FILING DATE: 2000-10-30  
; PRIOR APPLICATION NUMBER: US 09/818,875  
; PRIOR FILING DATE: 2001-03-27  
; NUMBER OF SEQ ID NOS: 2717  
; SOFTWARE: Friedman macro Napro4  
; SEQ ID NO 956  
; LENGTH: 17  
; TYPE: DNA  
; ORGANISM: Eucalyptus camaldulensis  
US-10-307-005-956

Query Match 0.9%; Score 14; DB 1; Length 17;  
Best Local Similarity 100.0%; Pred. No. 3.2e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1202 GGTCCACCACGGTGG 1215  
Db 4 GGTCCACCACGGTGG 17

RESULT 427  
US-10-669-841-4134  
; Sequence 4134, Application US/10669841  
; Publication No. US2004012746A1  
; GENERAL INFORMATION:  
; APPLICANT: Sirna Therapeutics, Inc.  
; APPLICANT: Lawrence, Blatt  
; APPLICANT: Dennis, Macejak  
; APPLICANT: James, McSwiggen  
; APPLICANT: David, Morrissey  
; APPLICANT: Pamela, Pavco  
; APPLICANT: Patrice, Lee  
; APPLICANT: Kenneth, Draper  
; APPLICANT: Elisabeth, Roberts  
; TITLE OF INVENTION: OLIGONUCLEOTIDE MEDIATED INHIBITION OF HEPATITIS B VIRUS AND HEPATITIS C VIRUS  
; FILE REFERENCE: 400/042US (MBH02-249-E)  
; CURRENT APPLICATION NUMBER: US/10/669,841  
; CURRENT FILING DATE: 2003-09-23  
; PRIOR APPLICATION NUMBER: PCT/US02/09187  
; PRIOR FILING DATE: 2002-03-26  
; PRIOR APPLICATION NUMBER: US 60/296,876  
; PRIOR FILING DATE: 2001-06-08  
; PRIOR APPLICATION NUMBER: US 60/335,059  
; PRIOR FILING DATE: 2001-10-24  
; PRIOR APPLICATION NUMBER: US 60/337,055  
; PRIOR FILING DATE: 2001-12-05  
; PRIOR APPLICATION NUMBER: US 60/358,580  
; PRIOR FILING DATE: 2002-02-20  
; PRIOR APPLICATION NUMBER: US 60/363,124  
; PRIOR FILING DATE: 2002-03-11  
; PRIOR APPLICATION NUMBER: US 09/817,879  
; PRIOR FILING DATE: 2001-03-26  
; PRIOR APPLICATION NUMBER: US 09/740,332  
; PRIOR FILING DATE: 2000-12-18  
; PRIOR APPLICATION NUMBER: US 09/611,931  
; PRIOR FILING DATE: 2000-07-07  
; PRIOR APPLICATION NUMBER: US 09/504,321  
; PRIOR FILING DATE: 2000-02-15  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 16207  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 4134  
; LENGTH: 17  
; TYPE: RNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION:  
; OTHER INFORMATION: oligonucleotide substrate  
US-10-669-841-4134

Query Match 0.9%; Score 14; DB 1; Length 17;  
Best Local Similarity 71.4%; Pred. No. 3.2e+02;  
Matches 10; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy 766 TCCACGCCATGTC 779  
Db 4 UCCACGCCAUGUUC 17

RESULT 428

RESULT 429  
US-09-866-108-2643/c  
; Sequence 2643, Application US/09866108  
; Patent No. US20020048800A1  
; GENERAL INFORMATION:  
; APPLICANT: GU, Yizhong  
; APPLICANT: JI, Yonggang  
; APPLICANT: PENN, Sharon G.  
; APPLICANT: HANZEL, David K.  
; APPLICANT: RANK, David R.  
; APPLICANT: CHEN, Wensheng

```

1  APPLICANT: SHANNON, Mark
2
3  TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
4
5  FILE REFERENCE: AEMICA-7
6
7  CURRENT APPLICATION NUMBER: US/09/866.108
8
9  CURRENT FILING DATE: 2001-05-25
10
11  PRIOR APPLICATION NUMBER: US 60/207,456
12
13  PRIOR FILING DATE: 2000-05-26
14
15  PRIOR APPLICATION NUMBER: GB 24263.6
16
17  PRIOR FILING DATE: 2000-10-04
18
19  PRIOR APPLICATION NUMBER: US 60/236,359
20

```

; PRIOR FILING DATE: 2000-09-27  
; PRIOR APPLICATION NUMBER: PCT/US01/00666  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00667  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00664  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00669  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00665  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00668  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00663  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00662  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00661  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00670  
; PRIOR FILING DATE: 2000-09-21  
; PRIOR APPLICATION NUMBER: US 60/234,687  
; PRIOR FILING DATE: 2000-09-21  
; PRIOR APPLICATION NUMBER: US 60/266,860  
; PRIOR FILING DATE: 2001-02-05  
; NUMBER OF SEQ ID NOS: 15752  
; SOFTWARE: Aecomica Sequence Listing Engine  
; SEQ ID NO 7355  
; LENGTH: 17  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-866-108-7355

Query Match 0.8%; Score 13.8; DB 1; Length 17;  
Best Local Similarity 88.2%; Pred. No. 3.3e+02;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 270 GAAGAAGCCCAAGAGAA 286  
DB 1 GAAGAGCCCGACAGAA 17  
|||||

## RESULT 431

US-09-866-108-7485/c  
; Sequence 7485, Application US/09866108  
; Patent No. US20020048800A1  
; GENERAL INFORMATION:  
; APPLICANT: GU, Yizhong  
; APPLICANT: JI, Yonggang  
; APPLICANT: PENN, Sharron G.  
; APPLICANT: HANZEL, David K.  
; APPLICANT: RANK, David R.  
; APPLICANT: CHEN, Wensheng  
; APPLICANT: SHANNON, Mark  
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE  
; FILE REFERENCE: AEOMICA-7  
; CURRENT APPLICATION NUMBER: US/09/866,108  
; CURRENT FILING DATE: 2001-05-25  
; PRIOR APPLICATION NUMBER: US 60/207,456  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: GB 24263.6  
; PRIOR FILING DATE: 2000-10-04  
; PRIOR APPLICATION NUMBER: US 60/236,359  
; PRIOR FILING DATE: 2000-09-27  
; PRIOR APPLICATION NUMBER: PCT/US01/00666  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00667  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00664  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00669  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00665  
; PRIOR FILING DATE: 2000-09-27  
; PRIOR APPLICATION NUMBER: PCT/US01/00666  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00667  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00664  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00669  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00665

; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00668  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00663  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00662  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00661  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00670  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: US 60/234,687  
; PRIOR FILING DATE: 2000-09-21  
; PRIOR APPLICATION NUMBER: US 60/266,860  
; PRIOR FILING DATE: 2001-02-05  
; NUMBER OF SEQ ID NOS: 15752  
; SOFTWARE: Aecomica Sequence Listing Engine  
; SEQ ID NO 7485  
; LENGTH: 17  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-866-108-7485

Query Match 0.8%; Score 13.8; DB 1; Length 17;  
Best Local Similarity 88.2%; Pred. No. 3.3e+02;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1530 GCCAGCCTCTCCCGC 1546  
DB 17 GTCCAGCCTCTCTCGC 1  
|||||

## RESULT 432

US-09-866-108-8568  
; Sequence 8568, Application US/09866108  
; Patent No. US20020048800A1  
; GENERAL INFORMATION:  
; APPLICANT: GU, Yizhong  
; APPLICANT: JI, Yonggang  
; APPLICANT: PENN, Sharron G.  
; APPLICANT: HANZEL, David K.  
; APPLICANT: RANK, David R.  
; APPLICANT: CHEN, Wensheng  
; APPLICANT: SHANNON, Mark  
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE  
; FILE REFERENCE: AEOMICA-7  
; CURRENT APPLICATION NUMBER: US/09/866,108  
; CURRENT FILING DATE: 2001-05-25  
; PRIOR APPLICATION NUMBER: US 60/207,456  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: GB 24263.6  
; PRIOR FILING DATE: 2000-10-04  
; PRIOR APPLICATION NUMBER: US 60/236,359  
; PRIOR FILING DATE: 2000-09-27  
; PRIOR APPLICATION NUMBER: PCT/US01/00666  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00667  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00664  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00669  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00665  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00668  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00663  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00662  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00661  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00670

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; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 60/266,860
; PRIOR FILING DATE: 2001-02-05
; NUMBER OF SEQ ID NOS: 15752
; SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 8568
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108-8568

```

Query Match 0.8%; Score 13.8; DB 1; Length 17;  
Best Local Similarity 88.2%; Pred. No. 3.3e+02;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 292 AGGATGCCCTAAATGAG 308  
Db 1 AGGATGACCTGAATGAG 17

```

RESULT 433
US-09-866-108-8660
; Sequence 8660, Application US/09866108
; Patent No. US20020048800A1
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOmica-7
; CURRENT APPLICATION NUMBER: US/09/866,108
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 60/266,860
; PRIOR FILING DATE: 2001-02-05
; NUMBER OF SEQ ID NOS: 15752
; SOFTWARE: AeoMica Sequence Listing Engine
; SEQ ID NO 8660
; LENGTH: 17
; TYPE: DNA

```

; ORGANISM: Homo sapiens  
US-09-866-108-8660

Query Match	0.8%	Score 13.8;	DB 1;	Length 17;
Best Local Similarity	88.2%	Pred. No. 3.3e+02;		
Matches 15;	Conservative	0;	Mismatches 2;	Indels 0; Gaps 0;

QY            267 CTAGAAGAGCCAAGAA 283  
               ||| ||||| |||||  
Db            1 CTGGAGGAGCCAAGAA 17

RESULT 434

US-09-866-108-8661  
; Sequence 8661, Application US/09866108  
; Patent No. US20020048800A1  
; GENERAL INFORMATION:  
; APPLICANT: GU, Yizhong  
; APPLICANT: JI, Yonggang  
; APPLICANT: PENN, Shaaron G.  
; APPLICANT: HANZEL, David K.  
; APPLICANT: RANK, David R.  
; APPLICANT: CHEN, Wensheng  
; APPLICANT: SHANNON, Mark  
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE  
; FILE REFERENCE: AEOmica-7  
; CURRENT APPLICATION NUMBER: US/09/866.108  
; CURRENT FILING DATE: 2001-05-25  
; PRIOR APPLICATION NUMBER: US 60/207,456  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: GB 24263.6  
; PRIOR FILING DATE: 2000-10-04  
; PRIOR APPLICATION NUMBER: US 60/236,359  
; PRIOR FILING DATE: 2000-09-27  
; PRIOR APPLICATION NUMBER: PCT/US01/00666  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00667  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00664  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00669  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00665  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00668  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00663  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00662  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00661  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00670  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: US 60/234,687  
; PRIOR FILING DATE: 2000-09-21  
; PRIOR APPLICATION NUMBER: US 60/266,860  
; PRIOR FILING DATE: 2001-02-05  
; NUMBER OF SEQ ID NOS: 15752  
; SOFTWARE: Aemica Sequence Listing Engine  
; SEQ ID NO 8661  
; LENGTH: 17  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-866-108-8661

```

Query Match      0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 3.3e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      268 TAGAAGAAGCCCAAGAAG 284
          | | | | | | | | | |
Db       1 TGGAGGAAGCCCAAGAAG 17
          | | | | | | | | | |

```

```

RESULT 435
US-09-866-108-8663
; Sequence 8663, Application US/09866108
; Patent No. US2002004800A1
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/006666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 60/266,860
; PRIOR FILING DATE: 2001-02-05
; NUMBER OF SEQ ID NOS: 15752
; SOFTWARE: Aeonica Sequence Listing Engine
; SEQ ID NO 8663
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108-8663

Query Match 0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. NO. 3.3e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps

QY 270 GAAGAAGCCCAAGAA 286
DB 1 GAGGAAGCCCAAGGA 17

RESULT 436
US-09-866-108-8664
; Sequence 8664, Application US/09866108
; Patent No. US2002004800A1
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: PENN, Sharron G.

```





; PRIOR APPLICATION NUMBER: PCT/US01/00661  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00670  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: US 60/234,687  
; PRIOR FILING DATE: 2000-09-21  
; PRIOR APPLICATION NUMBER: US 60/266,860  
; PRIOR FILING DATE: 2001-02-05  
; NUMBER OF SEQ ID NOS: 15752  
; SOFTWARE: Aecmica Sequence Listing Engine  
; SEQ ID NO 9689  
; LENGTH: 17  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-866-108-9689

Query Match 0.8%; Score 13.8; DB 1; Length 17;  
Best Local Similarity 88.2%; Pred. No. 3.3e+02;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 91 GGGAGAGTGGGCAGTCT 107  
Db 17 GGGAGAGTGGGCAGTCT 1

RESULT 440  
US-09-776-291A-4/c  
; Sequence 4, Application US/09776291A  
; Patent No. US20020123046A1  
; GENERAL INFORMATION:  
; APPLICANT: SMITH, Lloyd M.  
; APPLICANT: HOOD, Leroy E.  
; APPLICANT: HUNKAPILLER, Michael W.  
; APPLICANT: HUNKAPILLER, Tim J.  
; APPLICANT: CONNELL, Charles R.  
; TITLE OF INVENTION: AUTOMATED DNA SEQUENCING TECHNIQUE  
; FILE REFERENCE: 24313200106  
; CURRENT APPLICATION NUMBER: US/09/776,291A  
; CURRENT FILING DATE: 2001-02-02  
; PRIOR APPLICATION NUMBER: 08/484,340  
; PRIOR FILING DATE: 1995-06-07  
; PRIOR APPLICATION NUMBER: 08/361,176  
; PRIOR FILING DATE: 1994-12-21  
; PRIOR APPLICATION NUMBER: 07/898,019  
; PRIOR FILING DATE: 1992-06-12  
; PRIOR APPLICATION NUMBER: 07/660,160  
; PRIOR FILING DATE: 1991-02-21  
; PRIOR APPLICATION NUMBER: 07/106,232  
; PRIOR FILING DATE: 1987-10-07  
; PRIOR APPLICATION NUMBER: 06/722,742  
; PRIOR FILING DATE: 1985-04-11  
; PRIOR APPLICATION NUMBER: 06/689,013  
; PRIOR FILING DATE: 1985-01-02  
; PRIOR APPLICATION NUMBER: 06/570,973  
; PRIOR FILING DATE: 1984-01-16  
; NUMBER OF SEQ ID NOS: 7  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 4  
; LENGTH: 17  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: synthetic construct  
US-09-776-291A-4

Query Match 0.8%; Score 13.8; DB 1; Length 17;  
Best Local Similarity 88.2%; Pred. No. 3.3e+02;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1357 AAGCGCTGCAGATATC 1373  
Db 17 ATGCTCTGCAGGATATC 1

RESULT 441  
US-09-864-785-115  
; Sequence 115, Application US/09864785  
; Patent No. US20020177568A1  
; GENERAL INFORMATION:  
; APPLICANT: Ribozyme Pharmaceuticals, Inc.  
; APPLICANT: Stinchcomb, Dan  
; APPLICANT: Draper, Ken  
; APPLICANT: McSwiggen, Jim  
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Relate  
; FILE REFERENCE: 400/022 (MBHB00-812-D)  
; CURRENT APPLICATION NUMBER: US/09/864,785  
; CURRENT FILING DATE: 2001-05-23  
; NUMBER OF SEQ ID NOS: 3929  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 115  
; LENGTH: 17  
; TYPE: RNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid  
US-09-864-785-115

Query Match 0.8%; Score 13.8; DB 1; Length 17;  
Best Local Similarity 82.4%; Pred. No. 3.3e+02;  
Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 988 CCACCAACACCCCTCC 1004  
Db 1 CCAACACACCCCTCC 17

RESULT 442  
US-09-864-785-117  
; Sequence 117, Application US/09864785  
; Patent No. US20020177568A1  
; GENERAL INFORMATION:  
; APPLICANT: Ribozyme Pharmaceuticals, Inc.  
; APPLICANT: Stinchcomb, Dan  
; APPLICANT: Draper, Ken  
; APPLICANT: McSwiggen, Jim  
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Relate  
; FILE REFERENCE: 400/022 (MBHB00-812-D)  
; CURRENT APPLICATION NUMBER: US/09/864,785  
; CURRENT FILING DATE: 2001-05-23  
; NUMBER OF SEQ ID NOS: 3929  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 117  
; LENGTH: 17  
; TYPE: RNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid  
US-09-864-785-117

Query Match 0.8%; Score 13.8; DB 1; Length 17;  
Best Local Similarity 82.4%; Pred. No. 3.3e+02;  
Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 992 CAACACCCCTCCAGG 1008  
Db 1 CAACACCCCTCCAGG 17

RESULT 443  
US-09-864-785-213  
; Sequence 213, Application US/09864785  
; Patent No. US20020177568A1  
; GENERAL INFORMATION:  
; APPLICANT: Ribozyme Pharmaceuticals, Inc.

```
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Draper, Ken
; APPLICANT: McSwiggen, Jim
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related to
; TITLE OF INVENTION: Levels of NF-Kappa B
; FILE REFERENCE: 400/022 (MBHB00-812-D)
; CURRENT APPLICATION NUMBER: US/09/864,785
; CURRENT FILING DATE: 2001-05-23
; NUMBER OF SEQ ID NOS: 3929
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 213
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid
US-09-864-785-213

Query Match          0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 3.3e+02;
Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1501 CAGCCCCCAGCTCCAG 1517
Db 1 CAGACCCCGAGCCGCGAG 17

RESULT 444
US-09-864-785-215
; Sequence 215, Application US/09864785
; Patent No. US20020177568A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Draper, Ken
; APPLICANT: McSwiggen, Jim
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related to
; TITLE OF INVENTION: Levels of NF-Kappa B
; FILE REFERENCE: 400/022 (MBHB00-812-D)
; CURRENT APPLICATION NUMBER: US/09/864,785
; CURRENT FILING DATE: 2001-05-23
; NUMBER OF SEQ ID NOS: 3929
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 215
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid
US-09-864-785-215

Query Match          0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 3.3e+02;
Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1505 CCCCAGCTCCAGGCC 1521
Db 1 CCCCAGCCGCGAGGCUC 17

RESULT 445
US-09-864-785-336
; Sequence 336, Application US/09864785
; Patent No. US20020177568A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Draper, Ken
; APPLICANT: McSwiggen, Jim
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related to
; TITLE OF INVENTION: Levels of NF-Kappa B
; FILE REFERENCE: 400/022 (MBHB00-812-D)
; CURRENT APPLICATION NUMBER: US/09/864,785
```

```
; CURRENT FILING DATE: 2001-05-23
; NUMBER OF SEQ ID NOS: 3929
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 336
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid
US-09-864-785-336

Query Match          0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 3.3e+02;
Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1505 CCCCAGCTCCAGGCC 1521
Db 1 CCCCAGGCCGCGAGCCCC 17

RESULT 446
US-09-864-785-1519
; Sequence 1519, Application US/09864785
; Patent No. US20020177568A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Draper, Ken
; APPLICANT: McSwiggen, Jim
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related to
; TITLE OF INVENTION: Levels of NF-Kappa B
; FILE REFERENCE: 400/022 (MBHB00-812-D)
; CURRENT APPLICATION NUMBER: US/09/864,785
; CURRENT FILING DATE: 2001-05-23
; NUMBER OF SEQ ID NOS: 3929
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1519
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid
US-09-864-785-1519

Query Match          0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 3.3e+02;
Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1502 AGCCCCCAGCTCCAGG 1518
Db 1 AGACCCCGAGCCGCGAGG 17

RESULT 447
US-09-864-785-1520
; Sequence 1520, Application US/09864785
; Patent No. US20020177568A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Draper, Ken
; APPLICANT: McSwiggen, Jim
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related to
; TITLE OF INVENTION: Levels of NF-Kappa B
; FILE REFERENCE: 400/022 (MBHB00-812-D)
; CURRENT APPLICATION NUMBER: US/09/864,785
; CURRENT FILING DATE: 2001-05-23
; NUMBER OF SEQ ID NOS: 3929
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1520
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Artificial Sequence
```

```
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid
US-09-864-785-1520

Query Match          0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 3.3e+02;
Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1506 CCCAGCTCCAGGCC 1522
Db 1 CCCAGCCUAGGCCUCC 17

RESULT 448
US-09-864-785-2036
; Sequence 2036, Application US/09864785
; Patent No. US20020177568A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Draper, Ken
; APPLICANT: McSwiggen, Jim
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related to
; TITLE OF INVENTION: Levels of NF-kappa B
; FILE REFERENCE: 400/022 (MBHB00-812-D)
; CURRENT APPLICATION NUMBER: US/09/864,785
; CURRENT FILING DATE: 2001-05-23
; NUMBER OF SEQ ID NOS: 3929
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2036
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid
US-09-864-785-2036

Query Match          0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 3.3e+02;
Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 989 CACCAACACCCCTCCC 1005
Db 1 CACCAACACCCCUCC 17

RESULT 449
US-09-961-077-687/c
; Sequence 687, Application US/09961077
; Publication No. US20030014775A1
; GENERAL INFORMATION:
; APPLICANT: Zwick, Michael G.
; Edington, Brent E.
; McSwiggen, James A.
; Merlo, Patricia Ann Owens
; Guo, Lining
; Skokut, Thomas A.
; Young, Scott A.
; Folkerts, Otto
; Merlo, Donald J.
; TITLE OF INVENTION: COMPOSITION AND METHODS FOR
; MODULATION OF GENE EXPRESSION
; IN PLANTS
; NUMBER OF SEQUENCES: 1263
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
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; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/961,077
; FILING DATE: 21-Sep-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/679,645
; FILING DATE: July 12, 1996
; APPLICATION NUMBER: 60/001,135
; FILING DATE: July 13, 1995
; APPLICATION NUMBER: 08/300,726
; FILING DATE: September 2, 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 219/247
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 687:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 687:
US-09-961-077-687

Query Match          0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 3.3e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1213 TGGCTTCCACACTTCT 1229
Db 17 TGGCTGCCACACTTCT 1

RESULT 450
US-09-780-533A-1053/c
; Sequence 1053, Application US/09780533A
; Publication No. US20030060611A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Blatt, Larry
; APPLICANT: McSwiggen, Jim
; APPLICANT: Chowrira, Bharat
; APPLICANT: Haerberli, Pete
; TITLE OF INVENTION: Method and Reagent for the Inhibition of NOGO Gene
; FILE REFERENCE: MBHB00,878-A (400/011)
; CURRENT APPLICATION NUMBER: US/09/780,533A
; CURRENT FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: US 60/181,797
; PRIOR FILING DATE: 2000-02-11
; NUMBER OF SEQ ID NOS: 6679
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1053
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
; ORGANISM: Homo sapiens
US-09-780-533A-1053

Query Match          0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 3.3e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1622 AATAAACTGCTTTGTG 1638
Db 17 ATTAAAACTGCTTTTG 1
```

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RESULT 451
US-09-780-533A-1885/c
; Sequence 1885, Application US/09780533A
; Publication No. US20030060611A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Blatt, Larry
; APPLICANT: McSwiggen, Jim
; APPLICANT: Chowrira, Bharat
; APPLICANT: Haeblerli, Pete
; TITLE OF INVENTION: Method and Reagent for the Inhibition of NOGO Gene
; FILE REFERENCE: MBHB00,878-A (400/011)
; CURRENT APPLICATION NUMBER: US/09/780,533A
; CURRENT FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: US 60/181,797
; PRIOR FILING DATE: 2000-02-11
; NUMBER OF SEQ ID NOS: 6679
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1885
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-780-533A-1885

Query Match      0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 3.3e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1621 CAATAAACTGCTCTGT 1637
||| ||||| |||||
Db 17 CATTAAACTGCTCTTT 1

RESULT 452
US-09-093-972C-874/c
; Sequence 874, Application US/09093972C
; Publication No. US20030087845A1
; GENERAL INFORMATION:
; APPLICANT: Nyce, Jonathan W.
; TITLE OF INVENTION: COMPOSITION, FORMULATIONS & METHOD FOR PREVENTION
& TREATMENT OF DISEASES & CONDITIONS ASSOCIATED WITH
BRONCHOCONSTRICTION, ALLERGY (IES) & INFLAMMATION
; NUMBER OF SEQUENCES: 996
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: EPIGENESIS PHARMACEUTICALS, INC.
; STREET: 7 Clarke Drive
; CITY: Cranbury
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 08512
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/093,972C
; FILING DATE: 09-Jun-1998
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/472,527
; FILING DATE: 7-June-1995
; APPLICATION NUMBER: US 08/757,024
; FILING DATE: 26-11-1996
; APPLICATION NUMBER: US 08/472,527
; FILING DATE: 7-June-1995
; APPLICATION NUMBER: US 09/016,464
; FILING DATE: 30-January-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Amzel, Viviana
; REGISTRATION NUMBER: 30,930
; REFERENCE/DOCKET NUMBER: EPI-00672
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 609-409-3035
; TELEFAX: 413-254-9245
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 944:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear

RESULT 453
US-09-093-972C-944/c
; Sequence 944, Application US/09093972C
; Publication No. US20030087845A1
; GENERAL INFORMATION:
; APPLICANT: Nyce, Jonathan W.
; TITLE OF INVENTION: COMPOSITION, FORMULATIONS & METHOD FOR PREVENTION
& TREATMENT OF DISEASES & CONDITIONS ASSOCIATED WITH
BRONCHOCONSTRICTION, ALLERGY (IES) & INFLAMMATION
; NUMBER OF SEQUENCES: 996
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: EPIGENESIS PHARMACEUTICALS, INC.
; STREET: 7 Clarke Drive
; CITY: Cranbury
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 08512
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/093,972C
; FILING DATE: 09-Jun-1998
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/472,527
; FILING DATE: 7-June-1995
; APPLICATION NUMBER: US 08/757,024
; FILING DATE: 26-11-1996
; APPLICATION NUMBER: US 08/472,527
; FILING DATE: 7-June-1995
; APPLICATION NUMBER: US 09/016,464
; FILING DATE: 30-January-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Amzel, Viviana
; REGISTRATION NUMBER: 30,930
; REFERENCE/DOCKET NUMBER: EPI-00672
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 609-409-3035
; TELEFAX: 413-254-9245
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 944:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
```

[illegible]

```

; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related
; TITLE OF INVENTION: Hepatitis C Virus Infection
; FILE REFERENCE: RPI 400/003
; CURRENT APPLICATION NUMBER: US/09/740,332
; CURRENT FILING DATE: 2001-03-26
; NUMBER OF SEQ ID NOS: 9704
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3012
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
; NAME/KEY: misc_feature
; FEATURE:
; LOCATION:
; OTHER INFORMATION: oligonucleotide substrate
US-09-740-332-3012

Query Match      0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 3.3e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      769  AGCCCATGTTCCAGCCC 785
Db      17   AGCCCATGTTCCGCTC 1

RESULT 459
US-09-792-818-440/c
; Sequence 440, Application US/09792818
; Publication No. US20030134806A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Jarvis, Thale
; APPLICANT: Von Carlowitz, Ira
; APPLICANT: McSwiggen, Jim
; APPLICANT: Hamblin, Paul
; APPLICANT: Ellis, Jonathan
; TITLE OF INVENTION: Method and Reagent for the Inhibition of Grb-2-related with Inse
; TITLE OF INVENTION: (GRD) Gens
; FILE REFERENCE: MBH00-901-A (400/013)
; CURRENT APPLICATION NUMBER: US/09/792,818
; CURRENT FILING DATE: 2001-02-23
; NUMBER OF SEQ ID NOS: 2304
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 440
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-792-818-440

Query Match      0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 3.3e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1539  CTCCCCGCTCTGGATCC 1555
Db      17   CTCCCCGCTGTGGAACC 1

RESULT 460
US-09-745-237A-57/c
; Sequence 57, Application US/09745237A
; Publication No. US20030143708A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Blatt, Larry
; APPLICANT: McSwiggen, Jim
; TITLE OF INVENTION: Method and Reagent for the Treatment of Alzheimer's Disease
; FILE REFERENCE: 400/007 (MBH00-918-A)
; CURRENT APPLICATION NUMBER: US/09/745,237A
; CURRENT FILING DATE: 2002-04-15
; NUMBER OF SEQ ID NOS: 4550
; SOFTWARE: PatentIn version 3.0

```

```

; SEQ ID NO 57
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-745-237A-57

Query Match      0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 3.3e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      643  AGCCCCAGGATACCTAC 659
Db      17   AGCCCCAGGATGCCTTC 1

RESULT 461
US-09-817-879-632
; Sequence 632, Application US/09817879
; Publication No. US20030171311A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals Inc.
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related
; FILE REFERENCE: MBH00-801-F
; CURRENT APPLICATION NUMBER: US/09/817,879
; CURRENT FILING DATE: 2001-03-26
; NUMBER OF SEQ ID NOS: 9703
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 632
; LENGTH: 17
; TYPE: RNA
; ORGANISM: artificial sequence
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION:
; OTHER INFORMATION: oligonucleotide substrate
US-09-817-879-632

Query Match      0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 47.1%; Pred. No. 3.3e+02;
Matches 8; Conservative 7; Mismatches 2; Indels 0; Gaps 0;

QY      1400  TGTGGATGTTGCTTTTG 1416
Db      1   UGUGGAUGAUGCUGUUG 17

RESULT 462
US-09-817-879-2161
; Sequence 2161, Application US/09817879
; Publication No. US20030171311A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals Inc.
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related
; FILE REFERENCE: MBH00-801-F
; CURRENT APPLICATION NUMBER: US/09/817,879
; CURRENT FILING DATE: 2001-03-26
; NUMBER OF SEQ ID NOS: 9703
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2161
; LENGTH: 17
; TYPE: RNA
; ORGANISM: artificial sequence
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION:
; OTHER INFORMATION: oligonucleotide substrate
US-09-817-879-2161

Query Match      0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 52.9%; Pred. No. 3.3e+02;
Matches 9; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

```

```
Qy 689 GAGGCTCACTTCTTCT 705
Db 1 GAUGACUCACUUCUUCU 17

RESULT 463
US-09-817-879-3012/c
; Sequence 3012, Application US/09817879
; Publication No. US20030171311A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals Inc.
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related to Hepatitis C Virus Infection
; FILE REFERENCE: MHB00-801-F
; CURRENT APPLICATION NUMBER: US/09/817,879
; CURRENT FILING DATE: 2001-03-26
; NUMBER OF SEQ ID NOS: 9703
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3012
; LENGTH: 17
; TYPE: RNA
; ORGANISM: artificial sequence
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION:
; OTHER INFORMATION: oligonucleotide substrate
US-09-817-879-3012

Query Match 0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 3.3e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 769 AGCCATGTTCCAGCCC 785
Db 17 AGCCATGTTCCGGGTC 1

RESULT 464
US-10-079-625-25
; Sequence 25, Application US/10079625
; Publication No. US20020182676A1
; GENERAL INFORMATION:
; APPLICANT: Tartaglia, Louis A.
; APPLICANT: Tepper, Robert I.
; APPLICANT: Culpepper, Janice A.
; APPLICANT: White, David W.
; TITLE OF INVENTION: THE OB RECEPTOR AND METHODS FOR THE OB RECEPTOR AND METHODS FOR
; TITLE OF INVENTION: THE DIAGNOSIS AND TREATMENT OF BODY WEIGHT DISORDERS,
; TITLE OF INVENTION: INCLUDING OBESITY AND CACHEXIA
; NUMBER OF SEQUENCES: 50
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/079,625
; FILING DATE: 2002-FEB-19
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/864,564
; FILING DATE: 28-MAY-1997
; APPLICATION NUMBER: 08/708,123
; FILING DATE: 03-SEP-1996
; APPLICATION NUMBER: 08/638,524
; FILING DATE: 26-APR-1996

Qy 689 GAGGCTCACTTCTTCT 705
Db 1 GAUGACUCACUUCUUCU 17

RESULT 465
US-10-079-625-27
; Sequence 27, Application US/10079625
; Publication No. US20020182676A1
; GENERAL INFORMATION:
; APPLICANT: Tartaglia, Louis A.
; APPLICANT: Tepper, Robert I.
; APPLICANT: Culpepper, Janice A.
; APPLICANT: White, David W.
; TITLE OF INVENTION: THE OB RECEPTOR AND METHODS FOR THE OB RECEPTOR AND METHODS FOR
; TITLE OF INVENTION: THE DIAGNOSIS AND TREATMENT OF BODY WEIGHT DISORDERS,
; TITLE OF INVENTION: INCLUDING OBESITY AND CACHEXIA
; NUMBER OF SEQUENCES: 50
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/079,625
; FILING DATE: 2002-FEB-19
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/864,564
; FILING DATE: 28-MAY-1997
; APPLICATION NUMBER: 08/708,123
; FILING DATE: 03-SEP-1996
; APPLICATION NUMBER: 08/638,524
; FILING DATE: 26-APR-1996

Qy 660 CACTACCTGCCTTCAG 676
Db 1 CACTATTTGCCTTCAG 17

RESULT 466
US-10-079-625-25
; Sequence 25, Application US/10079625
; Publication No. US20020182676A1
; GENERAL INFORMATION:
; APPLICANT: Tartaglia, Louis A.
; APPLICANT: Tepper, Robert I.
; APPLICANT: Culpepper, Janice A.
; APPLICANT: White, David W.
; TITLE OF INVENTION: THE OB RECEPTOR AND METHODS FOR THE OB RECEPTOR AND METHODS FOR
; TITLE OF INVENTION: THE DIAGNOSIS AND TREATMENT OF BODY WEIGHT DISORDERS,
; TITLE OF INVENTION: INCLUDING OBESITY AND CACHEXIA
; NUMBER OF SEQUENCES: 50
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/079,625
; FILING DATE: 2002-FEB-19
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/864,564
; FILING DATE: 28-MAY-1997
; APPLICATION NUMBER: 08/708,123
; FILING DATE: 03-SEP-1996
; APPLICATION NUMBER: 08/638,524
; FILING DATE: 26-APR-1996
```

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; APPLICATION NUMBER: 08/599,455
; FILING DATE: 22-JAN-1996
; APPLICATION NUMBER: 08/583,153
; FILING DATE: 28-DEC-1995
; APPLICATION NUMBER: 08/570,142
; FILING DATE: 11-DEC-1995
; APPLICATION NUMBER: 08/569,485
; FILING DATE: 08-DEC-1995
; APPLICATION NUMBER: 08/566,622
; FILING DATE: 04-DEC-1995
; APPLICATION NUMBER: 08/562,663
; FILING DATE: 27-NOV-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Meiklejohn, Ph.D., Anita L.
; REGISTRATION NUMBER: 35,283
; REFERENCE/DOCKET NUMBER: 07334/019002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-542-5070
; TELEFAX: 617-542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 27:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-10-079-625-27

Query Match          0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 3.3e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 660 CACTACCTGCCCTTCAG 676
DB 1 CACTATTGCCCTTCAG 17

RESULT 466
US-10-060-756A-748
; Sequence 748, Application US/10060756A
; Publication No. US20030046717A1
; GENERAL INFORMATION:
; APPLICANT: Zhang, Jian
; TITLE OF INVENTION: HUMAN TESTIS EXPRESSED PATCHED LIKE PROTEIN
; FILE REFERENCE: PB0177
; CURRENT APPLICATION NUMBER: US/10/060,756A
; CURRENT FILING DATE: 2002-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/327,898
; PRIOR FILING DATE: 2001-10-09
; NUMBER OF SEQ ID NOS: 4804
; SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 748
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-060-756A-748

Query Match          0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 3.3e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 660 CACTACCTGCCCTTCAG 676
DB 1 CACTATTGCCCTTCAG 17

RESULT 466
US-10-060-756A-748
; Sequence 748, Application US/10060756A
; Publication No. US20030046717A1
; GENERAL INFORMATION:
; APPLICANT: Zhang, Jian
; TITLE OF INVENTION: HUMAN TESTIS EXPRESSED PATCHED LIKE PROTEIN
; FILE REFERENCE: PB0177
; CURRENT APPLICATION NUMBER: US/10/060,756A
; CURRENT FILING DATE: 2002-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/327,898
; PRIOR FILING DATE: 2001-10-09
; NUMBER OF SEQ ID NOS: 4804
; SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 748
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-060-756A-748

Query Match          0.8%; Score 13.8; DB 1; Length 17;
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Best Local Similarity 88.2%; Pred. No. 3.3e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 521 CATCGACTCCCTGCTGG 537
DB 1 CAGCGACTCACTGCTGG 17

RESULT 467
US-10-060-756A-749
; Sequence 749, Application US/10060756A
; Publication No. US20030046717A1
; GENERAL INFORMATION:
; APPLICANT: Zhang, Jian
; TITLE OF INVENTION: HUMAN TESTIS EXPRESSED PATCHED LIKE PROTEIN
; FILE REFERENCE: PB0177
; CURRENT APPLICATION NUMBER: US/10/060,756A
; CURRENT FILING DATE: 2002-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/327,898
; PRIOR FILING DATE: 2001-10-09
; NUMBER OF SEQ ID NOS: 4804
; SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 749
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-060-756A-749

Query Match          0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 3.3e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 522 ATCGACTCCCTGCTGGA 538
DB 1 AGCGACTCACTGCTGGA 17

RESULT 468
US-10-060-756A-1238
; Sequence 1238, Application US/10060756A
; Publication No. US20030046717A1
; GENERAL INFORMATION:
; APPLICANT: Zhang, Jian
; TITLE OF INVENTION: HUMAN TESTIS EXPRESSED PATCHED LIKE PROTEIN
; FILE REFERENCE: PB0177
; CURRENT APPLICATION NUMBER: US/10/060,756A
; CURRENT FILING DATE: 2002-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
```



Query Match 0.8%; Score 13.8; DB 1; Length 17;  
Best Local Similarity 58.8%; Pred. No. 3.3e+02;  
Matches 10; Conservative 5; Mismatches 2; Indels

Qy 1117 CCTTCTGGAGCAGCTG 1133

Db 1 CCCUCCUGGAGCAGCUG 17

## RESULT 473

US-10-138-674-3543  
; Sequence 3543, Application US/10138674  
; Publication No. US20040077565A1  
; GENERAL INFORMATION: Ribozyme Pharmaceuticals, Inc.  
; APPLICANT: Pavco, Pam  
; APPLICANT: McSwiggen, Jim  
; APPLICANT: Stinchcomb, Dan  
; APPLICANT: Escobedo, Jaime  
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re  
; FILE REFERENCE: MBHB00-876-N (400/049)  
; CURRENT APPLICATION NUMBER: US/10/138,674  
; CURRENT FILING DATE: 2002-05-03  
; NUMBER OF SEQ ID NOS: 20822  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 3543  
; LENGTH: 17  
; TYPE: RNA  
; ORGANISM: Mus musculus  
US-10-138-674-3543

Query Match 0.8%; Score 13.8; DB 1; Length 17;  
Best Local Similarity 64.7%; Pred. No. 3.3e+02;  
Matches 11; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1112 CTCCTCTGCTGGAGC 1128

Db 1 CUCCCCUUGCUGAGC 17

## RESULT 474

US-10-138-674-4182  
; Sequence 4182, Application US/10138674  
; Publication No. US20040077565A1  
; GENERAL INFORMATION: Ribozyme Pharmaceuticals, Inc.  
; APPLICANT: Pavco, Pam  
; APPLICANT: McSwiggen, Jim  
; APPLICANT: Stinchcomb, Dan  
; APPLICANT: Escobedo, Jaime  
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re  
; FILE REFERENCE: MBHB00-876-N (400/049)  
; CURRENT APPLICATION NUMBER: US/10/138,674  
; CURRENT FILING DATE: 2002-05-03  
; NUMBER OF SEQ ID NOS: 20822  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 4182  
; LENGTH: 17  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-10-138-674-4182

Query Match 0.8%; Score 13.8; DB 1; Length 17;  
Best Local Similarity 70.6%; Pred. No. 3.3e+02;  
Matches 12; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1115 CTCCTGCTGGAGCAGC 1131

Db 1 CUCCUGGCGUGAGCCGC 17

## RESULT 475

US-10-287-949A-3543  
; Sequence 3543, Application US/10287949A  
; Publication No. US20040102389A1  
; GENERAL INFORMATION: Ribozyme Pharmaceuticals, Inc.  
; APPLICANT: Pavco, Pam  
; APPLICANT: McSwiggen, Jim  
; APPLICANT: Stinchcomb, Dan  
; APPLICANT: Escobedo, Jaime  
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re  
; FILE REFERENCE: MBHB00-876-N (400/049)  
; CURRENT APPLICATION NUMBER: US/10/287,949A  
; CURRENT FILING DATE: 2003-04-11  
; NUMBER OF SEQ ID NOS: 20822  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 3543  
; LENGTH: 17  
; TYPE: RNA  
; ORGANISM: Mus musculus  
US-10-287-949A-3543

Query Match 0.8%; Score 13.8; DB 1; Length 17;  
Best Local Similarity 64.7%; Pred. No. 3.3e+02;  
Matches 11; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1112 CTCCTCTGCTGGAGC 1128

Db 1 CUCCCCUUGCUGAGC 17

## RESULT 476

US-10-287-949A-4182  
; Sequence 4182, Application US/10287949A  
; Publication No. US20040102389A1  
; GENERAL INFORMATION: Ribozyme Pharmaceuticals, Inc.  
; APPLICANT: Pavco, Pam  
; APPLICANT: McSwiggen, Jim  
; APPLICANT: Stinchcomb, Dan  
; APPLICANT: Escobedo, Jaime  
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re  
; FILE REFERENCE: MBHB00-876-N (400/049)  
; CURRENT APPLICATION NUMBER: US/10/287,949A  
; CURRENT FILING DATE: 2003-04-11  
; NUMBER OF SEQ ID NOS: 20822  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 4182  
; LENGTH: 17  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-10-287-949A-4182

Query Match 0.8%; Score 13.8; DB 1; Length 17;  
Best Local Similarity 70.6%; Pred. No. 3.3e+02;  
Matches 12; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1115 CTCCTGCTGGAGCAGC 1131

Db 1 CUCCUGGCGUGAGCCGC 17

## RESULT 477

US-10-712-672-564/C  
; Sequence 564, Application US/10712672  
; Publication No. US20040102413A1  
; GENERAL INFORMATION: Ribozyme Pharmaceuticals, Inc.  
; APPLICANT: Chowrira, Bharat  
; APPLICANT: McSwiggen, Jim  
; APPLICANT: Stinchcomb, Dan  
; TITLE OF INVENTION: Method and Reagent for the Inhibition of Telomerase Enzyme  
; FILE REFERENCE: MBHB00-882-C (400/019)  
; CURRENT APPLICATION NUMBER: US/10/712,672  
; CURRENT FILING DATE: 2003-11-13  
; PRIOR APPLICATION NUMBER: US/09/653,225  
; PRIOR FILING DATE: 2000-08-31

; PRIOR APPLICATION NUMBER: 60/197,769  
; PRIOR FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/150,713  
; PRIOR FILING DATE: 1999-08-31  
; NUMBER OF SEQ ID NOS: 5586  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 564  
; LENGTH: 17  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-10-712-672-564

Query Match 0.8%; Score 13.8; DB 1; Length 17;  
Best Local Similarity 88.2%; Pred. No. 3.3e+02;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 101 GCAGGTCCTGGGGACC 117  
Db 17 GCAGGCCACGGGGACC 1

## RESULT 478

US-10-712-672-1193  
; Sequence 1193, Application US/10712672  
; Publication No. US20040102413A1  
; GENERAL INFORMATION:  
; APPLICANT: Ribozyme Pharmaceuticals, Inc.  
; APPLICANT: Chowrira, Bharat  
; APPLICANT: McSwiggen, Jim  
; APPLICANT: Stinchcomb, Dan

; TITLE OF INVENTION: Method and Reagent for the Inhibition of Telomerase Enzyme  
; FILE REFERENCE: MBH00-882-C (400/019)  
; CURRENT APPLICATION NUMBER: US/10712,672  
; CURRENT FILING DATE: 2003-11-13  
; PRIOR APPLICATION NUMBER: US/09/653,225  
; PRIOR FILING DATE: 2000-08-31  
; PRIOR APPLICATION NUMBER: 60/197,769  
; PRIOR FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/150,713  
; PRIOR FILING DATE: 1999-08-31  
; NUMBER OF SEQ ID NOS: 5586  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 1193  
; LENGTH: 17  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-10-712-672-1193

Query Match 0.8%; Score 13.8; DB 1; Length 17;  
Best Local Similarity 70.6%; Pred. No. 3.3e+02;  
Matches 12; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 1321 GGAGGACCCCTAATTT 1337  
Db 1 GGAAGACCCCAUAUU 17

## RESULT 479

US-10-669-841-3225  
; Sequence 3225, Application US/10669841  
; Publication No. US20040127446A1  
; GENERAL INFORMATION:  
; APPLICANT: Sirna Therapeutics, Inc.  
; APPLICANT: Lawrence, Blatt  
; APPLICANT: Dennis, Macejak  
; APPLICANT: James, McSwiggen  
; APPLICANT: David, Morrissey  
; APPLICANT: Pamela, Pavco  
; APPLICANT: Patrice, Lee  
; APPLICANT: Kenneth, Draper  
; APPLICANT: Elisabeth, Roberts

; TITLE OF INVENTION: OLIGONUCLEOTIDE MEDIATED INHIBITION OF HEPATITIS B VIRUS AND HEP  
; FILE REFERENCE: 400/042US (MBH02-249-E)  
; CURRENT APPLICATION NUMBER: US/10/669,841  
; CURRENT FILING DATE: 2003-09-23  
; PRIOR APPLICATION NUMBER: PCT/US02/09187  
; PRIOR FILING DATE: 2002-03-26  
; PRIOR APPLICATION NUMBER: US 60/296,876  
; PRIOR FILING DATE: 2001-06-08  
; PRIOR APPLICATION NUMBER: US 60/335,059  
; PRIOR FILING DATE: 2001-10-24  
; PRIOR APPLICATION NUMBER: US 60/337,055

; FILE REFERENCE: 400/042US (MBH02-249-E)  
; CURRENT APPLICATION NUMBER: US/10/669,841  
; CURRENT FILING DATE: 2003-09-23  
; PRIOR APPLICATION NUMBER: PCT/US02/09187  
; PRIOR FILING DATE: 2002-03-26  
; PRIOR APPLICATION NUMBER: US 60/296,876  
; PRIOR FILING DATE: 2001-06-08  
; PRIOR APPLICATION NUMBER: US 60/335,059  
; PRIOR FILING DATE: 2001-10-24  
; PRIOR APPLICATION NUMBER: US 60/337,055  
; PRIOR FILING DATE: 2001-12-05  
; PRIOR APPLICATION NUMBER: US 60/358,580  
; PRIOR FILING DATE: 2002-02-20  
; PRIOR APPLICATION NUMBER: US 60/363,134  
; PRIOR FILING DATE: 2002-03-11  
; PRIOR APPLICATION NUMBER: US 09/817,879  
; PRIOR FILING DATE: 2001-03-26  
; PRIOR APPLICATION NUMBER: US 09/740,332  
; PRIOR FILING DATE: 2000-12-18  
; PRIOR APPLICATION NUMBER: US 09/611,931  
; PRIOR FILING DATE: 2000-07-07  
; PRIOR APPLICATION NUMBER: US 09/504,321  
; PRIOR FILING DATE: 2000-02-15  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 16207  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 3225  
; LENGTH: 17  
; TYPE: RNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION:  
; OTHER INFORMATION: oligonucleotide substrate  
US-10-669-841-3225

Query Match 0.8%; Score 13.8; DB 1; Length 17;  
Best Local Similarity 47.1%; Pred. No. 3.3e+02;  
Matches 8; Conservative 7; Mismatches 2; Indels 0; Gaps 0;

Qy 1400 TGTGGATGTGCTTTTG 1416  
Db 1 UGUGGAUGAUGCUGUG 17

## RESULT 480

US-10-669-841-4754  
; Sequence 4754, Application US/10669841  
; Publication No. US20040127446A1  
; GENERAL INFORMATION:  
; APPLICANT: Sirna Therapeutics, Inc.  
; APPLICANT: Lawrence, Blatt  
; APPLICANT: Dennis, Macejak  
; APPLICANT: James, McSwiggen  
; APPLICANT: David, Morrissey  
; APPLICANT: Pamela, Pavco  
; APPLICANT: Patrice, Lee  
; APPLICANT: Kenneth, Draper  
; APPLICANT: Elisabeth, Roberts

; TITLE OF INVENTION: OLIGONUCLEOTIDE MEDIATED INHIBITION OF HEPATITIS B VIRUS AND HEP  
; FILE REFERENCE: 400/042US (MBH02-249-E)  
; CURRENT APPLICATION NUMBER: US/10/669,841  
; CURRENT FILING DATE: 2003-09-23  
; PRIOR APPLICATION NUMBER: PCT/US02/09187  
; PRIOR FILING DATE: 2002-03-26  
; PRIOR APPLICATION NUMBER: US 60/296,876  
; PRIOR FILING DATE: 2001-06-08  
; PRIOR APPLICATION NUMBER: US 60/335,059  
; PRIOR FILING DATE: 2001-10-24  
; PRIOR APPLICATION NUMBER: US 60/337,055

; PRIOR FILING DATE: 2001-12-05  
; PRIOR APPLICATION NUMBER: US 60/358,580  
; PRIOR FILING DATE: 2002-02-20  
; PRIOR APPLICATION NUMBER: US 60/363,124  
; PRIOR FILING DATE: 2002-03-11  
; PRIOR APPLICATION NUMBER: US 09/817,879  
; PRIOR FILING DATE: 2001-03-26  
; PRIOR APPLICATION NUMBER: US 09/740,332  
; PRIOR FILING DATE: 2000-12-18  
; PRIOR APPLICATION NUMBER: US 09/611,931  
; PRIOR FILING DATE: 2000-07-07  
; PRIOR APPLICATION NUMBER: US 09/504,321  
; PRIOR FILING DATE: 2000-02-15  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 16207  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 4754  
; LENGTH: 17  
; TYPE: RNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION:  
; OTHER INFORMATION: oligonucleotide substrate  
US-10-669-841-4754

Query Match 0.8%; Score 13.8; DB 1; Length 17;  
Best Local Similarity 52.9%; Pred. No. 3.3e+02;  
Matches 9; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

Qy 689 GAGGCGCTCACTCTCT 705  
Db 1 GAUGACUCACUUCUCU 17  
|||||:|:|:|

RESULT 481  
US-10-669-841-5605/c  
; Sequence 5605, Application US/10669841  
; Publication No. US20040127446A1  
; GENERAL INFORMATION:  
; APPLICANT: Sirna Therapeutics, Inc.  
; APPLICANT: Lawrence, Blatt  
; APPLICANT: Dennis, Macsjak  
; APPLICANT: James, McSwiggen  
; APPLICANT: David, Morrissey  
; APPLICANT: Pamela, Pavco  
; APPLICANT: Patricia, Lee  
; APPLICANT: Kenneth, Draper  
; APPLICANT: Elisabeth, Roberts  
; TITLE OF INVENTION: OLIGONUCLEOTIDE MEDIATED INHIBITION OF HEPATITIS B VIRUS AND HEPATITIS C VIRUS  
; FILE REFERENCE: 400/042US (MEHB02-249-E)  
; CURRENT APPLICATION NUMBER: US/10/669,841  
; CURRENT FILING DATE: 2003-09-23  
; PRIOR APPLICATION NUMBER: PCT/US02/09187  
; PRIOR FILING DATE: 2002-03-26  
; PRIOR APPLICATION NUMBER: US 60/296,876  
; PRIOR FILING DATE: 2001-06-08  
; PRIOR APPLICATION NUMBER: US 60/335,059  
; PRIOR FILING DATE: 2001-10-24  
; PRIOR APPLICATION NUMBER: US 60/337,055  
; PRIOR FILING DATE: 2001-12-05  
; PRIOR APPLICATION NUMBER: US 60/358,580  
; PRIOR FILING DATE: 2002-02-20  
; PRIOR APPLICATION NUMBER: US 60/363,124  
; PRIOR FILING DATE: 2002-03-11  
; PRIOR APPLICATION NUMBER: US 09/817,879  
; PRIOR FILING DATE: 2001-03-26  
; PRIOR APPLICATION NUMBER: US 09/740,332  
; PRIOR FILING DATE: 2000-12-18  
; PRIOR APPLICATION NUMBER: US 09/611,931

; PRIOR FILING DATE: 2000-07-07  
; PRIOR APPLICATION NUMBER: US 09/504,321  
; PRIOR FILING DATE: 2000-02-15  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 16207  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 5605  
; LENGTH: 17  
; TYPE: RNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION:  
; OTHER INFORMATION: oligonucleotide substrate  
US-10-669-841-5605

Query Match 0.8%; Score 13.8; DB 1; Length 17;  
Best Local Similarity 88.2%; Pred. No. 3.3e+02;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 769 AGCCCATGTTCCAGCCC 785  
Db 17 AGCCCATGTTCCGGCTC 1  
|||||:|:|:|

RESULT 482  
US-10-723-361-1895/c  
; Sequence 1895, Application US/10723361  
; Publication No. US20040137589A1  
; GENERAL INFORMATION:  
; APPLICANT: GU, Yizhong  
; APPLICANT: JI, Yonggang  
; APPLICANT: PENN, Sharron G.  
; APPLICANT: HANZEL, David K.  
; APPLICANT: RANK, David R.  
; APPLICANT: CHEN, Wensheng  
; APPLICANT: SHANNON, Mark  
; TITLE OF INVENTION: HUMAN MYOSIN-LIKE POLYPEPTIDE EXPRESSED PREDOMINANTLY IN HEART AN  
; FILE REFERENCE: PB0105  
; CURRENT APPLICATION NUMBER: US/10/723,361  
; CURRENT FILING DATE: 2003-11-26  
; PRIOR APPLICATION NUMBER: US 09/866,108  
; PRIOR FILING DATE: 2001-05-25  
; PRIOR APPLICATION NUMBER: US 60/207,456  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: GB 24263.6  
; PRIOR FILING DATE: 2000-10-04  
; PRIOR APPLICATION NUMBER: US 60/236,359  
; PRIOR FILING DATE: 2000-09-27  
; PRIOR APPLICATION NUMBER: PCT/US01/00666  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00667  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00664  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00669  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00665  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00668  
; PRIOR FILING DATE: 2001-01-30  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 15755  
; SOFTWARE: Aecomica Sequence Listing Engine  
; SEQ ID NO 1895  
; LENGTH: 17  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-723-361-1895

Query Match 0.8%; Score 13.8; DB 1; Length 17;

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Best Local Similarity 88.2%; Pred. No. 3.3e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 93 GAGAGTGGCGAGGTCTCT 109
   ||||| |||||
Db 17 GAGAGAGCCGAGGTCTCT 1

RESULT 483
US-10-723-361-2643/c
; Sequence 2643, Application US/10723361
; Publication No. US20040137589A1
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: HUMAN MYOSIN-LIKE POLYPEPTIDE EXPRESSED PREDOMINANTLY IN HEART AN
; FILE REFERENCE: PB0105
; CURRENT APPLICATION NUMBER: US/10/723,361
; CURRENT FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: US 09/866,108
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aeonica Sequence Listing Engine
; SEQ ID NO 2643
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-723-361-2643

Query Match 0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 3.3e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 845 CTTCCAGCACCCGCCAA 861
   ||||| |||||
Db 17 CTGCCAGGACCCGCCAA 1

RESULT 484
US-10-723-361-7355
; Sequence 7355, Application US/10723361
; Publication No. US20040137589A1
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng

```

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; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Acomica Sequence Listing Engine
; SEQ ID NO 7485
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-723-361-7485

Query Match      0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 3.3e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1530 GCCAGCCTCTCCCGC 1546
Db 17 GTCCAGCCTCTCCCGC 1

RESULT 486
US-10-723-361-8568
; Sequence 8568, Application US/10723361
; Publication No. US20040137589A1
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: HUMAN MYOSIN-LIKE POLYPEPTIDE EXPRESSED PREDOMINANTLY IN HEART AN
; FILE REFERENCE: PB0105
; CURRENT APPLICATION NUMBER: US/10723,361
; CURRENT FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: US 09/866,108
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Acomica Sequence Listing Engine
; SEQ ID NO 8568
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-723-361-8568

Query Match      0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 3.3e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1530 GCCAGCCTCTCCCGC 1546
Db 17 GTCCAGCCTCTCCCGC 1

RESULT 486
US-10-723-361-8568
; Sequence 8568, Application US/10723361
; Publication No. US20040137589A1
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: HUMAN MYOSIN-LIKE POLYPEPTIDE EXPRESSED PREDOMINANTLY IN HEART AN
; FILE REFERENCE: PB0105
; CURRENT APPLICATION NUMBER: US/10723,361
; CURRENT FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: US 09/866,108
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Acomica Sequence Listing Engine
; SEQ ID NO 8568
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-723-361-8568

Query Match      0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 3.3e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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Qy 292 AGGATGCCCTAAATGAG 308
Db 1 AGGATGACCTGAATGAG 17

RESULT 487
US-10-723-361-8660
; Sequence 8660, Application US/10723361
; Publication No. US20040137589A1
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: HUMAN MYOSIN-LIKE POLYPEPTIDE EXPRESSED PREDOMINANTLY IN HEART AN
; FILE REFERENCE: PB0105
; CURRENT APPLICATION NUMBER: US/10723,361
; CURRENT FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: US 09/866,108
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Acomica Sequence Listing Engine
; SEQ ID NO 8660
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-723-361-8660

Query Match      0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 3.3e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 267 CTAGAAGAGCCCAAGAA 283
Db 1 CTGGAGAGGACCAAGAA 17

RESULT 488
US-10-723-361-8661
; Sequence 8661, Application US/10723361
; Publication No. US20040137589A1
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: HUMAN MYOSIN-LIKE POLYPEPTIDE EXPRESSED PREDOMINANTLY IN HEART AN
; FILE REFERENCE: PB0105
```

; CURRENT APPLICATION NUMBER: US/10/723,361  
; CURRENT FILING DATE: 2003-11-26  
; PRIOR APPLICATION NUMBER: US 09/866,108  
; PRIOR FILING DATE: 2001-05-25  
; PRIOR APPLICATION NUMBER: US 60/207,456  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: GB 24263.6  
; PRIOR FILING DATE: 2000-10-04  
; PRIOR APPLICATION NUMBER: US 60/236,359  
; PRIOR FILING DATE: 2000-09-27  
; PRIOR APPLICATION NUMBER: PCT/US01/00666  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00667  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00664  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00669  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00665  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00668  
; PRIOR FILING DATE: 2001-01-30  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 15755  
; SOFTWARE: Acomica Sequence Listing Engine  
; SEQ ID NO 8661  
; LENGTH: 17  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-723-361-8661

Query Match 0.8%; Score 13.8; DB 1; Length 17;  
Best Local Similarity 88.2%; Pred. No. 3.3e+02;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 268 TAGAAGAGCCCAAGAG 284  
Db 1 TGGAGGAGCCCAAGAG 17

RESULT 489  
US-10-723-361-8663  
; Sequence 8663, Application US/10723361  
; Publication No. US20040137589A1  
; GENERAL INFORMATION:  
; APPLICANT: GU, Yizhong  
; APPLICANT: JI, Yonggang  
; APPLICANT: PENN, Sharron G.  
; APPLICANT: HANZEL, David K.  
; APPLICANT: RANK, David R.  
; APPLICANT: CHEN, Wensheng  
; APPLICANT: SHANNON, Mark  
; TITLE OF INVENTION: HUMAN MYOSIN-LIKE POLYPEPTIDE EXPRESSED PREDOMINANTLY IN HEART AN  
; FILE REFERENCE: PB0105  
; CURRENT APPLICATION NUMBER: US/10/723,361  
; CURRENT FILING DATE: 2003-11-26  
; PRIOR APPLICATION NUMBER: US 09/866,108  
; PRIOR FILING DATE: 2001-05-25  
; PRIOR APPLICATION NUMBER: US 60/207,456  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: GB 24263.6  
; PRIOR FILING DATE: 2000-10-04  
; PRIOR APPLICATION NUMBER: US 60/236,359  
; PRIOR FILING DATE: 2000-09-27  
; PRIOR APPLICATION NUMBER: PCT/US01/00666  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00667  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00664  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00669  
; PRIOR FILING DATE: 2001-01-30  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 15755  
; SOFTWARE: Acomica Sequence Listing Engine  
; SEQ ID NO 8662  
; LENGTH: 17  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-723-361-8662

; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00668  
; PRIOR FILING DATE: 2001-01-30  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 15755  
; SOFTWARE: Acomica Sequence Listing Engine  
; SEQ ID NO 8663  
; LENGTH: 17  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-723-361-8663

Query Match 0.8%; Score 13.8; DB 1; Length 17;  
Best Local Similarity 88.2%; Pred. No. 3.3e+02;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 270 GAAGAAGCCCAAGAGAA 286  
Db 1 GAGGAAGCCCAAGAGGA 17

RESULT 490  
US-10-723-361-8664  
; Sequence 8664, Application US/10723361  
; Publication No. US20040137589A1  
; GENERAL INFORMATION:  
; APPLICANT: GU, Yizhong  
; APPLICANT: JI, Yonggang  
; APPLICANT: PENN, Sharron G.  
; APPLICANT: HANZEL, David K.  
; APPLICANT: RANK, David R.  
; APPLICANT: CHEN, Wensheng  
; APPLICANT: SHANNON, Mark  
; TITLE OF INVENTION: HUMAN MYOSIN-LIKE POLYPEPTIDE EXPRESSED PREDOMINANTLY IN HEART AN

; FILE REFERENCE: PB0105  
; CURRENT APPLICATION NUMBER: US/10/723,361  
; CURRENT FILING DATE: 2003-11-26  
; PRIOR APPLICATION NUMBER: US 09/866,108  
; PRIOR FILING DATE: 2001-05-25  
; PRIOR APPLICATION NUMBER: US 60/207,456  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: GB 24263.6  
; PRIOR FILING DATE: 2000-10-04  
; PRIOR APPLICATION NUMBER: US 60/236,359  
; PRIOR FILING DATE: 2000-09-27  
; PRIOR APPLICATION NUMBER: PCT/US01/00666  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00667  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00664  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00669  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00665  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00668  
; PRIOR FILING DATE: 2001-01-30  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 15755  
; SOFTWARE: Acomica Sequence Listing Engine  
; SEQ ID NO 8664  
; LENGTH: 17  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-723-361-8664

Query Match 0.8%; Score 13.8; DB 1; Length 17;  
Best Local Similarity 88.2%; Pred. No. 3.3e+02;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 271 AAGAAGCCCAAGAGAG 287  
Db 1 AGGAAGCCCAAGAGAG 17

## RESULT 491

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US-10-723-361-9687/c
; Sequence 9687, Application US/10723361
; Publication No. US20040137589A1
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: HUMAN MYOSIN-LIKE POLYPEPTIDE EXPRESSED PREDOMINANTLY IN HEART AN
; FILE REFERENCE: PB0105
; CURRENT APPLICATION NUMBER: US/10/723,361
; CURRENT FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: US 09/866,108
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aecomica Sequence Listing Engine
; SEQ ID NO 9687
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-723-361-9687
```

```
Query Match      0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 3.3e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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QY 93 GAGAGTGGCGAGGTCT 109

Db 17 GAGAGTGGCGAGTCT 1

## RESULT 492

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US-10-723-361-9688/c
; Sequence 9688, Application US/10723361
; Publication No. US20040137589A1
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: HUMAN MYOSIN-LIKE POLYPEPTIDE EXPRESSED PREDOMINANTLY IN HEART AN
; FILE REFERENCE: PB0105
; CURRENT APPLICATION NUMBER: US/10/723,361
; CURRENT FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: US 09/866,108
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; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aecomica Sequence Listing Engine
; SEQ ID NO 9688
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-723-361-9688
```

```
Query Match      0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 3.3e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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QY 92 GGAGAGTGGCGAGTCT 108

Db 17 GGAGAGTGGCGAGTCT 1

## RESULT 493

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US-10-723-361-9689/c
; Sequence 9689, Application US/10723361
; Publication No. US20040137589A1
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: HUMAN MYOSIN-LIKE POLYPEPTIDE EXPRESSED PREDOMINANTLY IN HEART AN
; FILE REFERENCE: PB0105
; CURRENT APPLICATION NUMBER: US/10/723,361
; CURRENT FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: US 09/866,108
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
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; Remaining Prior Application data removed - See File Wrapper or PALM.

; NUMBER OF SEQ ID NOS: 15755  
; SOFTWARE: Aeomica Sequence Listing Engine  
; SEQ ID NO 9689  
; LENGTH: 17  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-723-361-9689

Query Match 0.8%; Score 13.8; DB 1; Length 17;  
Best Local Similarity 88.2%; Pred. No. 3.3e+02;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 91 GGGAGAGTGGCAGGTC 107  
Db 17 GGGAGAGTGGCAGGTC 1

## RESULT 494

US-10-758-451-944/c  
; Sequence 944, Application US/10758451  
; Publication No. US20050014711A1  
; GENERAL INFORMATION:  
; APPLICANT: East Carolina University  
; TITLE OF INVENTION: COMPOSITION, FORMULATION & METHOD FOR PREVENTION & TREATMENT OF D  
; TITLE OF INVENTION: AND CONDITIONS ASSOCIATED WITH BRONCHOCONSTRICTION, ALLERGY (IES)  
; TITLE OF INVENTION: INFLAMMATION  
; FILE REFERENCE: 30775-706.301  
; CURRENT APPLICATION NUMBER: US/10758,451  
; CURRENT FILING DATE: 2004-01-14  
; PRIOR APPLICATION NUMBER: 09/093,972  
; PRIOR FILING DATE: 1998-06-09  
; NUMBER OF SEQ ID NOS: 996  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 944  
; LENGTH: 17  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-758-451-944

Query Match 0.8%; Score 13.8; DB 1; Length 17;  
Best Local Similarity 88.2%; Pred. No. 3.3e+02;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1530 GCCCAGCCTCTCCCGCG 1546  
Db 17 GCCCAGCCTGTGCCCGC 1

## RESULT 495

US-10-890-776A-748  
; Sequence 748, Application US/10890776A  
; Publication No. US20050129683A1  
; GENERAL INFORMATION:  
; APPLICANT: Zhang, Jian  
; TITLE OF INVENTION: HUMAN TESTIS EXPRESSED PATCHED LIKE PROTEIN  
; FILE REFERENCE: PB0177  
; CURRENT APPLICATION NUMBER: US/10890,776A  
; CURRENT FILING DATE: 2004-07-14  
; PRIOR APPLICATION NUMBER: US 10/060,756  
; PRIOR FILING DATE: 2002-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00663  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00664  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00665  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00667  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00668  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00669  
; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: US 09/864,761  
; PRIOR FILING DATE: 2001-05-23  
; PRIOR APPLICATION NUMBER: US 60/327,898  
; PRIOR FILING DATE: 2001-10-09  
; NUMBER OF SEQ ID NOS: 4809  
; SOFTWARE: Aeomica Sequence Listing Engine  
; SEQ ID NO 748  
; LENGTH: 17  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-890-776A-748

Query Match 0.8%; Score 13.8; DB 1; Length 17;  
Best Local Similarity 88.2%; Pred. No. 3.3e+02;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 521 CATCGACTCCCTGCTGG 537  
Db 1 CAGCGACTCACTGCTGG 17

## RESULT 496

US-10-890-776A-749  
; Sequence 749, Application US/10890776A  
; Publication No. US20050129683A1  
; GENERAL INFORMATION:  
; APPLICANT: Zhang, Jian  
; TITLE OF INVENTION: HUMAN TESTIS EXPRESSED PATCHED LIKE PROTEIN  
; FILE REFERENCE: PB0177  
; CURRENT APPLICATION NUMBER: US/10890,776A  
; CURRENT FILING DATE: 2004-07-14  
; PRIOR APPLICATION NUMBER: US 10/060,756  
; PRIOR FILING DATE: 2002-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00663  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00664  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00665  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00667  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00668  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00669  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: US 09/864,761  
; PRIOR FILING DATE: 2001-05-23  
; PRIOR APPLICATION NUMBER: US 60/327,898  
; PRIOR FILING DATE: 2001-10-09  
; NUMBER OF SEQ ID NOS: 4809  
; SOFTWARE: Aeomica Sequence Listing Engine  
; SEQ ID NO 749  
; LENGTH: 17  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-890-776A-749

Query Match 0.8%; Score 13.8; DB 1; Length 17;  
Best Local Similarity 88.2%; Pred. No. 3.3e+02;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 522 ATCGACTCCCTGCTGGA 538  
Db 1 AGCGACTCACTGCTGGA 17

## RESULT 497

US-10-890-776A-1238  
; Sequence 1238, Application US/10890776A  
; Publication No. US20050129683A1  
; GENERAL INFORMATION:  
; APPLICANT: Zhang, Jian  
; TITLE OF INVENTION: HUMAN TESTIS EXPRESSED PATCHED LIKE PROTEIN

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; FILE REFERENCE: PB0177
; CURRENT APPLICATION NUMBER: US/10/890,776A
; CURRENT FILING DATE: 2004-07-14
; PRIOR APPLICATION NUMBER: US 10/060,756
; PRIOR FILING DATE: 2002-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 09/864,761
; PRIOR FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/327,898
; PRIOR FILING DATE: 2001-10-09
; NUMBER OF SEQ ID NOS: 4809
; SOFTWARE: Ascomica Sequence Listing Engine
; SEQ ID NO 1238
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-890-776A-1238
```

```
Query Match      0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 3.3e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1273 TCTTTGACTCTGATCCC 1289
Db      1 TCTGTGACTGTGATCCC 17
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Search completed: September 13, 2005, 10:47:07  
Job time : 12 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 13, 2005, 10:39:51 ; Search time 5 Seconds  
(without alignments)  
3.649 Million cell updates/sec

Title: us-10-828-394-1  
Perfect score: 1643  
Sequence: 1 gaattccgcgtgaccgag.....taaaactgtctgtgagctg 1643

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 0.5

Searched: 298 seqs, 5552 residues

Total number of hits satisfying chosen parameters: 596

Minimum DB seq length: 8  
Maximum DB seq length: 50

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 298 summaries

Database : rgedb.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	27.2	1.7	32	1	ACCESSION:A21575
2	26	1.6	26	1	ACCESSION:AR090627
3	26	1.6	26	1	ACCESSION:AR197662
4	26	1.6	26	1	ACCESSION:AR259816
5	25	1.5	25	1	ACCESSION:AR090628
6	25	1.5	25	1	ACCESSION:AR197663
7	25	1.5	25	1	ACCESSION:AR259817
8	23	1.4	23	1	ACCESSION:AR259817
9	23	1.4	23	1	ACCESSION:AR259817
10	23	1.4	23	1	ACCESSION:AR259817
11	23	1.4	23	1	ACCESSION:AR259817
12	23	1.4	23	1	ACCESSION:AR259817
13	21	1.3	21	1	ACCESSION:AR038687
14	21	1.3	21	1	ACCESSION:AR038687
15	21	1.3	21	1	ACCESSION:AR038687
16	21	1.3	21	1	ACCESSION:AR038687
17	21	1.3	21	1	ACCESSION:AR038687
18	21	1.3	21	1	ACCESSION:AR038687
19	21	1.3	21	1	ACCESSION:AR038687
20	21	1.3	21	1	ACCESSION:AR038687
21	21	1.3	21	1	ACCESSION:AR038687
22	21	1.3	21	1	ACCESSION:AR038687
23	21	1.3	21	1	ACCESSION:AR038687
24	21	1.3	21	1	ACCESSION:AR038687
25	21	1.3	21	1	ACCESSION:AR038687
26	21	1.3	21	1	ACCESSION:AR038687
27	21	1.3	21	1	ACCESSION:AR038687
28	21	1.3	21	1	ACCESSION:AR038687
29	21	1.3	21	1	ACCESSION:AR038687
30	21	1.3	21	1	ACCESSION:AR038687
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32	21	1.3	21	1	ACCESSION:AR038687
33	21	1.3	21	1	ACCESSION:AR038687

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ACCESSION: CQ786633  
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ACCESSION: CQ786650  
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ACCESSION: AR208707  
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ACCESSION: BD230318  
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ACCESSION: AX097246  
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C 107	20	1.2	20	1	AR208762	ACCESSION:AR208762	C 180	14.4	0.9	17	1	AR466360	ACCESSION:AR466360
C 108	20	1.2	20	1	AR208763	ACCESSION:AR208763	C 181	14.4	0.9	17	1	AR466361	ACCESSION:AR466361
C 109	20	1.2	20	1	AR208764	ACCESSION:AR208764	C 182	14.4	0.9	17	1	AX214729	ACCESSION:AX214729
C 110	20	1.2	20	1	AR208765	ACCESSION:AR208765	C 183	14.4	0.9	17	1	AX688718	ACCESSION:AX688718
C 111	20	1.2	20	1	AR208766	ACCESSION:AR208766	C 184	14.4	0.9	17	1	AX688720	ACCESSION:AX688720
C 112	20	1.2	20	1	AR208767	ACCESSION:AR208767	C 185	14.4	0.9	17	1	AX732888	ACCESSION:AX732888
C 113	20	1.2	20	1	AR208768	ACCESSION:AR208768	C 186	14.4	0.9	17	1	AX760623	ACCESSION:AX760623
C 114	20	1.2	20	1	AR208769	ACCESSION:AR208769	C 187	14.4	0.9	18	1	AR067404	ACCESSION:AR067404
C 115	20	1.2	20	1	AR208770	ACCESSION:AR208770	C 188	14.4	0.9	18	1	AX837978	ACCESSION:AX837978
C 116	20	1.2	20	1	AR208771	ACCESSION:AR208771	C 189	14	0.9	17	1	AX324817	ACCESSION:AX324817
C 117	20	1.2	20	1	AR208772	ACCESSION:AR208772	C 190	14	0.9	17	1	AX324818	ACCESSION:AX324818
C 118	20	1.2	20	1	AR208773	ACCESSION:AR208773	C 191	13.8	0.8	17	1	AR039619	ACCESSION:AR039619
C 119	20	1.2	20	1	AR208774	ACCESSION:AR208774	C 192	13.8	0.8	17	1	AR081753	ACCESSION:AR081753
C 120	20	1.2	20	1	AR208775	ACCESSION:AR208775	C 193	13.8	0.8	17	1	AR081755	ACCESSION:AR081755
C 121	20	1.2	20	1	AR208776	ACCESSION:AR208776	C 194	13.8	0.8	17	1	AR094983	ACCESSION:AR094983
C 122	20	1.2	20	1	AR208777	ACCESSION:AR208777	C 195	13.8	0.8	17	1	AR167987	ACCESSION:AR167987
C 123	20	1.2	20	1	AR208778	ACCESSION:AR208778	C 196	13.8	0.8	17	1	AR167987	ACCESSION:AR167987
C 124	20	1.2	20	1	AR208781	ACCESSION:AR208781	C 197	13.8	0.8	17	1	BD254845	ACCESSION:BD254845
C 125	20	1.2	21	1	CQ786121	ACCESSION:CQ786121	C 198	13.8	0.8	17	1	CQ617155	ACCESSION:CQ617155
C 126	19.4	1.2	21	1	AR236281	ACCESSION:AR236281	C 199	13.8	0.8	17	1	CQ622615	ACCESSION:CQ622615
C 127	19	1.2	19	1	CQ786179	ACCESSION:CQ786179	C 200	13.8	0.8	17	1	CQ622745	ACCESSION:CQ622745
C 128	19	1.2	19	1	CQ786180	ACCESSION:CQ786180	C 201	13.8	0.8	17	1	CQ623828	ACCESSION:CQ623828
C 129	19	1.2	19	1	CQ786653	ACCESSION:CQ786653	C 202	13.8	0.8	17	1	CQ623920	ACCESSION:CQ623920
C 130	19	1.2	19	1	CQ786654	ACCESSION:CQ786654	C 203	13.8	0.8	17	1	CQ623921	ACCESSION:CQ623921
C 131	19	1.2	21	1	CQ786122	ACCESSION:CQ786122	C 204	13.8	0.8	17	1	CQ623923	ACCESSION:CQ623923
C 132	19	1.2	21	1	CQ786640	ACCESSION:CQ786640	C 205	13.8	0.8	17	1	CQ623924	ACCESSION:CQ623924
C 133	18.8	1.1	22	1	AR071119	ACCESSION:AR071119	C 206	13.8	0.8	17	1	CQ624947	ACCESSION:CQ624947
C 134	18.8	1.1	22	1	E15141	ACCESSION:E15141	C 207	13.8	0.8	17	1	CQ624948	ACCESSION:CQ624948
C 135	18	1.1	22	1	AR038688	ACCESSION:AR038688	C 208	13.8	0.8	17	1	CQ624949	ACCESSION:CQ624949
C 136	18	1.1	18	1	AX208705	ACCESSION:AX208705	C 209	13.8	0.8	17	1	E65210	ACCESSION:E65210
C 137	17	1.0	17	1	AX728619	ACCESSION:AX728619	C 210	13.8	0.8	17	1	AR192271	ACCESSION:AR192271
C 138	17	1.0	17	1	AR167026	ACCESSION:AR167026	C 211	13.8	0.8	17	1	AR196222	ACCESSION:AR196222
C 139	16.8	1.0	20	1	AR210681	ACCESSION:AR210681	C 212	13.8	0.8	17	1	AR213316	ACCESSION:AR213316
C 140	16.8	1.0	20	1	A39125	ACCESSION:A39125	C 213	13.8	0.8	17	1	AR213318	ACCESSION:AR213318
C 141	16	1.0	16	1	AR063448	ACCESSION:AR063448	C 214	13.8	0.8	17	1	AR256153	ACCESSION:AR256153
C 142	16	1.0	16	1	AR123639	ACCESSION:AR123639	C 215	13.8	0.8	17	1	AR256155	ACCESSION:AR256155
C 143	16	1.0	16	1	AR267380	ACCESSION:AR267380	C 216	13.8	0.8	17	1	AR275110	ACCESSION:AR275110
C 144	16	1.0	16	1	AR305790	ACCESSION:AR305790	C 217	13.8	0.8	17	1	AR275112	ACCESSION:AR275112
C 145	16	1.0	16	1	AX023187	ACCESSION:AX023187	C 218	13.8	0.8	17	1	AR306243	ACCESSION:AR306243
C 146	16	1.0	16	1	AX417393	ACCESSION:AX417393	C 219	13.8	0.8	17	1	AR306245	ACCESSION:AR306245
C 147	16	1.0	16	1	AR029848	ACCESSION:AR029848	C 220	13.8	0.8	17	1	AR326141	ACCESSION:AR326141
C 148	16	1.0	17	1	CQ881900	ACCESSION:CQ881900	C 221	13.8	0.8	17	1	AR326780	ACCESSION:AR326780
C 149	16	1.0	19	1	CQ786119	ACCESSION:CQ786119	C 222	13.8	0.8	17	1	AR371631	ACCESSION:AR371631
C 150	15.8	1.0	19	1	CQ786120	ACCESSION:CQ786120	C 223	13.8	0.8	17	1	AR371633	ACCESSION:AR371633
C 151	15.8	1.0	19	1	CQ786635	ACCESSION:CQ786635	C 224	13.8	0.8	17	1	AR458218	ACCESSION:AR458218
C 152	15.8	1.0	19	1	CQ786637	ACCESSION:CQ786637	C 225	13.8	0.8	17	1	AR458966	ACCESSION:AR458966
C 153	15.8	1.0	19	1	CQ786638	ACCESSION:CQ786638	C 226	13.8	0.8	17	1	AR463678	ACCESSION:AR463678
C 154	15.8	1.0	19	1	CQ623926	ACCESSION:CQ623926	C 227	13.8	0.8	17	1	AR463808	ACCESSION:AR463808
C 155	15.4	0.9	17	1	I37522	ACCESSION:I37522	C 228	13.8	0.8	17	1	AR464891	ACCESSION:AR464891
C 156	15.4	0.9	17	1	I94372	ACCESSION:I94372	C 229	13.8	0.8	17	1	AR464983	ACCESSION:AR464983
C 157	15.4	0.9	17	1	AR464989	ACCESSION:AR464989	C 230	13.8	0.8	17	1	AR464984	ACCESSION:AR464984
C 158	15.4	0.9	17	1	AX214728	ACCESSION:AX214728	C 231	13.8	0.8	17	1	AR464986	ACCESSION:AR464986
C 159	15.4	0.9	17	1	AX688719	ACCESSION:AX688719	C 232	13.8	0.8	17	1	AR464987	ACCESSION:AR464987
C 160	15.4	0.9	17	1	AX762505	ACCESSION:AX762505	C 233	13.8	0.8	17	1	AR466010	ACCESSION:AR466010
C 161	15.4	0.9	17	1	AR011407	ACCESSION:AR011407	C 234	13.8	0.8	17	1	AR466011	ACCESSION:AR466011
C 162	14.8	0.9	18	1	AR040105	ACCESSION:AR040105	C 235	13.8	0.8	17	1	AR466012	ACCESSION:AR466012
C 163	14.8	0.9	18	1	AX115178	ACCESSION:AX115178	C 236	13.8	0.8	17	1	AX215611	ACCESSION:AX215611
C 164	14.8	0.9	18	1	AX776586	ACCESSION:AX776586	C 237	13.8	0.8	17	1	AX216443	ACCESSION:AX216443
C 165	14.8	0.9	17	1	AR173373	ACCESSION:AR173373	C 238	13.8	0.8	17	1	AX272871	ACCESSION:AX272871
C 166	14.4	0.9	17	1	CQ623612	ACCESSION:CQ623612	C 239	13.8	0.8	17	1	AX423446	ACCESSION:AX423446
C 167	14.4	0.9	17	1	CQ623613	ACCESSION:CQ623613	C 240	13.8	0.8	17	1	AX423446	ACCESSION:AX423446
C 168	14.4	0.9	17	1	CQ623925	ACCESSION:CQ623925	C 241	13.8	0.8	17	1	AX475287	ACCESSION:AX475287
C 169	14.4	0.9	17	1	CQ623927	ACCESSION:CQ623927	C 242	13.8	0.8	17	1	AX475288	ACCESSION:AX475288
C 170	14.4	0.9	17	1	CQ623927	ACCESSION:CQ623927	C 243	13.8	0.8	17	1	AX475289	ACCESSION:AX475289
C 171	14.4	0.9	17	1	CQ625297	ACCESSION:CQ625297	C 244	13.8	0.8	17	1	AX475290	ACCESSION:AX475290
C 172	14.4	0.9	17	1	CQ625298	ACCESSION:CQ625298	C 245	13.8	0.8	17	1	AX475291	ACCESSION:AX475291
C 173	14.4	0.9	17	1	I37523	ACCESSION:I37523	C 246	13.8	0.8	17	1	AX475293	ACCESSION:AX475293
C 174	14.4	0.9	17	1	I94373	ACCESSION:I94373	C 247	13.8	0.8	17	1	AX475720	ACCESSION:AX475720
C 175	14.4	0.9	17	1	AR464675	ACCESSION:AR464675	C 248	13.8	0.8	17	1	AX499441	ACCESSION:AX499441
C 176	14.4	0.9	17	1	AR464676	ACCESSION:AR464676	C 249	13.8	0.8	17	1	AX499442	ACCESSION:AX499442
C 177	14.4	0.9	17	1	AR464988	ACCESSION:AR464988	C 250	13.8	0.8	17	1	AX499931	ACCESSION:AX499931
C 178	14.4	0.9	17	1	AR464990	ACCESSION:AR464990	C 251	13.8	0.8	17	1	AX687958	ACCESSION:AX687958
C 179	14.4	0.9	17	1			C 252	13.8	0.8	17	1		

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c 253 13.8 0.8 17 1 AX688721
254 13.8 0.8 17 1 AX690667
255 13.8 0.8 17 1 AX727197
c 256 13.8 0.8 17 1 AX728423
257 13.8 0.8 17 1 AX731740
258 13.8 0.8 17 1 AX734894
c 259 13.8 0.8 17 1 AX756729
260 13.4 0.8 15 1 I61606
c 261 13.4 0.8 15 1 AR180106
c 262 13.4 0.8 15 1 AR180715
c 263 13.4 0.8 15 1 AR532147
c 264 13.4 0.8 15 1 AX157089
265 13.4 0.8 15 1 AX635964
c 266 13.4 0.8 16 1 AR029843
267 13.4 0.8 16 1 AR131574
c 268 13.4 0.8 16 1 AR131575
c 269 13.4 0.8 16 1 CO796994
c 270 13.4 0.8 16 1 CO858546
271 13.4 0.8 16 1 AR199508
272 13.4 0.8 16 1 AR199509
273 13.4 0.8 16 1 AR200979
274 13.4 0.8 16 1 AR200980
275 13.4 0.8 16 1 AR488738
276 13.4 0.8 16 1 AR488739
277 13.4 0.8 16 1 AX419730
278 13.4 0.8 16 1 AX419731
279 13.4 0.8 16 1 BD084992
280 13.4 0.8 16 1 BD084993
c 281 13.4 0.8 16 1 S81287
c 282 13 0.8 14 1 AR066302
c 283 13 0.8 15 1 AX377347
c 284 13 0.8 15 1 ATH551605
285 13 0.8 16 1 CO806753
286 12.8 0.8 16 1 A88141
287 12.8 0.8 16 1 A89435
c 288 12.8 0.8 16 1 A90108
c 289 12.8 0.8 16 1 AR104209
c 290 12.8 0.8 16 1 CO786338
c 291 12.8 0.8 16 1 AR196058
292 12.8 0.8 16 1 AX003952
293 12.8 0.8 16 1 AX255603
294 12.8 0.8 16 1 AX255637
295 12.8 0.8 16 1 AX713247
296 12.8 0.8 16 1 BD065654
297 12.8 0.8 16 1 BD066948
c 298 12.8 0.8 16 1 BD086293
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## ALIGNMENTS

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RESULT 1
A21575 A21575 32 bp DNA linear PAT 26-JUL-1994
LOCUS oligonucleotide.
DEFINITION A21575
ACCESSION A21575
VERSION A21575.1 GI:583580
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1 (bases 1 to 32)
AUTHORS
TITLE CYTOLYSIS INHIBITOR PROTEINS (CLI) AND DNA SEQUENCES CODING FOR
SAID PROTEINS
JOURNAL Patent: WO 9105043-A 1 18-APR-1991;
FEATURES Location/Qualifiers
source
1 .32
/mol_type="synthetic construct"
/db_xref="taxon:32630"

Query Match 1.7%; Score 27.2; DB 1; Length 32;
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Best Local Similarity 90.6%; Pred. No. 8.1;
Matches 29; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 129 GACAATGAGCTCCAGGAATGTCCAATCAGGG 160
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Db 1 GACAATGAGCTCCAGGAGATGTCCAACACAGG 32
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RESULT 2
AR090627 26 bp DNA linear PAT 07-SEP-2000
LOCUS Sequence 747 from patent US 5994076.
DEFINITION AR090627
ACCESSION AR090627
VERSION AR090627.1 GI:10017382
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 26)
AUTHORS Chenchik,A., Jokhadze,G. and Bibilashvilli,R.
TITLE Methods of assaying differential expression
JOURNAL Patent: US 5994076-A 747 30-NOV-1999;
FEATURES Location/Qualifiers
source
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/organism="unknown"
/mol_type="unassigned DNA"

Query Match 1.6%; Score 26; DB 1; Length 26;
Best Local Similarity 100.0%; Pred. No. 6.5;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 934 TCGCGATGAAGCACCAGTGTGACAAG 959
|||||
Db 1 TCGCGATGAAGCACCAGTGTGACAAG 26
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RESULT 3
AR197662 26 bp DNA linear PAT 20-APR-2002
LOCUS Sequence 747 from patent US 6352829.
DEFINITION AR197662
ACCESSION AR197662
VERSION AR197662.1 GI:20247511
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 26)
AUTHORS Chenchik,A., Jokhadze,G. and Bibilashvilli,R.
TITLE Methods of assaying differential expression
JOURNAL Patent: US 6352829-A 747 05-MAR-2002;
FEATURES Location/Qualifiers
source
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/mol_type="unassigned DNA"

Query Match 1.6%; Score 26; DB 1; Length 26;
Best Local Similarity 100.0%; Pred. No. 6.5;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 934 TCGCGATGAAGCACCAGTGTGACAAG 959
|||||
Db 1 TCGCGATGAAGCACCAGTGTGACAAG 26
|||||

RESULT 4
AR259816 26 bp DNA linear PAT 20-DEC-2002
LOCUS Sequence 747 from patent US 6489455.
DEFINITION AR259816
ACCESSION AR259816
VERSION AR259816.1 GI:27310327
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
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Unclassified.
1 (bases 1 to 26)
REFERENCE   AR259817/c
AUTHORS     Chenchik,A., Jokhadze,G. and Bibilashvilli,R.
TITLE       Methods of assaying differential expression
JOURNAL     Patent: US 6489455-A 747 03-DEC-2002;
FEATURES    Location/Qualifiers
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            1..26
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            /mol_type="genomic DNA"

Query Match      1.6%; Score 26; DB 1; Length 26;
Best Local Similarity 100.0%; Pred. No. 6.5;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY   934  TCGGGATGAAGCACCAGTGTGACAAG 959
      1..26
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      1..25
      /organism="unknown"
      /mol_type="genomic DNA"

RESULT 5
LOCUS       AR090628/c
DEFINITION Sequence 748 from patent US 5994076.
ACCESSION   AR090628
VERSION     AR090628.1 GI:10017383
KEYWORDS    .
SOURCE      Unknown.
ORGANISM    Unclassified.
REFERENCE   1 (bases 1 to 25)
AUTHORS     Chenchik,A., Jokhadze,G. and Bibilashvilli,R.
TITLE       Methods of assaying differential expression
JOURNAL     Patent: US 5994076-A 748 30-NOV-1999;
FEATURES    Location/Qualifiers
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            1..25
            /organism="unknown"
            /mol_type="unassigned DNA"

Query Match      1.5%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 8.2;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY   1190 GTACTATCTCGGGTCCACCACGGTG 1214
      1..25
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      Db

RESULT 6
LOCUS       AR197663/c
DEFINITION Sequence 748 from patent US 6352829.
ACCESSION   AR197663
VERSION     AR197663.1 GI:20247512
KEYWORDS    .
SOURCE      Unknown.
ORGANISM    Unclassified.
REFERENCE   1 (bases 1 to 25)
AUTHORS     Chenchik,A., Jokhadze,G. and Bibilashvilli,R.
TITLE       Methods of assaying differential expression
JOURNAL     Patent: US 6352829-A 748 05-MAR-2002;
FEATURES    Location/Qualifiers
            source
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            /organism="unknown"
            /mol_type="unassigned DNA"

Query Match      1.5%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 8.2;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY   1190 GTACTATCTCGGGTCCACCACGGTG 1214
      1..25
      GTACTATCTCGGGTCCACCACGGTG 1
      Db

RESULT 7
LOCUS       AR259817/c
DEFINITION Sequence 748 from patent US 6489455.
ACCESSION   AR259817
VERSION     AR259817.1 GI:27310328
KEYWORDS    .
SOURCE      Unknown.
ORGANISM    Unclassified.
REFERENCE   1 (bases 1 to 25)
AUTHORS     Chenchik,A., Jokhadze,G. and Bibilashvilli,R.
TITLE       Methods of assaying differential expression
JOURNAL     Patent: US 6489455-A 748 03-DEC-2002;
FEATURES    Location/Qualifiers
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            1..25
            /organism="unknown"
            /mol_type="genomic DNA"

Query Match      1.5%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 8.2;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY   1190 GTACTATCTCGGGTCCACCACGGTG 1214
      1..25
      GTACTATCTCGGGTCCACCACGGTG 1
      Db

RESULT 8
LOCUS       CQ786169
DEFINITION Sequence 57 from Patent WO2004018676.
ACCESSION   CQ786169
VERSION     CQ786169.1 GI:45721272
KEYWORDS    .
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
REFERENCE   1
AUTHORS     Jansen,B., Gleave,M.E., Signaevsky,M., Beraldi,E., Trougakos,I. and Gonos,E.
TITLE       Rnai probes targeting cancer-related proteins
JOURNAL     Patent: WO 2004018676-A 57 04-MAR-2004;
            The University of British Columbia (CA)
FEATURES    Location/Qualifiers
            source
            1..23
            /organism="Homo sapiens"
            /mol_type="unassigned DNA"
            /db_xref="taxon:9606"

Query Match      1.4%; Score 23; DB 1; Length 23;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY   480  AACAGAGCTCGCCCTTCTACTT 502
      1..23
      AACAGAGCTCGCCCTTCTACTT 23
      Db

RESULT 9
LOCUS       CQ786172
DEFINITION Sequence 60 from Patent WO2004018676.
ACCESSION   CQ786172
VERSION     CQ786172.1 GI:45721275
KEYWORDS    .
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
REFERENCE   1
AUTHORS     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE       Rnai probes targeting cancer-related proteins
JOURNAL     Patent: WO 2004018676-A 57 04-MAR-2004;
            The University of British Columbia (CA)
FEATURES    Location/Qualifiers
            source
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Query Match      1.4%; Score 23; DB 1; Length 23;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY   480  AACAGAGCTCGCCCTTCTACTT 502
      1..23
      AACAGAGCTCGCCCTTCTACTT 23
      Db

RESULT 10
LOCUS       CQ786172
DEFINITION Sequence 60 from Patent WO2004018676.
ACCESSION   CQ786172
VERSION     CQ786172.1 GI:45721275
KEYWORDS    .
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
REFERENCE   1
AUTHORS     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE       Rnai probes targeting cancer-related proteins
JOURNAL     Patent: WO 2004018676-A 57 04-MAR-2004;
            The University of British Columbia (CA)
FEATURES    Location/Qualifiers
            source
            1..23
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Query Match      1.4%; Score 23; DB 1; Length 23;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY   480  AACAGAGCTCGCCCTTCTACTT 502
      1..23
      AACAGAGCTCGCCCTTCTACTT 23
      Db
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REFERENCE 1  
AUTHORS Jansen,B., Gleave,M.E., Signaevsky,M., Beraldi,E., Trougakos,I. and Gonos,E.  
TITLE Rnai probes targeting cancer-related proteins  
JOURNAL Patent: WO 2004018676-A 60 04-MAR-2004;  
The University of British Columbia (CA)  
FEATURES Location/Qualifiers  
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Query Match 1.4%; Score 23; DB 1; Length 23;  
Best Local Similarity 100.0%; Pred. No. 13;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 711 AAGTCCCGCATCGCCGAGCTT 733  
|||||  
Db 1 AAGTCCCGCATCGCCGAGCTT 23

RESULT 10  
LOCUS CQ786175 23 bp DNA linear PAT 24-MAR-2004  
DEFINITION Sequence 63 from Patent WO2004018676.  
ACCESSION CQ786175  
VERSION CQ786175.1 GI:45721278  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens

REFERENCE 1  
AUTHORS Jansen,B., Gleave,M.E., Signaevsky,M., Beraldi,E., Trougakos,I. and Gonos,E.  
TITLE Rnai probes targeting cancer-related proteins  
JOURNAL Patent: WO 2004018676-A 63 04-MAR-2004;  
The University of British Columbia (CA)  
FEATURES Location/Qualifiers  
source 1. .23  
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/mol\_type="unassigned DNA"  
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Query Match 1.4%; Score 23; DB 1; Length 23;  
Best Local Similarity 100.0%; Pred. No. 13;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1613 AACTAATTCATAAACTGCTT 1635  
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Db 1 AACTAATTCATAAACTGCTT 23

RESULT 11  
LOCUS CQ786178 23 bp DNA linear PAT 24-MAR-2004  
DEFINITION Sequence 66 from Patent WO2004018676.  
ACCESSION CQ786178  
VERSION CQ786178.1 GI:45721281  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens

REFERENCE 1  
AUTHORS Jansen,B., Gleave,M.E., Signaevsky,M., Beraldi,E., Trougakos,I. and Gonos,E.  
TITLE Rnai probes targeting cancer-related proteins  
JOURNAL Patent: WO 2004018676-A 66 04-MAR-2004;  
The University of British Columbia (CA)  
FEATURES Location/Qualifiers  
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/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"

Query Match 1.4%; Score 23; DB 1; Length 23;  
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Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 46 GCATGATGAAGACTCTGCTGCTG 68  
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Db 1 GCATGATGAAGACTCTGCTGCTG 23

RESULT 12  
LOCUS AR208706/c 23 bp DNA linear PAT 20-JUN-2002  
DEFINITION Sequence 5 from patent US 6383808.  
ACCESSION AR208706  
VERSION AR208706.1 GI:21509931  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.

REFERENCE 1 (bases 1 to 23)  
AUTHORS Monia,B.P. and Priester,S.M.  
TITLE Antisense inhibition of Clusterin expression  
JOURNAL Patent: US 6383808-A 5 07-MAY-2002;  
FEATURES Location/Qualifiers  
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/organism="unknown"  
/mol\_type="unassigned DNA"

Query Match 1.4%; Score 23; DB 1; Length 23;  
Best Local Similarity 100.0%; Pred. No. 13;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 789 CTTGAGATGATACACGAGGCTCA 811  
|||||  
Db 23 CTTGAGATGATACACGAGGCTCA 1

RESULT 13  
LOCUS AR038687 21 bp DNA linear PAT 29-SEP-1999  
DEFINITION Sequence 21 from patent US 5807678.  
ACCESSION AR038687  
VERSION AR038687.1 GI:5958050  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.

REFERENCE 1 (bases 1 to 21)  
AUTHORS Miller,W.L., Lin,D. and Strauss,J.F. III.  
TITLE Identification of gene mutations associated with congenital lipoid adrenal hyperplasia  
JOURNAL Patent: US 5807678-A 21 15-SEP-1998;  
FEATURES Location/Qualifiers  
source 1. .21  
/organism="unknown"  
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Query Match 1.3%; Score 21; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 20;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1354 AGAAGCGCTGCAGGATACC 1374  
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Db 1 AGAAGCGCTGCAGGATACC 21

RESULT 14  
LOCUS CQ786113 21 bp DNA linear PAT 24-MAR-2004  
DEFINITION Sequence 1 from Patent WO2004018676.

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ACCESSION      CQ786113
VERSION        CQ786113.1  GI:45721216
FEATURES
SOURCE        .
              synthetic construct
              other sequences; artificial sequences.
REFERENCE
AUTHORS       Jansen,B., Gleave,M.E., Signaevsky,M., Beraldi,E., Trougakos,I. and
              Gonos,E.
TITLE         Rnai probes targeting cancer-related proteins
JOURNAL       Patent: WO 2004018676-A 1 04-MAR-2004;
              The University of British Columbia (CA)
FEATURES
SOURCE        1. .21
              /organism="synthetic construct"
              /mol_type="unassigned DNA"
              /db_xref="taxon:32630"
              /note="RNAi for human clusterin"

Query Match      1.3%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      482  CCAGAGCTCGCCTTCTACTT 502
          |||||
          1  CCAGAGCTCGCCTTCTACTT 21

Db

RESULT 15
CQ786114/c
LOCUS      CQ786114          21 bp      DNA          linear          PAT 24-MAR-2004
DEFINITION Sequence 2 from Patent WO2004018676.
ACCESSION  CQ786114
VERSION    CQ786114.1  GI:45721217
KEYWORDS   .
SOURCE     synthetic construct
ORGANISM   other sequences; artificial sequences.
REFERENCE
AUTHORS    Jansen,B., Gleave,M.E., Signaevsky,M., Beraldi,E., Trougakos,I. and
              Gonos,E.
TITLE      Rnai probes targeting cancer-related proteins
JOURNAL    Patent: WO 2004018676-A 2 04-MAR-2004;
              The University of British Columbia (CA)
FEATURES
SOURCE     1. .21
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              /mol_type="unassigned DNA"
              /db_xref="taxon:32630"
              /note="RNAi for human clusterin"

Query Match      1.3%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      480  AACGAGCTCGCCTTCTAC 500
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          21  AACGAGCTCGCCTTCTAC 1

Db

RESULT 16
CQ786115
LOCUS      CQ786115          21 bp      DNA          linear          PAT 24-MAR-2004
DEFINITION Sequence 3 from Patent WO2004018676.
ACCESSION  CQ786115
VERSION    CQ786115.1  GI:45721218
KEYWORDS   .
SOURCE     synthetic construct
ORGANISM   other sequences; artificial sequences.
REFERENCE
AUTHORS    Jansen,B., Gleave,M.E., Signaevsky,M., Beraldi,E., Trougakos,I. and
              Gonos,E.
TITLE      Rnai probes targeting cancer-related proteins
JOURNAL    Patent: WO 2004018676-A 3 04-MAR-2004;
              The University of British Columbia (CA)
FEATURES
SOURCE     1. .21
              /organism="synthetic construct"
              /mol_type="unassigned DNA"
              /db_xref="taxon:32630"
              /note="RNAi for human clusterin"

Query Match      1.3%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      480  AACGAGCTCGCCTTCTAC 500
          |||||
          21  AACGAGCTCGCCTTCTAC 1

Db

RESULT 17
CQ786116/c
LOCUS      CQ786116          21 bp      DNA          linear          PAT 24-MAR-2004
DEFINITION Sequence 4 from Patent WO2004018676.
ACCESSION  CQ786116
VERSION    CQ786116.1  GI:45721219
KEYWORDS   .
SOURCE     synthetic construct
ORGANISM   other sequences; artificial sequences.
REFERENCE
AUTHORS    Jansen,B., Gleave,M.E., Signaevsky,M., Beraldi,E., Trougakos,I. and
              Gonos,E.
TITLE      Rnai probes targeting cancer-related proteins
JOURNAL    Patent: WO 2004018676-A 4 04-MAR-2004;
              The University of British Columbia (CA)
FEATURES
SOURCE     1. .21
              /organism="synthetic construct"
              /mol_type="unassigned DNA"
              /db_xref="taxon:32630"
              /note="RNAi for human clusterin"

Query Match      1.3%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1098  AAGATGCTCAACACCTCTCTCC 1118
          |||||
          21  AAGATGCTCAACACCTCTCTCC 1

Db

RESULT 18
CQ786117
LOCUS      CQ786117          21 bp      DNA          linear          PAT 24-MAR-2004
DEFINITION Sequence 5 from Patent WO2004018676.
ACCESSION  CQ786117
VERSION    CQ786117.1  GI:45721220
KEYWORDS   .
SOURCE     synthetic construct
ORGANISM   other sequences; artificial sequences.
REFERENCE
AUTHORS    Jansen,B., Gleave,M.E., Signaevsky,M., Beraldi,E., Trougakos,I. and
              Gonos,E.
TITLE      Rnai probes targeting cancer-related proteins
JOURNAL    Patent: WO 2004018676-A 5 04-MAR-2004;
              The University of British Columbia (CA)
FEATURES
SOURCE     1. .21
              /organism="synthetic construct"
              /mol_type="unassigned DNA"
              /db_xref="taxon:32630"
              /note="RNAi for human clusterin"
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Query Match      1.3%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1615 CTAATTCAATAAACTGCTT 1635
      |||||
Db 1 CTAATTCAATAAACTGCTT 21

RESULT 19
CQ786118/c
LOCUS      21 bp DNA linear PAT 24-MAR-2004
DEFINITION Sequence 6 from Patent WO2004018676.
ACCESSION  CQ786118
VERSION     CQ786118.1 GI:45721221
KEYWORDS   .
SOURCE     synthetic construct
ORGANISM   other sequences; artificial sequences.
REFERENCE  1
AUTHORS    Jansen,B., Gleave,M.E., Signaevsky,M., Beraldi,E., Trougakos,I. and
            Gonos,E.
TITLE      Rnai probes targeting cancer-related proteins
JOURNAL    Patent: WO 2004018676-A 6 04-MAR-2004;
            The University of British Columbia (CA)
FEATURES   Location/Qualifiers
            source
            1..21
                /organism="synthetic construct"
                /mol_type="unassigned DNA"
                /db_xref="taxon:32630"
                /note="RNAi for human clusterin"

Query Match      1.3%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 480 ACCAGAGCTCGCCCTTCTAC 500
      |||||
Db 21 AACAGAGCTCGCCCTTCTAC 1

RESULT 20
CQ786170
LOCUS      21 bp DNA linear PAT 24-MAR-2004
DEFINITION Sequence 58 from Patent WO2004018676.
ACCESSION  CQ786170
VERSION     CQ786170.1 GI:45721273
KEYWORDS   .
SOURCE     synthetic construct
ORGANISM   other sequences; artificial sequences.
REFERENCE  1
AUTHORS    Jansen,B., Gleave,M.E., Signaevsky,M., Beraldi,E., Trougakos,I. and
            Gonos,E.
TITLE      Rnai probes targeting cancer-related proteins
JOURNAL    Patent: WO 2004018676-A 58 04-MAR-2004;
            The University of British Columbia (CA)
FEATURES   Location/Qualifiers
            source
            1..21
                /organism="synthetic construct"
                /mol_type="unassigned DNA"
                /db_xref="taxon:32630"
                /note="RNAi for human clusterin"

Query Match      1.3%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1613 AACTAATTCATAAACTGTC 1633
      |||||
Db 21 AACTAATTCATAAACTGTC 1

RESULT 20
CQ786170
LOCUS      21 bp DNA linear PAT 24-MAR-2004
DEFINITION Sequence 58 from Patent WO2004018676.
ACCESSION  CQ786170
VERSION     CQ786170.1 GI:45721273
KEYWORDS   .
SOURCE     synthetic construct
ORGANISM   other sequences; artificial sequences.
REFERENCE  1
AUTHORS    Jansen,B., Gleave,M.E., Signaevsky,M., Beraldi,E., Trougakos,I. and
            Gonos,E.
TITLE      Rnai probes targeting cancer-related proteins
JOURNAL    Patent: WO 2004018676-A 58 04-MAR-2004;
            The University of British Columbia (CA)
FEATURES   Location/Qualifiers
            source
            1..21
                /organism="synthetic construct"
                /mol_type="unassigned DNA"
                /db_xref="taxon:32630"
                /note="RNAi for human clusterin"

Query Match      1.3%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 482 CCAGAGCTCGCCCTTCTACTT 502
      |||||
Db 1 CCAGAGCTCGCCCTTCTACTT 21

RESULT 21
CQ786171/c
LOCUS      21 bp DNA linear PAT 24-MAR-2004
DEFINITION Sequence 59 from Patent WO2004018676.
ACCESSION  CQ786171
VERSION     CQ786171.1 GI:45721274
KEYWORDS   .
SOURCE     synthetic construct
ORGANISM   other sequences; artificial sequences.
REFERENCE  1
AUTHORS    Jansen,B., Gleave,M.E., Signaevsky,M., Beraldi,E., Trougakos,I. and
            Gonos,E.
TITLE      Rnai probes targeting cancer-related proteins
JOURNAL    Patent: WO 2004018676-A 59 04-MAR-2004;
            The University of British Columbia (CA)
FEATURES   Location/Qualifiers
            source
            1..21
                /organism="synthetic construct"
                /mol_type="unassigned DNA"
                /db_xref="taxon:32630"
                /note="RNAi for human clusterin"

Query Match      1.3%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 480 ACCAGAGCTCGCCCTTCTAC 500
      |||||
Db 21 AACAGAGCTCGCCCTTCTAC 1

RESULT 22
CQ786173
LOCUS      21 bp DNA linear PAT 24-MAR-2004
DEFINITION Sequence 61 from Patent WO2004018676.
ACCESSION  CQ786173
VERSION     CQ786173.1 GI:45721276
KEYWORDS   .
SOURCE     synthetic construct
ORGANISM   other sequences; artificial sequences.
REFERENCE  1
AUTHORS    Jansen,B., Gleave,M.E., Signaevsky,M., Beraldi,E., Trougakos,I. and
            Gonos,E.
TITLE      Rnai probes targeting cancer-related proteins
JOURNAL    Patent: WO 2004018676-A 61 04-MAR-2004;
            The University of British Columbia (CA)
FEATURES   Location/Qualifiers
            source
            1..21
                /organism="synthetic construct"
                /mol_type="unassigned DNA"
                /db_xref="taxon:32630"
                /note="RNAi for human clusterin"

Query Match      1.3%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 713 GTCCCGCATCGTCCGAGCTT 733
      |||||
Db 1 GTCCCGCATCGTCCGAGCTT 21

RESULT 23
CQ786174/c
LOCUS      21 bp DNA linear PAT 24-MAR-2004
DEFINITION Sequence 62 from Patent WO2004018676.
ACCESSION  CQ786174
VERSION     CQ786174.1 GI:45721277
KEYWORDS   .
SOURCE     synthetic construct
```

```
ORGANISM      synthetic construct
other sequences; artificial sequences.
REFERENCE
AUTHORS      Jansen,B., Gleave,M.E., Signaevsky,M., Beraldi,E., Trougakos,I. and
              Gonos,E.
TITLE        Rnai probes targeting cancer-related proteins
JOURNAL      Patent: WO 2004018676-A 62 04-MAR-2004;
              The University of British Columbia (CA)
FEATURES
source
1. .21
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/notes="RNAi for human clusterin"

Query Match      1.3%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 711 AAGTCCCGCATCGTCCGCAGC 731
Db 21 AAGTCCCGCATCGTCCGCAGC 1

RESULT 24
LOCUS      CQ786176          21 bp      DNA          linear          PAT 24-MAR-2004
DEFINITION      Sequence 64 from Patent WO2004018676.
ACCESSION      CQ786176
VERSION      CQ786176.1 GI:45721279
KEYWORDS
SOURCE      synthetic construct
ORGANISM      other sequences; artificial sequences.
REFERENCE
AUTHORS      Jansen,B., Gleave,M.E., Signaevsky,M., Beraldi,E., Trougakos,I. and
              Gonos,E.
TITLE        Rnai probes targeting cancer-related proteins
JOURNAL      Patent: WO 2004018676-A 64 04-MAR-2004;
              The University of British Columbia (CA)
FEATURES
source
1. .21
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/notes="RNAi for human clusterin"

Query Match      1.3%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1615 CTAATTCATATAAACTGCTT 1635
Db 1 CTAATTCATATAAACTGCTT 21

RESULT 25
LOCUS      CQ786177/c          21 bp      DNA          linear          PAT 24-MAR-2004
DEFINITION      Sequence 65 from Patent WO2004018676.
ACCESSION      CQ786177
VERSION      CQ786177.1 GI:45721280
KEYWORDS
SOURCE      synthetic construct
ORGANISM      other sequences; artificial sequences.
REFERENCE
AUTHORS      Jansen,B., Gleave,M.E., Signaevsky,M., Beraldi,E., Trougakos,I. and
              Gonos,E.
TITLE        Rnai probes targeting cancer-related proteins
JOURNAL      Patent: WO 2004018676-A 65 04-MAR-2004;
              The University of British Columbia (CA)
FEATURES
source
1. .21
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/notes="RNAi for human clusterin"

Query Match      1.3%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1615 CTAATTCATATAAACTGCTT 1635
Db 1 CTAATTCATATAAACTGCTT 21

RESULT 26
LOCUS      CQ786614/c          21 bp      DNA          linear          PAT 24-MAR-2004
DEFINITION      Sequence 3 from Patent WO2004018675.
ACCESSION      CQ786614
VERSION      CQ786614.1 GI:45721634
KEYWORDS
SOURCE      Homo sapiens (human)
ORGANISM      Homo sapiens
              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS      Jansen,B.
TITLE        Treatment of melanoma by reduction in clusterin levels
JOURNAL      Patent: WO 2004018675-A 3 04-MAR-2004;
              The University of British Columbia (CA); Gleave, Martin E. (CA)
FEATURES
source
1. .21
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match      1.3%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 CCGAGGCGTGCAAGACTCCA 36
Db 21 CCGAGGCGTGCAAGACTCCA 1

RESULT 27
LOCUS      CQ786615/c          21 bp      DNA          linear          PAT 24-MAR-2004
DEFINITION      Sequence 4 from Patent WO2004018675.
ACCESSION      CQ786615
VERSION      CQ786615.1 GI:45721635
KEYWORDS
SOURCE      Homo sapiens (human)
ORGANISM      Homo sapiens
              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS      Jansen,B.
TITLE        Treatment of melanoma by reduction in clusterin levels
JOURNAL      Patent: WO 2004018675-A 4 04-MAR-2004;
              The University of British Columbia (CA); Gleave, Martin E. (CA)
FEATURES
source
1. .21
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match      1.3%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 48 ATGATGNAGACTCTGCTGCTG 68
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|||||
Db 21 ATGATGAAGACTCTGCTGCTG 1

RESULT 28
CQ786616/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1
AUTHORS
Jansen, B.
TITLE
Treatment of melanoma by reduction in clusterin levels
JOURNAL
Patent: WO 2004018675-A 5 04-MAR-2004;
The University of British Columbia (CA); Gleave, Martin E. (CA)
FEATURES
Location/Qualifiers
1..21
source
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 1.3%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 114 GACCAGACGGTCTCAGACAAAT 134
|||||
Db 21 GACCAGACGGTCTCAGACAAAT 1

Query Match 1.3%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 114 GACCAGACGGTCTCAGACAAAT 134
|||||
Db 21 GACCAGACGGTCTCAGACAAAT 1

RESULT 29
CQ786617/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1
AUTHORS
Jansen, B.
TITLE
Treatment of melanoma by reduction in clusterin levels
JOURNAL
Patent: WO 2004018675-A 6 04-MAR-2004;
The University of British Columbia (CA); Gleave, Martin E. (CA)
FEATURES
Location/Qualifiers
1..21
source
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 1.3%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 316 AATCAGAGACAAAGCTGAAGG 336
|||||
Db 21 AATCAGAGACAAAGCTGAAGG 1

Query Match 1.3%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 316 AATCAGAGACAAAGCTGAAGG 336
|||||
Db 21 AATCAGAGACAAAGCTGAAGG 1

RESULT 30
CQ786618/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1
AUTHORS
Jansen, B.
TITLE
Treatment of melanoma by reduction in clusterin levels
JOURNAL
Patent: WO 2004018675-A 7 04-MAR-2004;
The University of British Columbia (CA); Gleave, Martin E. (CA)
FEATURES
Location/Qualifiers
1..21
source
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 1.3%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 316 AATCAGAGACAAAGCTGAAGG 336
|||||
Db 21 AATCAGAGACAAAGCTGAAGG 1

RESULT 31
CQ786619/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1
AUTHORS
Jansen, B.
TITLE
Treatment of melanoma by reduction in clusterin levels
JOURNAL
Patent: WO 2004018675-A 8 04-MAR-2004;
The University of British Columbia (CA); Gleave, Martin E. (CA)
FEATURES
Location/Qualifiers
1..21
source
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 1.3%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 515 TGACCGCATCGACTCCCTGCT 535
|||||
Db 21 TGACCGCATCGACTCCCTGCT 1

RESULT 32
CQ786620/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1
AUTHORS
Jansen, B.
TITLE
Treatment of melanoma by reduction in clusterin levels
JOURNAL
Patent: WO 2004018675-A 9 04-MAR-2004;
The University of British Columbia (CA); Gleave, Martin E. (CA)
FEATURES
Location/Qualifiers
1..21
source
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 1.3%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 716 CCGCATCGTCCGAGCTTGAT 736
|||||
Db 21 CCGCATCGTCCGAGCTTGAT 1

RESULT 33
CQ786621/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1
AUTHORS
Jansen, B.
TITLE
Treatment of melanoma by reduction in clusterin levels
JOURNAL
Patent: WO 2004018675-A 10 04-MAR-2004;
The University of British Columbia (CA); Gleave, Martin E. (CA)
FEATURES
Location/Qualifiers
1..21
source
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 1.3%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 716 CCGCATCGTCCGAGCTTGAT 736
|||||
Db 21 CCGCATCGTCCGAGCTTGAT 1
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/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 1.3%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 916 ACAACTCCACGGCGCTGCTGC 936
Db 21 ACAACTCCACGGCGCTGCTGC 1

RESULT 33
LOCUS CQ786621/c 21 bp DNA linear PAT 24-MAR-2004
DEFINITION Sequence 10 from Patent WO2004018675.
ACCESSION CQ786621
VERSION CQ786621.1 GI:45721641
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Jansen,B.
TITLE Treatment of melanoma by reduction in clusterin levels
JOURNAL Patent: WO 2004018675-A 10 04-MAR-2004;
The University of British Columbia (CA); Gleave, Martin E. (CA)
FEATURES
source
Location/Qualifiers
1..21
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 1.3%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1516 AGGCCCCCAACTCGCCGAGC 1536
Db 21 AGGCCCCCAACTCGCCGAGC 1

RESULT 36
LOCUS CQ786631 21 bp DNA linear PAT 24-MAR-2004
DEFINITION Sequence 20 from Patent WO2004018675.
ACCESSION CQ786631
VERSION CQ786631.1 GI:45721651
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1
AUTHORS Jansen,B.
TITLE Treatment of melanoma by reduction in clusterin levels
JOURNAL Patent: WO 2004018675-A 20 04-MAR-2004;
The University of British Columbia (CA); Gleave, Martin E. (CA)
FEATURES
source
Location/Qualifiers
1..21
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="RNAi for human clusterin"

Query Match 1.3%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 482 CCAGAGCTCGCCCTTCTACTT 502
Db 1 CCAGAGCTCGCCCTTCTACTT 21

RESULT 37
LOCUS CQ786632/c 21 bp DNA linear PAT 24-MAR-2004
DEFINITION Sequence 21 from Patent WO2004018675.
ACCESSION CQ786632
VERSION CQ786632.1 GI:45721652
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM synthetic construct
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/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 1.3%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 916 ACAACTCCACGGCGCTGCTGC 936
Db 21 ACAACTCCACGGCGCTGCTGC 1

RESULT 33
LOCUS CQ786621/c 21 bp DNA linear PAT 24-MAR-2004
DEFINITION Sequence 10 from Patent WO2004018675.
ACCESSION CQ786621
VERSION CQ786621.1 GI:45721641
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Jansen,B.
TITLE Treatment of melanoma by reduction in clusterin levels
JOURNAL Patent: WO 2004018675-A 10 04-MAR-2004;
The University of British Columbia (CA); Gleave, Martin E. (CA)
FEATURES
source
Location/Qualifiers
1..21
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 1.3%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1115 CTCCTTGCTGGAGCAGCTGAA 1135
Db 21 CTCCTTGCTGGAGCAGCTGAA 1

RESULT 34
LOCUS CQ786622/c 21 bp DNA linear PAT 24-MAR-2004
DEFINITION Sequence 11 from Patent WO2004018675.
ACCESSION CQ786622
VERSION CQ786622.1 GI:45721642
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Jansen,B.
TITLE Treatment of melanoma by reduction in clusterin levels
JOURNAL Patent: WO 2004018675-A 11 04-MAR-2004;
The University of British Columbia (CA); Gleave, Martin E. (CA)
FEATURES
source
Location/Qualifiers
1..21
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 1.3%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1316 CTCAGGAGAACCCCTAAATT 1336
Db 21 CTCAGGAGAACCCCTAAATT 1
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other sequences; artificial sequences.
1
REFERENCE
AUTHORS      Jansen,B.
TITLE        Treatment of melanoma by reduction in clusterin levels
JOURNAL      Patent: WO 2004018675-A 21 04-MAR-2004;
              The University of British Columbia (CA); Gleave, Martin E. (CA)
FEATURES
source
1. .21
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="RNAi for human clusterin"

Query Match      1.3%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 480 AACGAGCTCGCCCTTCTAC 500
Db 21 AACGAGCTCGCCCTTCTAC 1

RESULT 38
CQ786633
LOCUS          CQ786633      21 bp      DNA      linear      PAT 24-MAR-2004
DEFINITION    Sequence 22 from Patent WO2004018675.
ACCESSION     CQ786633
VERSION       CQ786633.1 GI:45721653
KEYWORDS      .
SOURCE        synthetic construct
ORGANISM      other sequences; artificial sequences.
REFERENCE     1
AUTHORS       Jansen,B.
TITLE         Treatment of melanoma by reduction in clusterin levels
JOURNAL       Patent: WO 2004018675-A 22 04-MAR-2004;
              The University of British Columbia (CA); Gleave, Martin E. (CA)
FEATURES
source
1. .21
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="RNAi for human clusterin"

Query Match      1.3%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1100 GATGCTCAACACCTCTCTT 1120
Db 1 GATGCTCAACACCTCTCTT 21

RESULT 39
CQ786634/c
LOCUS          CQ786634      21 bp      DNA      linear      PAT 24-MAR-2004
DEFINITION    Sequence 23 from Patent WO2004018675.
ACCESSION     CQ786634
VERSION       CQ786634.1 GI:45721654
KEYWORDS      .
SOURCE        synthetic construct
ORGANISM      other sequences; artificial sequences.
REFERENCE     1
AUTHORS       Jansen,B.
TITLE         Treatment of melanoma by reduction in clusterin levels
JOURNAL       Patent: WO 2004018675-A 23 04-MAR-2004;
              The University of British Columbia (CA); Gleave, Martin E. (CA)
FEATURES
source
1. .21
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"

other sequences; artificial sequences.
1
REFERENCE
AUTHORS      Jansen,B.
TITLE        Treatment of melanoma by reduction in clusterin levels
JOURNAL      Patent: WO 2004018675-A 21 04-MAR-2004;
              The University of British Columbia (CA); Gleave, Martin E. (CA)
FEATURES
source
1.3%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1098 AAGATGCTCAACACCTCTCTC 1118
Db 21 AAGATGCTCAACACCTCTCTC 1

RESULT 40
CQ786636/c
LOCUS          CQ786636      21 bp      DNA      linear      PAT 24-MAR-2004
DEFINITION    Sequence 25 from Patent WO2004018675.
ACCESSION     CQ786636
VERSION       CQ786636.1 GI:45721656
KEYWORDS      .
SOURCE        synthetic construct
ORGANISM      other sequences; artificial sequences.
REFERENCE     1
AUTHORS       Jansen,B.
TITLE         Treatment of melanoma by reduction in clusterin levels
JOURNAL       Patent: WO 2004018675-A 25 04-MAR-2004;
              The University of British Columbia (CA); Gleave, Martin E. (CA)
FEATURES
source
1. .21
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="RNAi for human clusterin"

Query Match      1.3%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1613 AACTAATTCATAAACTGTC 1633
Db 21 AACTAATTCATAAACTGTC 1

RESULT 41
CQ786647
LOCUS          CQ786647      21 bp      DNA      linear      PAT 24-MAR-2004
DEFINITION    Sequence 36 from Patent WO2004018675.
ACCESSION     CQ786647
VERSION       CQ786647.1 GI:45721667
KEYWORDS      .
SOURCE        synthetic construct
ORGANISM      other sequences; artificial sequences.
REFERENCE     1
AUTHORS       Jansen,B.
TITLE         Treatment of melanoma by reduction in clusterin levels
JOURNAL       Patent: WO 2004018675-A 36 04-MAR-2004;
              The University of British Columbia (CA); Gleave, Martin E. (CA)
FEATURES
source
1. .21
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="RNAi for human clusterin"

Query Match      1.3%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 482 CCAGAGCTCGCCCTTCTACTT 502
Db 1 CCAGAGCTCGCCCTTCTACTT 21
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RESULT 42
CQ786648/c
LOCUS          CQ786648          21 bp    DNA
DEFINITION     Sequence 37 from Patent WO2004018675.
ACCESSION      CQ786648
VERSION        CQ786648.1  GI:45721668
KEYWORDS       .
SOURCE         synthetic construct
ORGANISM       other sequences; artificial sequences.
REFERENCE      1
AUTHORS        Jansen,B.
TITLE          Treatment of melanoma by reduction in clusterin levels
JOURNAL        Patent: WO 2004018675-A 37 04-MAR-2004;
                The University of British Columbia (CA); Gleave, Martin E. (CA)
FEATURES       Location/Qualifiers
source         1..21
                /organism="synthetic construct"
                /mol_type="unassigned DNA"
                /db_xref="taxon:32630"
                /note="RNAi for human clusterin"
Query Match    1.3%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 20;
Matches        21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY             480 AACGAGGCTCGCCCTTCTAC 500
Db             21 AACGAGGCTCGCCCTTCTAC 1
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                /organism="synthetic construct"
                /mol_type="unassigned DNA"
                /db_xref="taxon:32630"
                /note="RNAi for human clusterin"
Query Match    1.3%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 20;
Matches        21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY             480 AACGAGGCTCGCCCTTCTAC 500
Db             21 AACGAGGCTCGCCCTTCTAC 1
                |||||
                /organism="synthetic construct"
                /mol_type="unassigned DNA"
                /db_xref="taxon:32630"
                /note="RNAi for human clusterin"
RESULT 43
CQ786649
LOCUS          CQ786649          21 bp    DNA
DEFINITION     Sequence 38 from Patent WO2004018675.
ACCESSION      CQ786649
VERSION        CQ786649.1  GI:45721669
KEYWORDS       .
SOURCE         synthetic construct
ORGANISM       other sequences; artificial sequences.
REFERENCE      1
AUTHORS        Jansen,B.
TITLE          Treatment of melanoma by reduction in clusterin levels
JOURNAL        Patent: WO 2004018675-A 38 04-MAR-2004;
                The University of British Columbia (CA); Gleave, Martin E. (CA)
FEATURES       Location/Qualifiers
source         1..21
                /organism="synthetic construct"
                /mol_type="unassigned DNA"
                /db_xref="taxon:32630"
                /note="RNAi for human clusterin"
Query Match    1.3%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 20;
Matches        21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY             713 GTCCCGCATCGTCGCAGCTT 733
Db             1 GTCCCGCATCGTCGCAGCTT 21
                |||||
                /organism="synthetic construct"
                /mol_type="unassigned DNA"
                /db_xref="taxon:32630"
                /note="RNAi for human clusterin"
RESULT 44
CQ786650/c
LOCUS          CQ786650          21 bp    DNA
DEFINITION     Sequence 39 from Patent WO2004018675.
ACCESSION      CQ786650
VERSION        CQ786650.1  GI:45721670
KEYWORDS       .
SOURCE         synthetic construct
ORGANISM       other sequences; artificial sequences.
REFERENCE      1
AUTHORS        Jansen,B.
TITLE          Treatment of melanoma by reduction in clusterin levels
JOURNAL        Patent: WO 2004018675-A 41 04-MAR-2004;
                The University of British Columbia (CA); Gleave, Martin E. (CA)
FEATURES       Location/Qualifiers
source         1..21
                /organism="synthetic construct"
                /mol_type="unassigned DNA"
                /db_xref="taxon:32630"
                /note="RNAi for human clusterin"
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AUTHORS        Jansen,B.
TITLE          Treatment of melanoma by reduction in clusterin levels
JOURNAL        Patent: WO 2004018675-A 39 04-MAR-2004;
                The University of British Columbia (CA); Gleave, Martin E. (CA)
FEATURES       Location/Qualifiers
source         1..21
                /organism="synthetic construct"
                /mol_type="unassigned DNA"
                /db_xref="taxon:32630"
                /note="RNAi for human clusterin"
Query Match    1.3%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 20;
Matches        21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY             711 AAGTCCCGCATCGTCGCAGC 731
Db             21 AAGTCCCGCATCGTCGCAGC 1
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                /organism="synthetic construct"
                /mol_type="unassigned DNA"
                /db_xref="taxon:32630"
                /note="RNAi for human clusterin"
RESULT 45
CQ786651
LOCUS          CQ786651          21 bp    DNA
DEFINITION     Sequence 40 from Patent WO2004018675.
ACCESSION      CQ786651
VERSION        CQ786651.1  GI:45721671
KEYWORDS       .
SOURCE         synthetic construct
ORGANISM       other sequences; artificial sequences.
REFERENCE      1
AUTHORS        Jansen,B.
TITLE          Treatment of melanoma by reduction in clusterin levels
JOURNAL        Patent: WO 2004018675-A 40 04-MAR-2004;
                The University of British Columbia (CA); Gleave, Martin E. (CA)
FEATURES       Location/Qualifiers
source         1..21
                /organism="synthetic construct"
                /mol_type="unassigned DNA"
                /db_xref="taxon:32630"
                /note="RNAi for human clusterin"
Query Match    1.3%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 20;
Matches        21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY             1615 CTAATTCATATAAACTGCTT 1635
Db             1 CTAATTCATATAAACTGCTT 21
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                /organism="synthetic construct"
                /mol_type="unassigned DNA"
                /db_xref="taxon:32630"
                /note="RNAi for human clusterin"
RESULT 46
CQ786652/c
LOCUS          CQ786652          21 bp    DNA
DEFINITION     Sequence 41 from Patent WO2004018675.
ACCESSION      CQ786652
VERSION        CQ786652.1  GI:45721672
KEYWORDS       .
SOURCE         synthetic construct
ORGANISM       other sequences; artificial sequences.
REFERENCE      1
AUTHORS        Jansen,B.
TITLE          Treatment of melanoma by reduction in clusterin levels
JOURNAL        Patent: WO 2004018675-A 41 04-MAR-2004;
                The University of British Columbia (CA); Gleave, Martin E. (CA)
FEATURES       Location/Qualifiers
source         1..21
                /organism="synthetic construct"
                /mol_type="unassigned DNA"
                /db_xref="taxon:32630"
                /note="RNAi for human clusterin"
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Query Match 1.3%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1613 AACTAATTCATAAACTGTC 1633
Db 21 AACTAATTCATAAACTGTC 1

RESULT 47
AR208707
LOCUS AR208707 21 bp DNA linear PAT 20-JUN-2002
DEFINITION Sequence 6 from patent US 6383808.
ACCESSION AR208707
VERSION AR208707.1 GI:21509932
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 21)
AUTHORS Monia,B.P. and Freier,S.M.
TITLE Antisense inhibition of clusterin expression
JOURNAL Patent: US 6383808-A 6 07-MAY-2002;
FEATURES
source Location/Qualifiers
1..21
/mol_type="unknown"
/mol_type="unassigned DNA"

Query Match 1.3%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 766 TCCACGCCATGTTCCAGCCCT 786
Db 1 TCCACGCCATGTTCCAGCCCT 21

RESULT 48
AR236282
LOCUS AR236282 21 bp DNA linear PAT 20-DEC-2002
DEFINITION Sequence 14 from patent US 6464975.
ACCESSION AR236282
VERSION AR236282.1 GI:27280110
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 21)
AUTHORS Millis,A.J.T.
TITLE Compositions and methods for altering cell migration
JOURNAL Patent: US 6464975-A 14 15-OCT-2002;
FEATURES
source Location/Qualifiers
1..21
/mol_type="unknown"
/mol_type="genomic DNA"

Query Match 1.3%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 274 AAGCCAAGAGAAGAAGAGG 294
Db 1 AAGCCAAGAGAAGAAGAGG 21

RESULT 49
BD230318
LOCUS BD230318 24 bp DNA linear PAT 17-JUL-2003
DEFINITION Total genome radiation hybrid map of canine genome and its use for
identification of interesting genes.
ACCESSION BD230318
VERSION BD230318.1 GI:33040088
KEYWORDS JP 2002530091-A/187.

SOURCE Canis familiaris (dog)
ORGANISM Canis familiaris
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Pisipedia; Canidae; Canis.
REFERENCE 1 (bases 1 to 24)
AUTHORS Galibert,F. and Andre,C.
TITLE Total genome radiation hybrid map of canine genome and its use for
identification of interesting genes
JOURNAL Patent: JP 2002530091-A 187 17-SEP-2002;
COMMENT CENTRE NATIONAL DE LA RECHERCHE SCIENTIFIQUE
OS Canis familiaris (dog)
PN JP 2002530091-A/187
PD 17-SEP-2002
PF 15-NOV-1999 JP 2000582596
PR 13-NOV-1998 US 60/108193
PI FRANCIS GALIBERT, CATHERINE ANDRE
PC C12N15/09,C12Q1/68,C12N15/00
CC A0133
FH Key Location/Qualifiers
FT source 1..24
/mol_type="genomic DNA"
/db_xref="taxon:9615"

FEATURES
source Location/Qualifiers
1..24
/mol_type="genomic DNA"
/db_xref="taxon:9615"

Query Match 1.3%; Score 20.8; DB 1; Length 24;
Best Local Similarity 91.7%; Pred. No. 32;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1467 CCCCAGAGAGAGAGCTCGCAGTC 1490
Db 1 CCCCAGAGAGAGAGCTCGCAGTC 24

RESULT 50
AR531218
LOCUS AR531218 21 bp DNA linear PAT 08-OCT-2004
DEFINITION Sequence 2421 from patent US 6727063.
ACCESSION AR531218
VERSION AR531218.1 GI:53919655
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 21)
AUTHORS Lander,S.S., Cargill,M., Ireland,J.S., Bolk,S., Daley,G.Q. and
McCarthy,J.J.
TITLE Single nucleotide polymorphisms in genes
JOURNAL Patent: US 6727063-A 2421 27-APR-2004;
FEATURES
source Location/Qualifiers
1..21
/mol_type="unknown"
/mol_type="genomic DNA"

Query Match 1.3%; Score 20.6; DB 1; Length 21;
Best Local Similarity 95.2%; Pred. No. 23;
Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1050 GAGAGGTTGACCGAGGAATAC 1070
Db 1 GAGAGGTTGACCGAGGAATAC 21

RESULT 51
AR531219
LOCUS AR531219 21 bp DNA linear PAT 08-OCT-2004
DEFINITION Sequence 2422 from patent US 6727063.
ACCESSION AR531219
VERSION AR531219.1 GI:53919656
KEYWORDS
SOURCE Unknown.
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QY	1105	TCAACACCTCCTCTGCTGG	1125
Db	1	TCAACACCTCYTCTTGCTGG	21
RESULT 54			
AX097243			
LOCUS	21 bp	DNA	linear PAT 30-MAR-2001
DEFINITION	Sequence 2421 from Patent WO0118250.		
ACCESSION	AX097243		
VERSION	AX097243.1 GI:13513638		
KEYWORDS	.		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
	1 Lander,E.S., Gargill,M., Ireland,J.S., Bolk,S., Daley,G.Q. and McCarthy,J.J.		
TITLE	Single nucleotide polymorphisms in genes		
JOURNAL	Patent: WO 0118250-A 2421 15-MAR-2001;		
	WHITEHEAD INSTITUTE FOR BIOMEDICAL RESEARCH (US) ; Millennium Pharmaceuticals, Inc. (US)		
FEATURES	Location/Qualifiers		
source	1..21		
	/organism="Homo sapiens"		
	/mol_type="unassigned DNA"		
	/db_xref="taxon:9606"		
Query Match	1.3%; Score 20.6; DB 1; Length 21;		
Best Local Similarity	95.2%; Pred. No. 23;		
Matches	20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;		
QY	1050	GAGAGTTGACCAGAAATAC	1070
Db	1	GAGAGTTTGAYCAGAAATAC	21
RESULT 55			
AX097244			
LOCUS	21 bp	DNA	linear PAT 30-MAR-2001
DEFINITION	Sequence 2422 from Patent WO0118250.		
ACCESSION	AX097244		
VERSION	AX097244.1 GI:13513640		
KEYWORDS	.		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
	1 Lander,E.S., Gargill,M., Ireland,J.S., Bolk,S., Daley,G.Q. and McCarthy,J.J.		
TITLE	Single nucleotide polymorphisms in genes		
JOURNAL	Patent: WO 0118250-A 2422 15-MAR-2001;		
	WHITEHEAD INSTITUTE FOR BIOMEDICAL RESEARCH (US) ; Millennium Pharmaceuticals, Inc. (US)		
FEATURES	Location/Qualifiers		
source	1..21		
	/organism="Homo sapiens"		
	/mol_type="unassigned DNA"		
	/db_xref="taxon:9606"		
Query Match	1.3%; Score 20.6; DB 1; Length 21;		
Best Local Similarity	95.2%; Pred. No. 23;		
Matches	20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;		
QY	999	CCCTCCCAGGCTAAGCTGCGG	1019
Db	1	CCTCCCAGGYTAAGCTGCGG	21
RESULT 56			



AX097245  
LOCUS 21 bp DNA linear PAT 30-MAR-2001  
DEFINITION Sequence 2423 from Patent WO0118250.  
ACCESSION AX097245  
VERSION AX097245.1 GI:13513642  
KEYWORDS Homo sapiens (human)  
SOURCE Homo sapiens  
ORGANISM Homo sapiens  
REFERENCE 1  
AUTHORS Lander, E.S., Gargill, M., Ireland, J.S., Bolk, S., Daley, G.Q. and McCarthy, J.J.  
TITLE Single nucleotide polymorphisms in genes  
JOURNAL Patent: WO 0118250-A 2423 15-MAR-2001;  
WHITEHEAD INSTITUTE FOR BIOMEDICAL RESEARCH (US) ; Millennium Pharmaceuticals, Inc. (US)  
FEATURES  
source Location/Qualifiers  
1..21  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"  
Query Match 1.3%; Score 20.6; DB 1; Length 21;  
Best Local Similarity 95.2%; Pred. No. 23;  
Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 1170 CTCACGCGAGCGGAGACCCAG 1190  
Db 1 CTCACGCGAGCGGAGACCCAG 21  
RESULT 57  
AX097246  
LOCUS 21 bp DNA linear PAT 30-MAR-2001  
DEFINITION Sequence 2424 from Patent WO0118250.  
ACCESSION AX097246  
VERSION AX097246.1 GI:13513644  
KEYWORDS Homo sapiens (human)  
SOURCE Homo sapiens  
ORGANISM Homo sapiens  
REFERENCE 1  
AUTHORS Lander, E.S., Gargill, M., Ireland, J.S., Bolk, S., Daley, G.Q. and McCarthy, J.J.  
TITLE Single nucleotide polymorphisms in genes  
JOURNAL Patent: WO 0118250-A 2424 15-MAR-2001;  
WHITEHEAD INSTITUTE FOR BIOMEDICAL RESEARCH (US) ; Millennium Pharmaceuticals, Inc. (US)  
FEATURES  
source Location/Qualifiers  
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/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"  
Query Match 1.3%; Score 20.6; DB 1; Length 21;  
Best Local Similarity 95.2%; Pred. No. 23;  
Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 1105 TCAACACCTCTCTCTGCTGG 1125  
Db 1 TCAACACCTCTCTCTGCTGG 21  
RESULT 58  
CQ803453  
LOCUS 20 bp DNA linear PAT 10-MAY-2004  
DEFINITION Sequence 5 from Patent WO2004035827.  
ACCESSION CQ803453  
VERSION CQ803453.1 GI:47110310  
KEYWORDS  
SOURCE unidentified

ORGANISM unidentified  
REFERENCE 1  
AUTHORS Breban, M., Gidrol, X., Marion, S. and Chiochia, G.  
TITLE Microarrays allowing molecular profiling of rheumatoid arthritis comparatively to osteoarthritis and their use  
JOURNAL Patent: WO 2004035827-A 5 29-APR-2004;  
INSERM, The French Institute of Health and Medical Research (FR); ASSISTANCE PUBLIQUE - HOPITAUX DE PARIS (FR); COMMISSARIAT A L'ENERGIE ATOMIQUE (FR)  
FEATURES  
source Location/Qualifiers  
1..20  
/organism="unidentified"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32644"  
misc\_feature 1..20  
/note="CLU forward primer for PCR"  
Query Match 1.2%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 24;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1180 GCGAAGACCAGTACTATCTG 1199  
Db 1 GCGAAGACCAGTACTATCTG 20  
RESULT 59  
CQ803454/c  
LOCUS 20 bp DNA linear PAT 10-MAY-2004  
DEFINITION Sequence 6 from Patent WO2004035827.  
ACCESSION CQ803454  
VERSION CQ803454.1 GI:47110311  
KEYWORDS  
SOURCE unidentified  
ORGANISM unidentified  
REFERENCE 1  
AUTHORS Breban, M., Gidrol, X., Marion, S. and Chiochia, G.  
TITLE Microarrays allowing molecular profiling of rheumatoid arthritis comparatively to osteoarthritis and their use  
JOURNAL Patent: WO 2004035827-A 6 29-APR-2004;  
INSERM, The French Institute of Health and Medical Research (FR); ASSISTANCE PUBLIQUE - HOPITAUX DE PARIS (FR); COMMISSARIAT A L'ENERGIE ATOMIQUE (FR)  
FEATURES  
source Location/Qualifiers  
1..20  
/organism="unidentified"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32644"  
misc\_feature 1..20  
/note="CLU reverse primer for PCR"  
Query Match 1.2%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 24;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1361 GCTGCAGGAATACCCGAAAA 1380  
Db 20 GCTGCAGGAATACCCGAAAA 1  
RESULT 60  
AR208715/c  
LOCUS 20 bp DNA linear PAT 20-JUN-2002  
DEFINITION Sequence 14 from patent US 6383808.  
ACCESSION AR208715  
VERSION AR208715.1 GI:21509942  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 20)

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AUTHORS      Monia,B.P. and Freier,S.M.
TITLE         Antisense inhibition of clusterin expression
JOURNAL       Patent: US 6383808-A 14 07-MAY-2002;
FEATURES      Location/Qualifiers
source        1..20
              /organism="unknown"
              /mol_type="unassigned DNA"

Query Match      1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 TGACCGAGGCGTCCAAAGAC 32
Db 20 TGACCGAGGCGTCCAAAGAC 1

RESULT 61
AR208716/c
LOCUS          AR208716          20 bp      DNA      linear      PAT 20-JUN-2002
DEFINITION     Sequence 15 from patent US 6383808.
ACCESSION      AR208716
VERSION        AR208716.1  GI:21509944
KEYWORDS       .
SOURCE         Unknown.
ORGANISM       Unclassified.
REFERENCE      1 (bases 1 to 20)
AUTHORS        Monia,B.P. and Freier,S.M.
TITLE          Antisense inhibition of clusterin expression
JOURNAL        Patent: US 6383808-A 15 07-MAY-2002;
FEATURES       Location/Qualifiers
source        1..20
              /organism="unknown"
              /mol_type="unassigned DNA"

Query Match      1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 21 GCGTGAAGACTCCAGAAT 40
Db 20 GCGTGAAGACTCCAGAAT 1

RESULT 62
AR208717/c
LOCUS          AR208717          20 bp      DNA      linear      PAT 20-JUN-2002
DEFINITION     Sequence 16 from patent US 6383808.
ACCESSION      AR208717
VERSION        AR208717.1  GI:21509945
KEYWORDS       .
SOURCE         Unknown.
ORGANISM       Unclassified.
REFERENCE      1 (bases 1 to 20)
AUTHORS        Monia,B.P. and Freier,S.M.
TITLE          Antisense inhibition of clusterin expression
JOURNAL        Patent: US 6383808-A 16 07-MAY-2002;
FEATURES       Location/Qualifiers
source        1..20
              /organism="unknown"
              /mol_type="unassigned DNA"

Query Match      1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 39 ATTGGAGGCATGATGAAGAC 58
Db 20 ATTGGAGGCATGATGAAGAC 1

AUTHORS      Monia,B.P. and Freier,S.M.
TITLE         Antisense inhibition of clusterin expression
JOURNAL       Patent: US 6383808-A 14 07-MAY-2002;
FEATURES      Location/Qualifiers
source        1..20
              /organism="unknown"
              /mol_type="unassigned DNA"

Query Match      1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 TGACCGAGGCGTCCAAAGAC 32
Db 20 TGACCGAGGCGTCCAAAGAC 1

RESULT 63
AR208718/c
LOCUS          AR208718          20 bp      DNA      linear      PAT 20-JUN-2002
DEFINITION     Sequence 17 from patent US 6383808.
ACCESSION      AR208718
VERSION        AR208718.1  GI:21509946
KEYWORDS       .
SOURCE         Unknown.
ORGANISM       Unclassified.
REFERENCE      1 (bases 1 to 20)
AUTHORS        Monia,B.P. and Freier,S.M.
TITLE          Antisense inhibition of clusterin expression
JOURNAL        Patent: US 6383808-A 17 07-MAY-2002;
FEATURES       Location/Qualifiers
source        1..20
              /organism="unknown"
              /mol_type="unassigned DNA"

Query Match      1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 77 GCTGCTGCTGACCTGGGAGA 96
Db 20 GCTGCTGCTGACCTGGGAGA 1

RESULT 64
AR208719/c
LOCUS          AR208719          20 bp      DNA      linear      PAT 20-JUN-2002
DEFINITION     Sequence 18 from patent US 6383808.
ACCESSION      AR208719
VERSION        AR208719.1  GI:21509947
KEYWORDS       .
SOURCE         Unknown.
ORGANISM       Unclassified.
REFERENCE      1 (bases 1 to 20)
AUTHORS        Monia,B.P. and Freier,S.M.
TITLE          Antisense inhibition of clusterin expression
JOURNAL        Patent: US 6383808-A 18 07-MAY-2002;
FEATURES       Location/Qualifiers
source        1..20
              /organism="unknown"
              /mol_type="unassigned DNA"

Query Match      1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 101 GCAGGTCTCTGGGGACCAGA 120
Db 20 GCAGGTCTCTGGGGACCAGA 1

RESULT 65
AR208720/c
LOCUS          AR208720          20 bp      DNA      linear      PAT 20-JUN-2002
DEFINITION     Sequence 19 from patent US 6383808.
ACCESSION      AR208720
VERSION        AR208720.1  GI:21509949
KEYWORDS       .
SOURCE         Unknown.
ORGANISM       Unclassified.
REFERENCE      1 (bases 1 to 20)
AUTHORS        Monia,B.P. and Freier,S.M.
TITLE          Antisense inhibition of clusterin expression
JOURNAL        Patent: US 6383808-A 19 07-MAY-2002;
FEATURES       Location/Qualifiers
source        1..20
              /organism="unknown"
              /mol_type="unassigned DNA"
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/mol_type="unassigned DNA"

Query Match      1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 122 GGTCTCAGACAAATGAGCTCC 141
|||||
DB 20 GGTCTCAGACAAATGAGCTCC 1

RESULT 66
AR208721/c
LOCUS AR208721 20 bp DNA linear PAT 20-JUN-2002
DEFINITION Sequence 20 from patent US 6383808.
ACCESSION AR208721
VERSION AR208721.1 GI:21509950
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Monia,B.P. and Freier,S.M.
TITLE Antisense inhibition of clusterin expression
JOURNAL Patent: US 6383808-A 20 07-MAY-2002;
FEATURES Location/Qualifiers
source 1..20
/mol_type="unassigned DNA"

Query Match      1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 201 GGGGTGAACAGATTAAGAC 220
|||||
DB 20 GGGGTGAACAGATTAAGAC 1

RESULT 69
AR208724/c
LOCUS AR208724 20 bp DNA linear PAT 20-JUN-2002
DEFINITION Sequence 23 from patent US 6383808.
ACCESSION AR208724
VERSION AR208724.1 GI:21509954
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Monia,B.P. and Freier,S.M.
TITLE Antisense inhibition of clusterin expression
JOURNAL Patent: US 6383808-A 23 07-MAY-2002;
FEATURES Location/Qualifiers
source 1..20
/mol_type="unassigned DNA"

Query Match      1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 281 GAAGAAGAAAGAGGATGCC 300
|||||
DB 20 GAAGAAGAAAGAGGATGCC 1

RESULT 70
AR208725/c
LOCUS AR208725 20 bp DNA linear PAT 20-JUN-2002
DEFINITION Sequence 24 from patent US 6383808.
ACCESSION AR208725
VERSION AR208725.1 GI:21509955
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Monia,B.P. and Freier,S.M.
TITLE Antisense inhibition of clusterin expression
JOURNAL Patent: US 6383808-A 24 07-MAY-2002;
FEATURES Location/Qualifiers
source 1..20
/mol_type="unassigned DNA"

Query Match      1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 166 AGTACGTCAATAGGAATT 185
|||||
DB 20 AGTACGTCAATAGGAATT 1

RESULT 68
AR208723/c
LOCUS AR208723 20 bp DNA linear PAT 20-JUN-2002
DEFINITION Sequence 22 from patent US 6383808.
ACCESSION AR208723
VERSION AR208723.1 GI:21509952
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KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Monia,B.P. and Freier,S.M.
TITLE Antisense inhibition of clusterin expression
JOURNAL Patent: US 6383808-A 22 07-MAY-2002;
FEATURES Location/Qualifiers
source 1..20
/mol_type="unassigned DNA"

Query Match      1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 201 GGGGTGAACAGATTAAGAC 220
|||||
DB 20 GGGGTGAACAGATTAAGAC 1

RESULT 69
AR208724/c
LOCUS AR208724 20 bp DNA linear PAT 20-JUN-2002
DEFINITION Sequence 23 from patent US 6383808.
ACCESSION AR208724
VERSION AR208724.1 GI:21509954
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Monia,B.P. and Freier,S.M.
TITLE Antisense inhibition of clusterin expression
JOURNAL Patent: US 6383808-A 23 07-MAY-2002;
FEATURES Location/Qualifiers
source 1..20
/mol_type="unassigned DNA"

Query Match      1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 281 GAAGAAGAAAGAGGATGCC 300
|||||
DB 20 GAAGAAGAAAGAGGATGCC 1

RESULT 70
AR208725/c
LOCUS AR208725 20 bp DNA linear PAT 20-JUN-2002
DEFINITION Sequence 24 from patent US 6383808.
ACCESSION AR208725
VERSION AR208725.1 GI:21509955
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Monia,B.P. and Freier,S.M.
TITLE Antisense inhibition of clusterin expression
JOURNAL Patent: US 6383808-A 24 07-MAY-2002;
FEATURES Location/Qualifiers
source 1..20
/mol_type="unassigned DNA"

Query Match      1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 166 AGTACGTCAATAGGAATT 185
|||||
DB 20 AGTACGTCAATAGGAATT 1

RESULT 68
AR208723/c
LOCUS AR208723 20 bp DNA linear PAT 20-JUN-2002
DEFINITION Sequence 22 from patent US 6383808.
ACCESSION AR208723
VERSION AR208723.1 GI:21509952
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QY 286 AGAAGAGGATGCCCTTAAT 305
Db 20 AGAAGAGGATGCCCTTAAT 1

RESULT 71
AR208726/c
LOCUS AR208726 20 bp DNA linear PAT 20-JUN-2002
DEFINITION Sequence 25 from patent US 6383808.
ACCESSION AR208726
VERSION AR208726.1 GI:21509956
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Monia,B.P. and Freier,S.M.
TITLE Antisense inhibition of clusterin expression
JOURNAL Patent: US 6383808-A 25 07-MAY-2002;
FEATURES
    Location/Qualifiers
        source
            1..20
                /organism="unknown"
                /mol_type="unassigned DNA"

Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 298 CCTAAATGAGACCGGAA 317
Db 20 CCTAAATGAGACCGGAA 1

RESULT 72
AR208727/c
LOCUS AR208727 20 bp DNA linear PAT 20-JUN-2002
DEFINITION Sequence 26 from patent US 6383808.
ACCESSION AR208727
VERSION AR208727.1 GI:21509957
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Monia,B.P. and Freier,S.M.
TITLE Antisense inhibition of clusterin expression
JOURNAL Patent: US 6383808-A 26 07-MAY-2002;
FEATURES
    Location/Qualifiers
        source
            1..20
                /organism="unknown"
                /mol_type="unassigned DNA"

Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 307 AGACGAGGAATCAGAGACA 326
Db 20 AGACGAGGAATCAGAGACA 1

RESULT 73
AR208728/c
LOCUS AR208728 20 bp DNA linear PAT 20-JUN-2002
DEFINITION Sequence 27 from patent US 6383808.
ACCESSION AR208728
VERSION AR208728.1 GI:21509959
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Monia,B.P. and Freier,S.M.

TITLE Antisense inhibition of clusterin expression
JOURNAL Patent: US 6383808-A 27 07-MAY-2002;
FEATURES
    Location/Qualifiers
        source
            1..20
                /organism="unknown"
                /mol_type="unassigned DNA"

Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 324 ACAAGAGCTGAAGAGCTCCC 343
Db 20 ACAAGAGCTGAAGAGCTCCC 1

RESULT 74
AR208729/c
LOCUS AR208729 20 bp DNA linear PAT 20-JUN-2002
DEFINITION Sequence 28 from patent US 6383808.
ACCESSION AR208729
VERSION AR208729.1 GI:21509960
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Monia,B.P. and Freier,S.M.
TITLE Antisense inhibition of clusterin expression
JOURNAL Patent: US 6383808-A 28 07-MAY-2002;
FEATURES
    Location/Qualifiers
        source
            1..20
                /organism="unknown"
                /mol_type="unassigned DNA"

Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 359 GACCATGATGCCCTCTGGG 378
Db 20 GACCATGATGCCCTCTGGG 1

RESULT 75
AR208730/c
LOCUS AR208730 20 bp DNA linear PAT 20-JUN-2002
DEFINITION Sequence 29 from patent US 6383808.
ACCESSION AR208730
VERSION AR208730.1 GI:21509961
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Monia,B.P. and Freier,S.M.
TITLE Antisense inhibition of clusterin expression
JOURNAL Patent: US 6383808-A 29 07-MAY-2002;
FEATURES
    Location/Qualifiers
        source
            1..20
                /organism="unknown"
                /mol_type="unassigned DNA"

Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 364 TGATGGCCCTCTGGGAGAG 383
Db 20 TGATGGCCCTCTGGGAGAG 1

RESULT 76
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AR208731/c  
LOCUS AR208731 20 bp DNA linear PAT 20-JUN-2002  
DEFINITION Sequence 30 from patent US 6383808.  
ACCESSION AR208731  
VERSION AR208731.1 GI:21509962  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 20)  
AUTHORS Monia,B.P. and Freier,S.M.  
TITLE Antisense inhibition of clusterin expression  
JOURNAL Patent: US 6383808-A 30 07-MAY-2002;  
FEATURES  
source  
1. .20  
/organism="unknown"  
/mol\_type="unassigned DNA"  
Query Match 1.2%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 24;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 380 AGAGTGTAAGCCTGCTGA 399  
|||||  
Db 20 AGAGTGTAAGCCTGCTGA 1  
RESULT 77  
AR208732/c  
LOCUS AR208732 20 bp DNA linear PAT 20-JUN-2002  
DEFINITION Sequence 31 from patent US 6383808.  
ACCESSION AR208732  
VERSION AR208732.1 GI:21509964  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 20)  
AUTHORS Monia,B.P. and Freier,S.M.  
TITLE Antisense inhibition of clusterin expression  
JOURNAL Patent: US 6383808-A 31 07-MAY-2002;  
FEATURES  
source  
1. .20  
/organism="unknown"  
/mol\_type="unassigned DNA"  
Query Match 1.2%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 24;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 407 CTGCATGAAGTTCTACGCAC 426  
|||||  
Db 20 CTGCATGAAGTTCTACGCAC 1  
RESULT 78  
AR208733/c  
LOCUS AR208733 20 bp DNA linear PAT 20-JUN-2002  
DEFINITION Sequence 32 from patent US 6383808.  
ACCESSION AR208733  
VERSION AR208733.1 GI:21509965  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 20)  
AUTHORS Monia,B.P. and Freier,S.M.  
TITLE Antisense inhibition of clusterin expression  
JOURNAL Patent: US 6383808-A 32 07-MAY-2002;  
FEATURES  
source  
1. .20  
/organism="unknown"  
/mol\_type="unassigned DNA"

Query Match 1.2%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 24;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 443 CTCAGGCCTGGTTGGCGGCC 462  
|||||  
Db 20 CTCAGGCCTGGTTGGCGGCC 1  
RESULT 79  
AR208734/c  
LOCUS AR208734 20 bp DNA linear PAT 20-JUN-2002  
DEFINITION Sequence 33 from patent US 6383808.  
ACCESSION AR208734  
VERSION AR208734.1 GI:21509966  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 20)  
AUTHORS Monia,B.P. and Freier,S.M.  
TITLE Antisense inhibition of clusterin expression  
JOURNAL Patent: US 6383808-A 33 07-MAY-2002;  
FEATURES  
source  
1. .20  
/organism="unknown"  
/mol\_type="unassigned DNA"  
Query Match 1.2%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 24;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 444 TCAGGCCTGGTTGGCGGCCA 463  
|||||  
Db 20 TCAGGCCTGGTTGGCGGCCA 1  
RESULT 80  
AR208735/c  
LOCUS AR208735 20 bp DNA linear PAT 20-JUN-2002  
DEFINITION Sequence 34 from patent US 6383808.  
ACCESSION AR208735  
VERSION AR208735.1 GI:21509967  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 20)  
AUTHORS Monia,B.P. and Freier,S.M.  
TITLE Antisense inhibition of clusterin expression  
JOURNAL Patent: US 6383808-A 34 07-MAY-2002;  
FEATURES  
source  
1. .20  
/organism="unknown"  
/mol\_type="unassigned DNA"  
Query Match 1.2%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 24;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 455 TGGCCGCCACGCTTGAGGACT 474  
|||||  
Db 20 TGGCCGCCACGCTTGAGGACT 1  
RESULT 81  
AR208736/c  
LOCUS AR208736 20 bp DNA linear PAT 20-JUN-2002  
DEFINITION Sequence 35 from patent US 6383808.  
ACCESSION AR208736  
VERSION AR208736.1 GI:21509969  
KEYWORDS

SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 20)  
AUTHORS Monia,B.P. and Freier,S.M.  
TITLE Antisense inhibition of clusterin expression  
JOURNAL Patent: US 6383808-A 35 07-MAY-2002;  
FEATURES Location/Qualifiers  
source  
1..20  
/organism="unknown"  
/mol\_type="unassigned DNA"

Query Match 1..2%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 24;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 482 CCAGAGCTCGCCCTTCTACT 501  
|||||  
Db 20 CCAGAGCTCGCCCTTCTACT 1

RESULT 82  
AR208737/c  
LOCUS 20 bp DNA linear PAT 20-JUN-2002  
DEFINITION Sequence 36 from patent US 6383808.  
ACCESSION AR208737  
VERSION AR208737.1 GI:21509970  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 20)  
AUTHORS Monia,B.P. and Freier,S.M.  
TITLE Antisense inhibition of clusterin expression  
JOURNAL Patent: US 6383808-A 36 07-MAY-2002;  
FEATURES Location/Qualifiers  
source  
1..20  
/organism="unknown"  
/mol\_type="unassigned DNA"

Query Match 1..2%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 24;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 492 CCCTTCTACTCTGGATGAA 511  
|||||  
Db 20 CCCTTCTACTCTGGATGAA 1

RESULT 83  
AR208738/c  
LOCUS 20 bp DNA linear PAT 20-JUN-2002  
DEFINITION Sequence 37 from patent US 6383808.  
ACCESSION AR208738  
VERSION AR208738.1 GI:21509971  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 20)  
AUTHORS Monia,B.P. and Freier,S.M.  
TITLE Antisense inhibition of clusterin expression  
JOURNAL Patent: US 6383808-A 37 07-MAY-2002;  
FEATURES Location/Qualifiers  
source  
1..20  
/organism="unknown"  
/mol\_type="unassigned DNA"

Query Match 1..2%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 24;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 517 ACCGCATCGACTCCCTGCTG 536  
|||||

Db 20 ACCGCATCGACTCCCTGCTG 1  
|||||

RESULT 84  
AR208739/c  
LOCUS 20 bp DNA linear PAT 20-JUN-2002  
DEFINITION Sequence 38 from patent US 6383808.  
ACCESSION AR208739  
VERSION AR208739.1 GI:21509972  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 20)  
AUTHORS Monia,B.P. and Freier,S.M.  
TITLE Antisense inhibition of clusterin expression  
JOURNAL Patent: US 6383808-A 38 07-MAY-2002;  
FEATURES Location/Qualifiers  
source  
1..20  
/organism="unknown"  
/mol\_type="unassigned DNA"

Query Match 1..2%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 24;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 533 GCTGGAGAACGCCGCCAGC 552  
|||||  
Db 20 GCTGGAGAACGCCGCCAGC 1

RESULT 85  
AR208740/c  
LOCUS 20 bp DNA linear PAT 20-JUN-2002  
DEFINITION Sequence 39 from patent US 6383808.  
ACCESSION AR208740  
VERSION AR208740.1 GI:21509974  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 20)  
AUTHORS Monia,B.P. and Freier,S.M.  
TITLE Antisense inhibition of clusterin expression  
JOURNAL Patent: US 6383808-A 39 07-MAY-2002;  
FEATURES Location/Qualifiers  
source  
1..20  
/organism="unknown"  
/mol\_type="unassigned DNA"

Query Match 1..2%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 24;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 551 GCACAGCGCACATGCTGGATG 570  
|||||  
Db 20 GCACAGCGCACATGCTGGATG 1

RESULT 86  
AR208741/c  
LOCUS 20 bp DNA linear PAT 20-JUN-2002  
DEFINITION Sequence 40 from patent US 6383808.  
ACCESSION AR208741  
VERSION AR208741.1 GI:21509975  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 20)  
AUTHORS Monia,B.P. and Freier,S.M.  
TITLE Antisense inhibition of clusterin expression

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JOURNAL Patent: US 6383808-A 40 07-MAY-2002;
FEATURES
  source
    Location/Qualifiers
      1..20
      /organism="unknown"
      /mol_type="unassigned DNA"

Query Match
Best Local Similarity 1.2%; Score 20; DB 1; Length 20;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 553 AGACGCACATGCTGGGATGTC 572
Db 20 AGACGCACATGCTGGGATGTC 1

RESULT 87
AR208742/c
LOCUS
DEFINITION Sequence 41 from patent US 6383808.
ACCESSION AR208742
VERSION AR208742.1 GI:21509976
KEYWORDS
SOURCE
ORGANISM
  Unknown.
  Unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS Monia,B.P. and Freier,S.M.
TITLE Antisense inhibition of clusterin expression
JOURNAL Patent: US 6383808-A 41 07-MAY-2002;
FEATURES
  source
    Location/Qualifiers
      1..20
      /organism="unknown"
      /mol_type="unassigned DNA"

Query Match
Best Local Similarity 1.2%; Score 20; DB 1; Length 20;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 565 TGGATGTCATGCAGGACCAC 584
Db 20 TGGATGTCATGCAGGACCAC 1

RESULT 88
AR208743/c
LOCUS
DEFINITION Sequence 42 from patent US 6383808.
ACCESSION AR208743
VERSION AR208743.1 GI:21509977
KEYWORDS
SOURCE
ORGANISM
  Unknown.
  Unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS Monia,B.P. and Freier,S.M.
TITLE Antisense inhibition of clusterin expression
JOURNAL Patent: US 6383808-A 42 07-MAY-2002;
FEATURES
  source
    Location/Qualifiers
      1..20
      /organism="unknown"
      /mol_type="unassigned DNA"

Query Match
Best Local Similarity 1.2%; Score 20; DB 1; Length 20;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 567 GATGTCATGCAGGACCATT 586
Db 20 GATGTCATGCAGGACCATT 1

RESULT 89
AR208744/c
LOCUS
DEFINITION Sequence 43 from patent US 6383808.
ACCESSION AR208744
VERSION AR208744.1 GI:21509979
KEYWORDS
SOURCE
ORGANISM
  Unknown.
  Unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS Monia,B.P. and Freier,S.M.
TITLE Antisense inhibition of clusterin expression
JOURNAL Patent: US 6383808-A 43 07-MAY-2002;
FEATURES
  source
    Location/Qualifiers
      1..20
      /organism="unknown"
      /mol_type="unassigned DNA"

Query Match
Best Local Similarity 1.2%; Score 20; DB 1; Length 20;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 604 TCATAGACGAGCTCTTCCAG 623
Db 20 TCATAGACGAGCTCTTCCAG 1

RESULT 90
AR208745/c
LOCUS
DEFINITION Sequence 44 from patent US 6383808.
ACCESSION AR208745
VERSION AR208745.1 GI:21509980
KEYWORDS
SOURCE
ORGANISM
  Unknown.
  Unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS Monia,B.P. and Freier,S.M.
TITLE Antisense inhibition of clusterin expression
JOURNAL Patent: US 6383808-A 44 07-MAY-2002;
FEATURES
  source
    Location/Qualifiers
      1..20
      /organism="unknown"
      /mol_type="unassigned DNA"

Query Match
Best Local Similarity 1.2%; Score 20; DB 1; Length 20;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 608 AGACGAGCTCTTCCAGGACA 627
Db 20 AGACGAGCTCTTCCAGGACA 1

RESULT 91
AR208746/c
LOCUS
DEFINITION Sequence 45 from patent US 6383808.
ACCESSION AR208746
VERSION AR208746.1 GI:21509981
KEYWORDS
SOURCE
ORGANISM
  Unknown.
  Unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS Monia,B.P. and Freier,S.M.
TITLE Antisense inhibition of clusterin expression
JOURNAL Patent: US 6383808-A 45 07-MAY-2002;
FEATURES
  source
    Location/Qualifiers
      1..20
      /organism="unknown"
      /mol_type="unassigned DNA"
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Query Match      1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      613 AGCTCTTCCAGGACAGGTTTC 632
Db      20 AGCTCTTCCAGGACAGGTTTC 1

RESULT 92
AR208747/c
LOCUS      AR208747      20 bp      DNA      linear      PAT 20-JUN-2002
DEFINITION Sequence 46 from patent US 6383808.
ACCESSION AR208747
VERSION    AR208747.1 GI:21509982
KEYWORDS   .
SOURCE     Unknown.
ORGANISM   Unknown.
REFERENCE   1 (bases 1 to 20)
AUTHORS    Monia,B.P. and Freier,S.M.
TITLE      Antisense inhibition of clusterin expression
JOURNAL    Patent: US 6383808-A 46 07-MAY-2002;
FEATURES   Location/Qualifiers
            source
              1..20
                /organism="unknown"
                /mol_type="unassigned DNA"

Query Match      1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      775 TGTTCACGCGCTTCCTTGAG 794
Db      20 TGTTCACGCGCTTCCTTGAG 1

RESULT 95
AR208750/c
LOCUS      AR208750      20 bp      DNA      linear      PAT 20-JUN-2002
DEFINITION Sequence 49 from patent US 6383808.
ACCESSION AR208750
VERSION    AR208750.1 GI:21509986
KEYWORDS   .
SOURCE     Unknown.
ORGANISM   Unknown.
REFERENCE   1 (bases 1 to 20)
AUTHORS    Monia,B.P. and Freier,S.M.
TITLE      Antisense inhibition of clusterin expression
JOURNAL    Patent: US 6383808-A 49 07-MAY-2002;
FEATURES   Location/Qualifiers
            source
              1..20
                /organism="unknown"
                /mol_type="unassigned DNA"

Query Match      1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      690 AGGCTCAGCTTCCTTTCC 709
Db      20 AGGCTCAGCTTCCTTTCC 1

RESULT 93
AR208748/c
LOCUS      AR208748      20 bp      DNA      linear      PAT 20-JUN-2002
DEFINITION Sequence 47 from patent US 6383808.
ACCESSION AR208748
VERSION    AR208748.1 GI:21509984
KEYWORDS   .
SOURCE     Unknown.
ORGANISM   Unknown.
REFERENCE   1 (bases 1 to 20)
AUTHORS    Monia,B.P. and Freier,S.M.
TITLE      Antisense inhibition of clusterin expression
JOURNAL    Patent: US 6383808-A 47 07-MAY-2002;
FEATURES   Location/Qualifiers
            source
              1..20
                /organism="unknown"
                /mol_type="unassigned DNA"

Query Match      1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      721 TCGTCCGAGCTTGATGCC 740
Db      20 TCGTCCGAGCTTGATGCC 1

RESULT 94
AR208749/c
LOCUS      AR208749      20 bp      DNA      linear      PAT 20-JUN-2002
DEFINITION Sequence 48 from patent US 6383808.
ACCESSION AR208749
VERSION    AR208749.1 GI:21509985
KEYWORDS   .
SOURCE     Unknown.

Query Match      1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      776 GTTCCAGCGCTTCCTTGAGA 795
Db      20 GTTCCAGCGCTTCCTTGAGA 1

RESULT 96
AR208751/c
LOCUS      AR208751      20 bp      DNA      linear      PAT 20-JUN-2002
DEFINITION Sequence 50 from patent US 6383808.
ACCESSION AR208751
VERSION    AR208751.1 GI:21509987
KEYWORDS   .
SOURCE     Unknown.
ORGANISM   Unknown.
REFERENCE   1 (bases 1 to 20)
AUTHORS    Monia,B.P. and Freier,S.M.
TITLE      Antisense inhibition of clusterin expression
JOURNAL    Patent: US 6383808-A 50 07-MAY-2002;
FEATURES   Location/Qualifiers
            source
              1..20
                /organism="unknown"
                /mol_type="unassigned DNA"

Query Match      1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      783 CCCTTCCTTGAGATGATACA 802
Db      783 CCCTTCCTTGAGATGATACA 802
```



```
Db      20  CCCTTCTCGATGATACA 1
RESULT 97
AR208752/c
LOCUS   AR208752          20 bp      DNA      linear      PAT 20-JUN-2002
DEFINITION   Sequence 51 from patent US 6383808.
ACCESSION   AR208752
VERSION     AR208752.1  GI:21509989
KEYWORDS
SOURCE      Unknown.
ORGANISM    Unknown.
REFERENCE   1 (bases 1 to 20)
AUTHORS    Monia,B.P. and Freier,S.M.
TITLE      Antisense inhibition of clusterin expression
JOURNAL    Patent: US 6383808-A 51 07-MAY-2002;
FEATURES
source
Location/Qualifiers
1..20
/mol_type="unassigned DNA"

Query Match      1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      820  TGGACATCCACTTCCACAGC 839
|||||
Db      20  TGGACATCCACTTCCACAGC 1

RESULT 98
AR208753/c
LOCUS   AR208753          20 bp      DNA      linear      PAT 20-JUN-2002
DEFINITION   Sequence 52 from patent US 6383808.
ACCESSION   AR208753
VERSION     AR208753.1  GI:21509990
KEYWORDS
SOURCE      Unknown.
ORGANISM    Unknown.
REFERENCE   1 (bases 1 to 20)
AUTHORS    Monia,B.P. and Freier,S.M.
TITLE      Antisense inhibition of clusterin expression
JOURNAL    Patent: US 6383808-A 52 07-MAY-2002;
FEATURES
source
Location/Qualifiers
1..20
/mol_type="unassigned DNA"

Query Match      1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      848  CCAGCACCCGCCCAACAGAAT 867
|||||
Db      20  CCAGCACCCGCCCAACAGAAT 1

RESULT 99
AR208754/c
LOCUS   AR208754          20 bp      DNA      linear      PAT 20-JUN-2002
DEFINITION   Sequence 53 from patent US 6383808.
ACCESSION   AR208754
VERSION     AR208754.1  GI:21509991
KEYWORDS
SOURCE      Unknown.
ORGANISM    Unknown.
REFERENCE   1 (bases 1 to 20)
AUTHORS    Monia,B.P. and Freier,S.M.
TITLE      Antisense inhibition of clusterin expression
JOURNAL    Patent: US 6383808-A 53 07-MAY-2002;

FEATURES
source
Location/Qualifiers
1..20
/mol_type="unassigned DNA"

Query Match      1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      853  ACCCGCCACAGAAATTCATA 872
|||||
Db      20  ACCCGCCACAGAAATTCATA 1

RESULT 100
AR208755/c
LOCUS   AR208755          20 bp      DNA      linear      PAT 20-JUN-2002
DEFINITION   Sequence 54 from patent US 6383808.
ACCESSION   AR208755
VERSION     AR208755.1  GI:21509992
KEYWORDS
SOURCE      Unknown.
ORGANISM    Unknown.
REFERENCE   1 (bases 1 to 20)
AUTHORS    Monia,B.P. and Freier,S.M.
TITLE      Antisense inhibition of clusterin expression
JOURNAL    Patent: US 6383808-A 54 07-MAY-2002;
FEATURES
source
Location/Qualifiers
1..20
/mol_type="unassigned DNA"

Query Match      1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      893  GACTGTGTGCGCGGAGATCC 912
|||||
Db      20  GACTGTGTGCGCGGAGATCC 1

RESULT 101
AR208756/c
LOCUS   AR208756          20 bp      DNA      linear      PAT 20-JUN-2002
DEFINITION   Sequence 55 from patent US 6383808.
ACCESSION   AR208756
VERSION     AR208756.1  GI:21509994
KEYWORDS
SOURCE      Unknown.
ORGANISM    Unknown.
REFERENCE   1 (bases 1 to 20)
AUTHORS    Monia,B.P. and Freier,S.M.
TITLE      Antisense inhibition of clusterin expression
JOURNAL    Patent: US 6383808-A 55 07-MAY-2002;
FEATURES
source
Location/Qualifiers
1..20
/mol_type="unassigned DNA"

Query Match      1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      894  ACTGTGTGCGCGGAGATCCG 913
|||||
Db      20  ACTGTGTGCGCGGAGATCCG 1

RESULT 102
AR208757/c
LOCUS   AR208757          20 bp      DNA      linear      PAT 20-JUN-2002
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```
DEFINITION Sequence 56 from patent US 6383808.
ACCESSION AR208757
VERSION AR208757.1 GI:21509995
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 20)
AUTHORS Monia,B.P. and Freier,S.M.
TITLE Antisense inhibition of clusterin expression
JOURNAL Patent: US 6383808-A 56 07-MAY-2002;
FEATURES
    Location/Qualifiers
        1..20
            /organism="unknown"
            /mol_type="unassigned DNA"

Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 906 GAGATCGGCACAACTCCAC 925
Db 20 GAGATCGGCACAACTCCAC 1

RESULT 103
AR208758/c
LOCUS AR208758 20 bp DNA linear PAT 20-JUN-2002
DEFINITION Sequence 57 from patent US 6383808.
ACCESSION AR208758
VERSION AR208758.1 GI:21509996
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 20)
AUTHORS Monia,B.P. and Freier,S.M.
TITLE Antisense inhibition of clusterin expression
JOURNAL Patent: US 6383808-A 57 07-MAY-2002;
FEATURES
    Location/Qualifiers
        1..20
            /organism="unknown"
            /mol_type="unassigned DNA"

Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 928 GTCGCTCGGATGAAGAC 947
Db 20 GTCGCTCGGATGAAGAC 1

RESULT 104
AR208759/c
LOCUS AR208759 20 bp DNA linear PAT 20-JUN-2002
DEFINITION Sequence 58 from patent US 6383808.
ACCESSION AR208759
VERSION AR208759.1 GI:21509997
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 20)
AUTHORS Monia,B.P. and Freier,S.M.
TITLE Antisense inhibition of clusterin expression
JOURNAL Patent: US 6383808-A 58 07-MAY-2002;
FEATURES
    Location/Qualifiers
        1..20
            /organism="unknown"
            /mol_type="unassigned DNA"

Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 967 AGATCTTGCTGTGGACTGT 986
Db 20 AGATCTTGCTGTGGACTGT 1

RESULT 105
AR208760/c
LOCUS AR208760 20 bp DNA linear PAT 20-JUN-2002
DEFINITION Sequence 59 from patent US 6383808.
ACCESSION AR208760
VERSION AR208760.1 GI:21509999
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 20)
AUTHORS Monia,B.P. and Freier,S.M.
TITLE Antisense inhibition of clusterin expression
JOURNAL Patent: US 6383808-A 59 07-MAY-2002;
FEATURES
    Location/Qualifiers
        1..20
            /organism="unknown"
            /mol_type="unassigned DNA"

Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1009 CTAAGCTCGCGGGAGCTC 1028
Db 20 CTAAGCTCGCGGGAGCTC 1

RESULT 106
AR208761/c
LOCUS AR208761 20 bp DNA linear PAT 20-JUN-2002
DEFINITION Sequence 60 from patent US 6383808.
ACCESSION AR208761
VERSION AR208761.1 GI:21510000
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 20)
AUTHORS Monia,B.P. and Freier,S.M.
TITLE Antisense inhibition of clusterin expression
JOURNAL Patent: US 6383808-A 60 07-MAY-2002;
FEATURES
    Location/Qualifiers
        1..20
            /organism="unknown"
            /mol_type="unassigned DNA"

Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1022 GGAGCTCGAGCAATCCCTCC 1041
Db 20 GGAGCTCGAGCAATCCCTCC 1

RESULT 107
AR208762/c
LOCUS AR208762 20 bp DNA linear PAT 20-JUN-2002
DEFINITION Sequence 61 from patent US 6383808.
ACCESSION AR208762
VERSION AR208762.1 GI:21510001
KEYWORDS
SOURCE
ORGANISM
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Unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS Monia,B.P. and Freier,S.M.
TITLE Antisense inhibition of clusterin expression
JOURNAL Patent: US 6383808-A 61 07-MAY-2002;
FEATURES Location/Qualifiers
source 1..20
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1083 AAGTCCTACCAAGTGGGAAGAT 1102
|||||
Db 20 AAGTCCTACCAAGTGGGAAGAT 1

RESULT 108
AR208763/c
LOCUS 20 bp DNA linear PAT 20-JUN-2002
DEFINITION Sequence 62 from patent US 6383808.
ACCESSION AR208763
VERSION AR208763.1 GI:21510002
FEATURES Location/Qualifiers
source Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Monia,B.P. and Freier,S.M.
TITLE Antisense inhibition of clusterin expression
JOURNAL Patent: US 6383808-A 62 07-MAY-2002;
FEATURES Location/Qualifiers
source 1..20
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1091 CCAGTGGAGATGCTCAACA 1110
|||||
Db 20 CCAGTGGAGATGCTCAACA 1

RESULT 109
AR208764/c
LOCUS 20 bp DNA linear PAT 20-JUN-2002
DEFINITION Sequence 63 from patent US 6383808.
ACCESSION AR208764
VERSION AR208764.1 GI:21510003
FEATURES Location/Qualifiers
source Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Monia,B.P. and Freier,S.M.
TITLE Antisense inhibition of clusterin expression
JOURNAL Patent: US 6383808-A 63 07-MAY-2002;
FEATURES Location/Qualifiers
source 1..20
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1113 TCCTCCTTGTGAGCAGCT 1132
|||||
Db 20 TCCTCCTTGTGAGCAGCT 1

Unclassified.
RESULT 110
AR208765/c
LOCUS 20 bp DNA linear PAT 20-JUN-2002
DEFINITION Sequence 64 from patent US 6383808.
ACCESSION AR208765
VERSION AR208765.1 GI:21510005
FEATURES Location/Qualifiers
source Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Monia,B.P. and Freier,S.M.
TITLE Antisense inhibition of clusterin expression
JOURNAL Patent: US 6383808-A 64 07-MAY-2002;
FEATURES Location/Qualifiers
source 1..20
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1121 GCTGGAGCAGCTGAACGAGC 1140
|||||
Db 20 GCTGGAGCAGCTGAACGAGC 1

RESULT 111
AR208766/c
LOCUS 20 bp DNA linear PAT 20-JUN-2002
DEFINITION Sequence 65 from patent US 6383808.
ACCESSION AR208766
VERSION AR208766.1 GI:21510006
FEATURES Location/Qualifiers
source Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Monia,B.P. and Freier,S.M.
TITLE Antisense inhibition of clusterin expression
JOURNAL Patent: US 6383808-A 65 07-MAY-2002;
FEATURES Location/Qualifiers
source 1..20
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1148 CTGGGTGTCCCGCTGGCAA 1167
|||||
Db 20 CTGGGTGTCCCGCTGGCAA 1

RESULT 112
AR208767/c
LOCUS 20 bp DNA linear PAT 20-JUN-2002
DEFINITION Sequence 66 from patent US 6383808.
ACCESSION AR208767
VERSION AR208767.1 GI:21510007
FEATURES Location/Qualifiers
source Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Monia,B.P. and Freier,S.M.
TITLE Antisense inhibition of clusterin expression
JOURNAL Patent: US 6383808-A 66 07-MAY-2002;
FEATURES Location/Qualifiers
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source
1. .20
/organism="unknown"
/mol_type="unassigned DNA"

Query Match
Best Local Similarity 1.2%; Score 20; DB 1; Length 20;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1182 GAAGACCACTACTATCTGCG 1201
|||||
Db 20 GAAGACCACTACTATCTGCG 1

RESULT 113
AR208768/c
LOCUS AR208768 20 bp DNA linear PAT 20-JUN-2002
DEFINITION Sequence 67 from patent US 6383808.
ACCESSION AR208768
VERSION AR208768.1 GI:21510008
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Monia,B.P. and Freier,S.M.
TITLE Antisense inhibition of clusterin expression
JOURNAL Patent: US 6383808-A 67 07-MAY-2002;
FEATURES Location/Qualifiers
source
1. .20
/organism="unknown"
/mol_type="unassigned DNA"

Query Match
Best Local Similarity 1.2%; Score 20; DB 1; Length 20;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1216 CTTCCACACTTCTGACTCG 1235
|||||
Db 20 CTTCCACACTTCTGACTCG 1

RESULT 115
AR208770/c
LOCUS AR208770 20 bp DNA linear PAT 20-JUN-2002
DEFINITION Sequence 69 from patent US 6383808.
ACCESSION AR208770
VERSION AR208770.1 GI:21510011
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Monia,B.P. and Freier,S.M.
TITLE Antisense inhibition of clusterin expression
JOURNAL Patent: US 6383808-A 69 07-MAY-2002;
FEATURES Location/Qualifiers
source
1. .20
/organism="unknown"
/mol_type="unassigned DNA"

Query Match
Best Local Similarity 1.2%; Score 20; DB 1; Length 20;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1275 TTGACTCTGATCCATCAC 1294
|||||
Db 20 TTGACTCTGATCCATCAC 1

RESULT 116
AR208771/c
LOCUS AR208771 20 bp DNA linear PAT 20-JUN-2002
DEFINITION Sequence 70 from patent US 6383808.
ACCESSION AR208771
VERSION AR208771.1 GI:21510012
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Monia,B.P. and Freier,S.M.
TITLE Antisense inhibition of clusterin expression
JOURNAL Patent: US 6383808-A 70 07-MAY-2002;
FEATURES Location/Qualifiers
source
1. .20
/organism="unknown"
/mol_type="unassigned DNA"

Query Match
Best Local Similarity 1.2%; Score 20; DB 1; Length 20;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1300 CGGTCCCTGTAGAGTCTCC 1319
|||||
Db 20 CGGTCCCTGTAGAGTCTCC 1

RESULT 117
AR208772/c
LOCUS AR208772 20 bp DNA linear PAT 20-JUN-2002
DEFINITION Sequence 71 from patent US 6383808.
ACCESSION AR208772
VERSION AR208772.1 GI:21510013
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Monia,B.P. and Freier,S.M.
TITLE Antisense inhibition of clusterin expression
JOURNAL Patent: US 6383808-A 71 07-MAY-2002;
FEATURES Location/Qualifiers
source
1. .20
/organism="unknown"
/mol_type="unassigned DNA"

Query Match
Best Local Similarity 1.2%; Score 20; DB 1; Length 20;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1319 CTTCCACACTTCTGACTCG 1335
|||||
Db 20 CTTCCACACTTCTGACTCG 1

RESULT 114
AR208769/c
LOCUS AR208769 20 bp DNA linear PAT 20-JUN-2002
DEFINITION Sequence 68 from patent US 6383808.
ACCESSION AR208769
VERSION AR208769.1 GI:21510010
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Monia,B.P. and Freier,S.M.
TITLE Antisense inhibition of clusterin expression
JOURNAL Patent: US 6383808-A 68 07-MAY-2002;
FEATURES Location/Qualifiers
source
1. .20
/organism="unknown"
/mol_type="unassigned DNA"

Query Match
Best Local Similarity 1.2%; Score 20; DB 1; Length 20;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1194 TATCTGGGGTCCACCGGT 1213
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Db 20 TATCTGGGGTCCACCGGT 1
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Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1332 AAATTTATGAGACCGTGC 1351
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Db 20 AAATTTATGAGACCGTGC 1

RESULT 118
AR208773/c
LOCUS AR208773 20 bp DNA linear PAT 20-JUN-2002
DEFINITION Sequence 72 from patent US 6383808.
ACCESSION AR208773
VERSION AR208773.1 GI:21510015
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 20)
AUTHORS Monia,B.P. and Freier,S.M.
TITLE Antisense inhibition of clusterin expression
JOURNAL Patent: US 6383808-A 72 07-MAY-2002;
FEATURES Location/Qualifiers
source
1..20
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1600 TGCTCTGCGATGCAACTAAT 1619
|||||
Db 20 TGCTCTGCGATGCAACTAAT 1

RESULT 121
AR208776/c
LOCUS AR208776 20 bp DNA linear PAT 20-JUN-2002
DEFINITION Sequence 75 from patent US 6383808.
ACCESSION AR208776
VERSION AR208776.1 GI:21510018
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 20)
AUTHORS Monia,B.P. and Freier,S.M.
TITLE Antisense inhibition of clusterin expression
JOURNAL Patent: US 6383808-A 75 07-MAY-2002;
FEATURES Location/Qualifiers
source
1..20
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/mol_type="unassigned DNA"

Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1615 CTAAATTCATAAACTGTCT 1634
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Db 20 CTAAATTCATAAACTGTCT 1

RESULT 122
AR208779/c
LOCUS AR208779 20 bp DNA linear PAT 20-JUN-2002
DEFINITION Sequence 78 from patent US 6383808.
ACCESSION AR208779
VERSION AR208779.1 GI:21510022
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 20)
AUTHORS Monia,B.P. and Freier,S.M.
TITLE Antisense inhibition of clusterin expression
JOURNAL Patent: US 6383808-A 78 07-MAY-2002;
FEATURES Location/Qualifiers
source
1..20
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/mol_type="unassigned DNA"

Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 979 TGGACTGTTCACCAACAC 998
|||||
Db 20 TGGACTGTTCACCAACAC 1

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1332 AAATTTATGAGACCGTGC 1351
|||||
Db 20 AAATTTATGAGACCGTGC 1

RESULT 118
AR208773/c
LOCUS AR208773 20 bp DNA linear PAT 20-JUN-2002
DEFINITION Sequence 72 from patent US 6383808.
ACCESSION AR208773
VERSION AR208773.1 GI:21510015
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 20)
AUTHORS Monia,B.P. and Freier,S.M.
TITLE Antisense inhibition of clusterin expression
JOURNAL Patent: US 6383808-A 72 07-MAY-2002;
FEATURES Location/Qualifiers
source
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/organism="unknown"
/mol_type="unassigned DNA"

Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1398 GATGTGGATGCTTTTGC 1417
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Db 20 GATGTGGATGCTTTTGC 1

RESULT 119
AR208774/c
LOCUS AR208774 20 bp DNA linear PAT 20-JUN-2002
DEFINITION Sequence 73 from patent US 6383808.
ACCESSION AR208774
VERSION AR208774.1 GI:21510016
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 20)
AUTHORS Monia,B.P. and Freier,S.M.
TITLE Antisense inhibition of clusterin expression
JOURNAL Patent: US 6383808-A 73 07-MAY-2002;
FEATURES Location/Qualifiers
source
1..20
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1545 GCTCTGGATCCTGCACTCTA 1564
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Db 20 GCTCTGGATCCTGCACTCTA 1

RESULT 120
AR208775/c
LOCUS AR208775 20 bp DNA linear PAT 20-JUN-2002
DEFINITION Sequence 74 from patent US 6383808.
ACCESSION AR208775
VERSION AR208775.1 GI:21510017
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 20)
AUTHORS Monia,B.P. and Freier,S.M.
TITLE Antisense inhibition of clusterin expression
JOURNAL Patent: US 6383808-A 74 07-MAY-2002;
FEATURES Location/Qualifiers
source
1..20
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1545 GCTCTGGATCCTGCACTCTA 1564
|||||
Db 20 GCTCTGGATCCTGCACTCTA 1

RESULT 120
AR208775/c
LOCUS AR208775 20 bp DNA linear PAT 20-JUN-2002
DEFINITION Sequence 74 from patent US 6383808.
ACCESSION AR208775
VERSION AR208775.1 GI:21510017
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 20)
AUTHORS Monia,B.P. and Freier,S.M.
TITLE Antisense inhibition of clusterin expression
JOURNAL Patent: US 6383808-A 74 07-MAY-2002;
FEATURES Location/Qualifiers
source
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/mol_type="unassigned DNA"

Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 979 TGGACTGTTCACCAACAC 998
|||||
Db 20 TGGACTGTTCACCAACAC 1

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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RESULT 123
AR208781/c
LOCUS
DEFINITION
ACCESSION AR208781
VERSION AR208781.1 GI:21510025
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS Monia,B.P. and Freier,S.M.
TITLE Antisense inhibition of clusterin expression
JOURNAL Patent: US 6383808-A 80 07-MAY-2002;
FEATURES
LOCATION/Qualifiers
1..20
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Query Match 1..2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1383 CACCGGGAGGAGTGAGATGT 1402
Db 20 CACCGGGAGGAGTGAGATGT 1
RESULT 124
CQ786121
LOCUS
DEFINITION
ACCESSION CQ786121
VERSION CQ786121.1 GI:45721224
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS Jansen,B., Gleave,M.E., Signaevsky,M., Beraldi,E., Trougakos,I. and
Gonos,E.
TITLE Rnai probes targeting cancer-related proteins
JOURNAL Patent: WO 2004018676-A 9 04-MAR-2004;
The University of British Columbia (CA)
FEATURES
LOCATION/Qualifiers
1..21
/mol_type="synthetic construct"
Query Match 1..2%; Score 20; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 48 ATGATGAAGACTCTGCTGCT 67
Db 1 ATGATGAAGACTCTGCTGCT 20
RESULT 125
CQ786639
LOCUS
DEFINITION
ACCESSION CQ786639
VERSION CQ786639.1 GI:45721659
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS Jansen,B.
TITLE Treatment of melanoma by reduction in clusterin levels
JOURNAL Patent: WO 2004018675-A 28 04-MAR-2004;
The University of British Columbia (CA); Gleave, Martin E. (CA)
FEATURES
LOCATION/Qualifiers
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/mol_type="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="RNAi for human clusterin"
Query Match 1..2%; Score 20; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 48 ATGATGAAGACTCTGCTGCT 67
Db 1 ATGATGAAGACTCTGCTGCT 20
RESULT 126
AR236281
LOCUS
DEFINITION
ACCESSION AR236281
VERSION AR236281.1 GI:27280109
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS Millis,A.J.T.
TITLE Compositions and methods for altering cell migration
JOURNAL Patent: US 6464975-A 13 15-OCT-2002;
LOCATION/Qualifiers
1..21
/mol_type="unknown"
Query Match 1..2%; Score 19.4; DB 1; Length 21;
Best Local Similarity 95.2%; Pred. No. 35;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 271 AAGAAGCCCAAGAAGAAGAAG 291
Db 1 AGGAAGCCCAAGAAGAAGAAG 21
RESULT 127
CQ786179
LOCUS
DEFINITION
ACCESSION CQ786179
VERSION CQ786179.1 GI:45721282
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS Jansen,B., Gleave,M.E., Signaevsky,M., Beraldi,E., Trougakos,I. and
Gonos,E.
TITLE Rnai probes targeting cancer-related proteins
JOURNAL Patent: WO 2004018676-A 67 04-MAR-2004;
The University of British Columbia (CA)
FEATURES
LOCATION/Qualifiers
1..19
/mol_type="synthetic construct"
/mol_type="unassigned RNA"
/db_xref="taxon:32630"
/note="RNAi for human clusterin"
Query Match 1..2%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 48 ATGATGAAGACTCTGCTGC 66  
Db 1 ATGATGAAGACTCTGCTGC 19

RESULT 128  
CQ786180/c  
LOCUS CQ786180.1 19 bp RNA linear PAT 24-MAR-2004  
DEFINITION Sequence 68 from Patent WO2004018676.  
ACCESSION CQ786180  
VERSION CQ786180.1 GI:45721283  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM synthetic construct  
other sequences; artificial sequences.  
REFERENCE 1  
AUTHORS Jansen,B., Gleave,M.E., Signaevsky,M., Beraldi,E., Trougakos,I. and Gonos,E.  
TITLE Rnai probes targeting cancer-related proteins  
JOURNAL Patent: WO 2004018676-A 68 04-MAR-2004;  
The University of British Columbia (CA)  
FEATURES  
source Location/Qualifiers  
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/db\_xref="taxon:32630"  
/note="RNAi for human clusterin"

Query Match 1.2%; Score 19; DB 1; Length 19;  
Best Local Similarity 100.0%; Pred. No. 30;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 48 ATGATGAAGACTCTGCTGC 66  
Db 19 ATGATGAAGACTCTGCTGC 1

RESULT 129  
CQ786653  
LOCUS CQ786653 19 bp RNA linear PAT 24-MAR-2004  
DEFINITION Sequence 42 from Patent WO2004018675.  
ACCESSION CQ786653  
VERSION CQ786653.1 GI:45721673  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM synthetic construct  
other sequences; artificial sequences.  
REFERENCE 1  
AUTHORS Jansen,B.  
TITLE Treatment of melanoma by reduction in clusterin levels  
JOURNAL Patent: WO 2004018675-A 42 04-MAR-2004;  
The University of British Columbia (CA); Gleave, Martin E. (CA)  
FEATURES  
source Location/Qualifiers  
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/mol\_type="unassigned RNA"  
/db\_xref="taxon:32630"  
/note="RNAi for human clusterin"

Query Match 1.2%; Score 19; DB 1; Length 19;  
Best Local Similarity 100.0%; Pred. No. 30;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 48 ATGATGAAGACTCTGCTGC 66  
Db 1 ATGATGAAGACTCTGCTGC 19

RESULT 130  
CQ786654/c  
LOCUS CQ786654 19 bp RNA linear PAT 24-MAR-2004  
DEFINITION Sequence 43 from Patent WO2004018675.

Qy 48 ATGATGAAGACTCTGCTGC 66  
Db 1 ATGATGAAGACTCTGCTGC 19

RESULT 131  
CQ786122/c  
LOCUS CQ786122 21 bp DNA linear PAT 24-MAR-2004  
DEFINITION Sequence 10 from Patent WO2004018676.  
ACCESSION CQ786122  
VERSION CQ786122.1 GI:45721225  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM synthetic construct  
other sequences; artificial sequences.  
REFERENCE 1  
AUTHORS Jansen,B., Gleave,M.E., Signaevsky,M., Beraldi,E., Trougakos,I. and Gonos,E.  
TITLE Rnai probes targeting cancer-related proteins  
JOURNAL Patent: WO 2004018676-A 10 04-MAR-2004;  
The University of British Columbia (CA)  
FEATURES  
source Location/Qualifiers  
1..21  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="RNAi for human clusterin"

Query Match 1.2%; Score 19; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 40;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 48 ATGATGAAGACTCTGCTGC 66  
Db 19 ATGATGAAGACTCTGCTGC 1

RESULT 132  
CQ786640/c  
LOCUS CQ786640 21 bp DNA linear PAT 24-MAR-2004  
DEFINITION Sequence 29 from Patent WO2004018675.  
ACCESSION CQ786640  
VERSION CQ786640.1 GI:45721660  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM synthetic construct  
other sequences; artificial sequences.  
REFERENCE 1  
AUTHORS Jansen,B.  
TITLE Treatment of melanoma by reduction in clusterin levels  
JOURNAL Patent: WO 2004018675-A 29 04-MAR-2004;

Qy 48 ATGATGAAGACTCTGCTGC 66  
Db 19 ATGATGAAGACTCTGCTGC 1

RESULT 133  
CQ786654/c  
LOCUS CQ786654 19 bp RNA linear PAT 24-MAR-2004  
DEFINITION Sequence 43 from Patent WO2004018675.

Qy 48 ATGATGAAGACTCTGCTGC 66  
Db 1 ATGATGAAGACTCTGCTGC 19

RESULT 134  
CQ786654/c  
LOCUS CQ786654 19 bp RNA linear PAT 24-MAR-2004  
DEFINITION Sequence 43 from Patent WO2004018675.

FEATURES  
source  
The University of British Columbia (CA) ; Gleave, Martin E. (CA)  
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Location/Qualifiers  
/organism="synthetic construct"  
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/note="RNAi for human clusterin"

Query Match 1.2%; Score 19; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 40;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 48 ATGATGAGAGACTCTGCTGC 66  
|||||  
Db 19 ATGATGAGAGCTCTGCTGC 1

RESULT 133  
AR071119  
LOCUS AR071119 22 bp DNA linear PAT 18-FEB-2000  
DEFINITION Sequence 10 from patent US 5910412.  
ACCESSION AR071119  
VERSION AR071119.1 GI:7222007  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 22)  
AUTHORS Akamatsu, T. and Suzuki, T.  
TITLE Method for identifying the sex of spinach by DNA markers  
JOURNAL Patent: US 5910412-A 10 08-JUN-1999;  
Location/Qualifiers  
FEATURES 1. .22  
source /organism="unknown"  
/mol\_type="unassigned DNA"

Query Match 1.1%; Score 18.8; DB 1; Length 22;  
Best Local Similarity 90.9%; Pred. No. 50;  
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 865 AATTCATACGAGAGCGGACGA 886  
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Db 1 AATTCATACGAGAAAGCTACGA 22

RESULT 134  
E15141  
LOCUS E15141 22 bp DNA linear PAT 28-JUL-1999  
DEFINITION PCR primer for detecting male spinach DNA.  
ACCESSION E15141  
VERSION E15141.1 GI:5709824  
KEYWORDS JP 1998052284-A/10.  
SOURCE unidentified  
ORGANISM unclassified.  
REFERENCE 1 (bases 1 to 22)  
AUTHORS Akamatsu, T., Suzuki, T. and Uchimiya, H.  
TITLE DETERMINATION OF MALE OR FEMALE OF SPINACH BY USING DNA MARKER  
JOURNAL Patent: JP 1998052284-A 10 24-FEB-1998;  
SAKATA NO TANE:KK  
COMMENT OS None  
OC Artificial sequences.  
PN JP 1998052284-A/10  
PD 24-FEB-1998  
PR 14-MAY-1997 JP 1997124012  
PF 14-MAY-1996 JP 96P 119124  
PI AKAMATSU TOYOKAZU, SUZUKI TAKAO, UCHIMIYA HIROBUMI PC  
C12N15/09, C07H21/04, C12Q1/68;  
CC strandedness: Single;  
CC topology: Linear;  
CC hypothetical: No;  
CC anti-sense: No; Location/Qualifiers  
FH Key

FEATURES  
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Location/Qualifiers  
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1. .22  
Location/Qualifiers  
/organism="unidentified"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:32644"

Query Match 1.1%; Score 18.8; DB 1; Length 22;  
Best Local Similarity 90.9%; Pred. No. 50;  
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 865 AATTCATACGAGAGCGGACGA 886  
|||||  
Db 1 AATTCATACGAGAAAGCTACGA 22

RESULT 135  
AR038688/c  
LOCUS AR038688 18 bp DNA linear PAT 29-SEP-1999  
DEFINITION Sequence 22 from patent US 5807678.  
ACCESSION AR038688  
VERSION AR038688.1 GI:5958051  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 18)  
AUTHORS Miller, W. L., Lin, D. and Strauss, J. F. III.  
TITLE Identification of gene mutations associated with congenital lipoid  
adrenal hyperplasia  
JOURNAL Patent: US 5807678-A 22 15-SEP-1998;  
Location/Qualifiers  
FEATURES 1. .18  
source /organism="unknown"  
/mol\_type="unassigned DNA"

Query Match 1.1%; Score 18; DB 1; Length 18;  
Best Local Similarity 100.0%; Pred. No. 36;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1475 GAGAGCTCTGCACGCTCAC 1492  
|||||  
Db 18 GAGAGCTCTGCACGCTCAC 1

RESULT 136  
AR208705  
LOCUS AR208705 18 bp DNA linear PAT 20-JUN-2002  
DEFINITION Sequence 4 from patent US 6383808.  
ACCESSION AR208705  
VERSION AR208705.1 GI:21509929  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 18)  
AUTHORS Monia, B. P. and Freier, S. M.  
TITLE Antisense inhibition of clusterin expression  
JOURNAL Patent: US 6383808-A 4 07-MAY-2002;  
Location/Qualifiers  
FEATURES 1. .18  
source /organism="unknown"  
/mol\_type="unassigned DNA"

Query Match 1.1%; Score 18; DB 1; Length 18;  
Best Local Similarity 100.0%; Pred. No. 36;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 746 TCCGTACGAGCCCTGAA 763  
|||||  
Db 1 TCCGTACGAGCCCTGAA 18



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RESULT 137
AX728619
LOCUS AX728619 17 bp DNA linear PAT 08-MAY-2003
DEFINITION Sequence 253 from Patent WO03025175.
ACCESSION AX728619
VERSION AX728619.1 GI:30507962
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Telerman,A., Anson,R. and Tuijnder,M.
TITLE Sequences involved in phenomena of tumour suppression, tumour
reversion, apoptosis and/or virus resistance and their use as
medicines
JOURNAL Patent: WO 03025175-A 253 27-MAR-2003;
Molecular Engines Laboratories (FR)
FEATURES
source
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/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
Query Match 1.0%; Score 17; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 43;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1551 GATCCTGCACTCTAACA 1567
|||||
Db 1 GATCCTGCACTCTAACA 17

RESULT 138
AX762710
LOCUS AX762710 17 bp DNA linear PAT 25-JUN-2003
DEFINITION Sequence 6031 from Patent WO03040369.
ACCESSION AX762710
VERSION AX762710.1 GI:32257326
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Telerman,A., Anson,R. and Tuijnder,M.
TITLE Sequences involved in tumoral suppression, tumoral reversion,
apoptosis and/or viral resistance phenomena and their use as
medicines
JOURNAL Patent: WO 03040369-A 6031 15-MAY-2003;
Molecular Engines Laboratories (FR)
FEATURES
source
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/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
Query Match 1.0%; Score 17; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 43;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1551 GATCCTGCACTCTAACA 1567
|||||
Db 1 GATCCTGCACTCTAACA 17

RESULT 139
AR167026/c
LOCUS AR167026/c 20 bp DNA linear PAT 17-OCT-2001
DEFINITION Sequence 43 from patent US 6284458.
ACCESSION AR167026
VERSION AR167026.1 GI:21513473
KEYWORDS virus-associated diseases
SOURCE virus-associated diseases
ORGANISM virus-associated diseases
REFERENCE 1 (bases 1 to 20)
AUTHORS Anderson,K.P., Hanecak,R.C., Hoshiko,K., Nozaki,C., Nishihara,T.,
Nakatake,H., Hamada,F., Eto,T. and Furukawa,S.
TITLE Compositions and methods for treatment of hepatitis C
virus-associated diseases
JOURNAL Patent: US 6284458-A 43 04-SEP-2001;
Molecular Engines Laboratories (FR)
FEATURES
source
1..20
/organism="unassigned DNA"
/mol_type="unassigned DNA"
Query Match 1.0%; Score 16.8; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 74;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1510 GCCTCCAGGCCCCCACTCC 1529
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Db 20 GCCTCCAGGCCCCCACTCC 1

RESULT 140
AR210681/c
LOCUS AR210681/c 20 bp DNA linear PAT 20-JUN-2002
DEFINITION Sequence 43 from patent US 6391542.
ACCESSION AR210681
VERSION AR210681.1 GI:21513473
KEYWORDS virus-associated diseases
SOURCE virus-associated diseases
ORGANISM virus-associated diseases
REFERENCE 1 (bases 1 to 20)
AUTHORS Anderson,K.P., Hanecak,R.C., Hoshiko,K., Nozaki,C., Nishihara,T.,
Nakatake,H., Hamada,F., Eto,T., Furukawa,S., Furusako,S.,
Bruce,T.W. and Lima,W.F.
TITLE Compositions and methods for treatment of Hepatitis C
virus-associated diseases
JOURNAL Patent: US 6391542-A 43 21-MAY-2002;
Molecular Engines Laboratories (FR)
FEATURES
source
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/organism="unassigned DNA"
/mol_type="unassigned DNA"
Query Match 1.0%; Score 16.8; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 74;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1510 GCCTCCAGGCCCCCACTCC 1529
|||||
Db 20 GCCTCCAGGCCCCCACTCC 1

RESULT 141
A39125/c
LOCUS A39125/c 16 bp DNA linear PAT 05-MAR-1997
DEFINITION Sequence 97 from Patent WO9412670.
ACCESSION A39125
VERSION A39125.1 GI:2295500
KEYWORDS unidentified
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 16)
AUTHORS Maertens,G., Stuyver,L., Rossau,R. and Van,H.H.
TITLE PROCESS FOR TYPING OF HCV ISOLATES
JOURNAL Patent: WO 9412670-A 97 09-JUN-1994;
INNOGENETICS NV (BE)
COMMENT Other publication AU 5628294 940622
Other publication CA 2128528 940609
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Other publication JP 7503143T 950406.
FEATURES
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    Location/Qualifiers
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        /organism="unidentified"
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        /db_xref="taxon:32644"

Query Match
  Best Local Similarity 1.0%; Score 16; DB 1; Length 16;
  Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1508 CAGCCTCCAGGCCCC 1523
  |||||||
Db 16 CAGCCTCCAGGCCCC 1

RESULT 142
AR063448/c
LOCUS AR063448 16 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 97 from patent US 5846704.
ACCESSION AR063448
VERSION AR063448.1 GI:5992756
KEYWORDS
SOURCE
  ORGANISM
    Unknown.
    Unclassified.
  REFERENCE
    1 (bases 1 to 16)
  AUTHORS
    Maertens,G., Stuyver,L., Rossau,R. and Van Heuverswyn,H.
  TITLE
    Process for typing of HCV isolates
  JOURNAL
    Patent: US 5846704-A 97 08-DEC-1998;
  FEATURES
    Location/Qualifiers
      1..16
        /organism="unknown"
        /mol_type="unassigned DNA"

Query Match
  Best Local Similarity 1.0%; Score 16; DB 1; Length 16;
  Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1508 CAGCCTCCAGGCCCC 1523
  |||||||
Db 16 CAGCCTCCAGGCCCC 1

RESULT 143
AR123639/c
LOCUS AR123639 16 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 97 from patent US 6171784.
ACCESSION AR123639
VERSION AR123639.1 GI:14109000
KEYWORDS
SOURCE
  ORGANISM
    Unknown.
    Unclassified.
  REFERENCE
    1 (bases 1 to 16)
  AUTHORS
    Maertens,G., Stuyver,L., Rossau,R. and Van Heuverswyn,H.
  TITLE
    Process for typing of HCV isolates
  JOURNAL
    Patent: US 6171784-A 97 09-JAN-2001;
  FEATURES
    Location/Qualifiers
      1..16
        /organism="unknown"
        /mol_type="unassigned DNA"

Query Match
  Best Local Similarity 1.0%; Score 16; DB 1; Length 16;
  Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1508 CAGCCTCCAGGCCCC 1523
  |||||||
Db 16 CAGCCTCCAGGCCCC 1

RESULT 144
AR123639/c
LOCUS AR123639 16 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 97 from patent US 6171784.
ACCESSION AR123639
VERSION AR123639.1 GI:14109000
KEYWORDS
SOURCE
  ORGANISM
    Unknown.
    Unclassified.
  REFERENCE
    1 (bases 1 to 16)
  AUTHORS
    Maertens,G., Stuyver,L., Rossau,R. and Van Heuverswyn,H.
  TITLE
    Process for typing of HCV isolates
  JOURNAL
    Patent: US 6171784-A 97 09-JAN-2001;
  FEATURES
    Location/Qualifiers
      1..16
        /organism="unknown"
        /mol_type="unassigned DNA"

Query Match
  Best Local Similarity 1.0%; Score 16; DB 1; Length 16;
  Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1508 CAGCCTCCAGGCCCC 1523
  |||||||
Db 16 CAGCCTCCAGGCCCC 1

RESULT 145
AR305790/c
LOCUS AR305790 16 bp mRNA linear PAT 12-JUN-2003
DEFINITION Sequence 97 from patent US 6548244.
ACCESSION AR305790
VERSION AR305790.1 GI:31695399
KEYWORDS
SOURCE
  ORGANISM
    Unknown.
    Unclassified.
  REFERENCE
    1 (bases 1 to 16)
  AUTHORS
    Maertens,G., Stuyver,L., Rossau,R. and Van Heuverswyn,H.
  TITLE
    Process for typing HCV isolates
  JOURNAL
    Patent: US 6548244-A 97 15-APR-2003;
  FEATURES
    Location/Qualifiers
      1..16
        /organism="unknown"
        /mol_type="mRNA"

Query Match
  Best Local Similarity 1.0%; Score 16; DB 1; Length 16;
  Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1508 CAGCCTCCAGGCCCC 1523
  |||||||
Db 16 CAGCCTCCAGGCCCC 1

RESULT 146
AR023187/c
LOCUS AR023187 16 bp DNA linear PAT 24-NOV-2000
DEFINITION Sequence 97 from Patent EP0905258.
ACCESSION AR023187
VERSION AR023187.1 GI:10046644
KEYWORDS
SOURCE
  ORGANISM
    unidentified
    unidentified
    unclassified.
  REFERENCE
    1
  AUTHORS
    .
  TITLE
    Method for detecting nucleic acid sequences based on the use of
    solid phase immobilised nucleotide probes (line probe assay)
  JOURNAL
    Patent: EP 0905258-A 97 31-MAR-1999;
  FEATURES
    Location/Qualifiers
      1..16
        /organism="unknown"
        /mol_type="mRNA"
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/organisms="unidentified"
/mol_type="unassigned DNA"
/db_xref="taxon:32644"

Query Match 1.0%; Score 16; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 50;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1508 CAGCCTCCAGGCCCCC 1523
|||||
Db 16 CAGCCTCCAGGCCCCC 1

RESULT 147
AX417393/c
LOCUS AX417393 16 bp DNA linear PAT 18-JUN-2002
DEFINITION Sequence 97 from Patent EP1197568.
ACCESSION AX417393
VERSION AX417393.1 GI:21522686
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
source
Hepatitis C virus
Hepatitis C virus
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
Hepacivirus.
1
Maertens,G., Rossau,R., Stuyver,L. and van Heuverswyn,H.
Detection and typing of hcv using 5'utr and ns5 nucleic acid
sequences
JOURNAL
Innogenetics N.V. (BE)
Patent: EP 1197568-A 97 17-APR-2002;
1. .16
Location/Qualifiers
/mol_type="unassigned DNA"
/db_xref="taxon:11103"

Query Match 1.0%; Score 16; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 50;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1508 CAGCCTCCAGGCCCCC 1523
|||||
Db 16 CAGCCTCCAGGCCCCC 1

RESULT 148
AR029848
LOCUS AR029848 17 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 37 from patent US 5861244.
ACCESSION AR029848
VERSION AR029848.1 GI:5943062
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
source
Wang,C.-G. and Hepburn,A.G.
Genetic sequence assay using DNA triple strand formation
Patent: US 5861244-A 37 19-JAN-1999;
1. .17
Location/Qualifiers
/mol_type="unassigned DNA"

Query Match 1.0%; Score 16; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 61;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 280 AGAAGAAGAAGAGGA 295
|||||
Db 1 AGAAGAAGAAGAGGA 16

/organisms="unidentified"
/mol_type="unassigned DNA"
/db_xref="taxon:32644"

Query Match 1.0%; Score 16; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 84;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 280 AGAAGAAGAAGAGGA 295
|||||
Db 17 AGAAGAAGAAGAGGA 2

RESULT 149
CQ881900/c
LOCUS CQ881900 19 bp RNA linear PAT 11-OCT-2004
DEFINITION Sequence 15 from Patent WO2004083446.
ACCESSION CQ881900
VERSION CQ881900.1 GI:54034672
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
source
synthetic construct
synthetic construct
other sequences; artificial sequences.
1
van Ommeren,G.J., van Deutekom,J.C., den Dunnen,J.T. and
Aartsma-Rus,A.
Modulation of exon recognition in pre-mrna by interfering with the
secondary rna structure
Patent: WO 2004083446-A 15 30-SEP-2004;
Academisch Ziekenhuis Leiden (NL)
Location/Qualifiers
1. .19
/mol_type="synthetic construct"
/mol_type="unassigned RNA"
/db_xref="taxon:32630"
/notes="Description of Artificial Sequence: h41AON1"

Query Match 1.0%; Score 16; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 84;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 280 AGAAGAAGAAGAGGA 295
|||||
Db 17 AGAAGAAGAAGAGGA 2

RESULT 150
CQ786119
LOCUS CQ786119 19 bp DNA linear PAT 24-MAR-2004
DEFINITION Sequence 7 from Patent WO2004018676.
ACCESSION CQ786119
VERSION CQ786119.1 GI:45721222
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
source
synthetic construct
synthetic construct
other sequences; artificial sequences.
1
Jansen,B., Gleave,M.E., Signaevsky,M., Beraldi,E., Trougakos,I. and
Conos,E.
Rnai probes targeting cancer-related proteins
Patent: WO 2004018676-A 7 04-MAR-2004;
The University of British Columbia (CA)
Location/Qualifiers
1. .19
/mol_type="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/notes="RNAi for human clusterin"

Query Match 1.0%; Score 15.8; DB 1; Length 19;
Best Local Similarity 89.5%; Pred. No. 90;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1616 TAATTCATAAAACTGTCT 1634
|||||
Db 1 TAATTCACAAAACGTGTT 19

RESULT 151
CQ786120/c
LOCUS CQ786120 19 bp DNA linear PAT 24-MAR-2004
DEFINITION Sequence 8 from Patent WO2004018676.
ACCESSION CQ786120
VERSION CQ786120.1 GI:45721223
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
source
synthetic construct
```

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ORGANISM      synthetic construct
REFERENCE      other sequences; artificial sequences.
AUTHORS       Jansen,B., Gleave,M.E., Signaevsky,M., Beraldi,E., Trougakos,I. and
              Gonos,E.
TITLE         Rnai probes targeting cancer-related proteins
JOURNAL       Patent: WO 2004018675-A 8 04-MAR-2004;
              The University of British Columbia (CA)
FEATURES      Location/Qualifiers
               1..19
               /organism="synthetic construct"
               /mol_type="unassigned DNA"
               /db_xref="taxon:32630"
               /note="RNAi for human clusterin"

Query Match   1.0%; Score 15.8; DB 1; Length 19;
Best Local Similarity 89.5%; Pred. No. 90;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1614 ACTAATTCATAAACTGCT 1632
Db 19 AATAATTCACAAACTGTT 1

RESULT 152
CQ786635
LOCUS          19 bp DNA linear PAT 24-MAR-2004
DEFINITION     Sequence 24 from Patent WO2004018675.
ACCESSION      CQ786635
VERSION        CQ786635.1 GI:45721655
KEYWORDS       .
SOURCE         synthetic construct
ORGANISM       other sequences; artificial sequences.
REFERENCE      1
AUTHORS        Jansen,B.
TITLE          Treatment of melanoma by reduction in clusterin levels
JOURNAL        Patent: WO 2004018675-A 27 04-MAR-2004;
              The University of British Columbia (CA); Gleave, Martin E. (CA)
FEATURES      Location/Qualifiers
               1..19
               /organism="synthetic construct"
               /mol_type="unassigned DNA"
               /db_xref="taxon:32630"
               /note="RNAi for human clusterin"

Query Match   1.0%; Score 15.8; DB 1; Length 19;
Best Local Similarity 89.5%; Pred. No. 90;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1614 ACTAATTCATAAACTGCT 1632
Db 19 AATAATTCACAAACTGTT 1

RESULT 153
CQ786637
LOCUS          19 bp DNA linear PAT 24-MAR-2004
DEFINITION     Sequence 26 from Patent WO2004018675.
ACCESSION      CQ786637
VERSION        CQ786637.1 GI:45721657
KEYWORDS       .
SOURCE         synthetic construct
ORGANISM       other sequences; artificial sequences.
REFERENCE      1
AUTHORS        Jansen,B.
TITLE          Treatment of melanoma by reduction in clusterin levels
JOURNAL        Patent: WO 2004018675-A 26 04-MAR-2004;
              The University of British Columbia (CA); Gleave, Martin E. (CA)
FEATURES      Location/Qualifiers
               1..19
               /organism="synthetic construct"

Query Match   1.0%; Score 15.8; DB 1; Length 19;
Best Local Similarity 89.5%; Pred. No. 90;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1616 TAATTCATAAACTGCT 1634
Db 1 TAATTCACAAACTGTT 19

RESULT 154
CQ786638/c
LOCUS          19 bp DNA linear PAT 24-MAR-2004
DEFINITION     Sequence 27 from Patent WO2004018675.
ACCESSION      CQ786638
VERSION        CQ786638.1 GI:45721658
KEYWORDS       .
SOURCE         synthetic construct
ORGANISM       other sequences; artificial sequences.
REFERENCE      1
AUTHORS        Jansen,B.
TITLE          Treatment of melanoma by reduction in clusterin levels
JOURNAL        Patent: WO 2004018675-A 27 04-MAR-2004;
              The University of British Columbia (CA); Gleave, Martin E. (CA)
FEATURES      Location/Qualifiers
               1..19
               /organism="synthetic construct"
               /mol_type="unassigned DNA"
               /db_xref="taxon:32630"
               /note="RNAi for human clusterin"

Query Match   1.0%; Score 15.8; DB 1; Length 19;
Best Local Similarity 89.5%; Pred. No. 90;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1614 ACTAATTCATAAACTGCT 1632
Db 19 AATAATTCACAAACTGTT 19

RESULT 155
CQ623926
LOCUS          17 bp DNA linear PAT 02-FEB-2004
DEFINITION     Sequence 8666 from Patent WO0192524.
ACCESSION      CQ623926
VERSION        CQ623926.1 GI:41674144
KEYWORDS       .
SOURCE         Homo sapiens (human)
ORGANISM       Homo sapiens
              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE      1
AUTHORS        Gu,Y., Ji,Y., Penn,S.G., Hanzel,D.K., Rank,D.R., Chen,W. and
              Shannon,M.E.
TITLE          Myosin-like gene expressed in human heart and muscle
JOURNAL        Patent: WO 0192524-A 8666 06-DEC-2001;
              Aeomica, Inc. (US)
FEATURES      Location/Qualifiers
               1..17
               /organism="Homo sapiens"
               /mol_type="unassigned DNA"
               /db_xref="taxon:9606"

Query Match   0.9%; Score 15.4; DB 1; Length 17;
Best Local Similarity 94.1%; Pred. No. 74;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 273 GAAGCCAAAGAGAGAA 289
              |||||||||

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Db 1 GAAGCCAGAGAGAGAA 17

RESULT 156  
I37522/c

LOCUS 17 bp DNA linear PAT 13-MAY-1997

DEFINITION Sequence 535 from patent US 5612215.

ACCESSION I37522

VERSION I37522.1 GI:2085482

KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

REFERENCE 1 (bases 1 to 17)  
Draper, K.G., Pavco, P., McSwiggen, J., Gustofson, J. and Stinchcomb, D.T.  
TITLE Stromelysin targeted ribozymes

JOURNAL Patent: US 5612215-A 535 18-MAR-1997;

FEATURES  
source  
1..17  
/organism="unknown"  
/mol\_type="unassigned DNA"

Query Match 0.9%; Score 15.4; DB 1; Length 17;  
Best Local Similarity 94.1%; Pred. No. 74;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1589 AAGAAGAGATTCTCTCC 1605  
|||||  
17 AAGACAGATTCTCC 1

Db 17 AAGACAGATTCTCC 1

RESULT 157  
I94372/c

LOCUS 17 bp DNA linear PAT 01-DEC-1998

DEFINITION Sequence 535 from patent US 5731295.

ACCESSION I94372

VERSION I94372.1 GI:3938842

KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

REFERENCE 1 (bases 1 to 17)  
Draper, K.G., Pavco, P., McSwiggen, J., Gustofson, J. and Stinchcomb, D.T.  
TITLE Method of reducing stromelysin RNA via ribozymes

JOURNAL Patent: US 5731295-A 535 24-MAR-1998;

FEATURES  
source  
1..17  
/organism="unknown"  
/mol\_type="unassigned DNA"

Query Match 0.9%; Score 15.4; DB 1; Length 17;  
Best Local Similarity 94.1%; Pred. No. 74;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1589 AAGAAGAGATTCTCTCC 1605  
|||||  
17 AAGACAGATTCTCC 1

Db 17 AAGACAGATTCTCC 1

RESULT 158  
AR464989

LOCUS 17 bp DNA linear PAT 20-FEB-2004

DEFINITION Sequence 8666 from patent US 6686188.

ACCESSION AR464989

VERSION AR464989.1 GI:42700046

KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

REFERENCE 1 (bases 1 to 17)  
Gu, Y., Ji, Y., Penn, S.G., Hanzel, D.K., Rank, D.R., Chen, W. and

Shannon, M.E.  
Polynucleotide encoding a human myosin-like polypeptide expressed predominantly in heart and muscle  
Patent: US 6686188-A 8666 03-FEB-2004;

JOURNAL Location/Qualifiers

FEATURES  
source  
1..17  
/organism="unknown"  
/mol\_type="genomic DNA"

Query Match 0.9%; Score 15.4; DB 1; Length 17;  
Best Local Similarity 94.1%; Pred. No. 74;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 273 GAAGCCAGAGAGAGAA 289  
|||||  
1 GAAGCCAGAGAGAGAA 17

Db 1 GAAGCCAGAGAGAGAA 17

RESULT 159  
AX214728/c

LOCUS 17 bp RNA linear PAT 07-SEP-2001

DEFINITION Sequence 170 from Patent WO0159103.

ACCESSION AX214728

VERSION AX214728.1 GI:15524771

KEYWORDS synthetic construct

SOURCE synthetic construct

ORGANISM other sequences; artificial sequences.

REFERENCE 1  
Blatt, L., McSwiggen, J. and Chowrira, B.M.  
AUTHORS Method and reagent for the modulation and diagnosis of cd20 and nogo gene expression

TITLE Patent: WO 0159103-A 170 16-AUG-2001;  
RIBOZYME PHARMACEUTICALS, INC. (US) ; Blatt, Lawrence (US) ; McSwiggen, James (US) ; Chowrira, Bharat M. (US)

JOURNAL Location/Qualifiers

FEATURES  
source  
1..17  
/organism="synthetic construct"  
/mol\_type="unassigned RNA"  
/db\_xref="taxon:32630"  
/note="Nucleic Acid"

Query Match 0.9%; Score 15.4; DB 1; Length 17;  
Best Local Similarity 94.1%; Pred. No. 74;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1619 TTCAATAAAACGTCTT 1635  
|||||  
17 TTCATTAACGTCTT 1

Db 17 TTCATTAACGTCTT 1

RESULT 160  
AX688719/c

LOCUS 17 bp DNA linear PAT 31-MAR-2003

DEFINITION Sequence 1451 from Patent EP1281758.

ACCESSION AX688719

VERSION AX688719.1 GI:29411423

KEYWORDS

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE 1  
Shannon, M., Gu, Y. and Nguyen, C.T.  
AUTHORS Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and mdz12

TITLE Patent: EP 1281758-A 1451 05-FEB-2003;

JOURNAL Aeomica, Inc. (US)

FEATURES  
source  
1..17  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"

Query Match 0.9%; Score 15.4; DB 1; Length 17;  
Best Local Similarity 94.1%; Pred. No. 74;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 928 GCTGCTGGCGATGAAG 944  
|||||  
Db 17 GCTGCTGGCGCTGAAG 1

RESULT 161  
AX762505  
LOCUS AX762505 17 bp DNA linear PAT 25-JUN-2003  
DEFINITION Sequence 5826 from Patent WO03040369.  
ACCESSION AX762505  
VERSION AX762505.1 GI:32257121  
KEYWORDS  
SOURCE  
ORGANISM Homo sapiens (human)  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
FEATURES  
source 1.17  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"

Query Match 0.9%; Score 15.4; DB 1; Length 17;  
Best Local Similarity 94.1%; Pred. No. 74;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1551 GATCCTGCACTCTAACA 1567  
|||||  
Db 1 GATCCTGCACTCTACCA 17

RESULT 162  
AR011407/c  
LOCUS AR011407 18 bp DNA linear PAT 04-DEC-1998  
DEFINITION Sequence 280 from patent US 5762938.  
ACCESSION AR011407  
VERSION AR011407.1 GI:3969397  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
FEATURES  
source 1.18  
/organism="unknown"  
/mol\_type="unassigned DNA"

Query Match 0.9%; Score 14.8; DB 1; Length 18;  
Best Local Similarity 88.9%; Pred. No. 1.1e+02;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 222 CTCATAGAAAAAACAAAC 239  
|||||  
Db 18 CTAATAGAAAAAACCAAC 1

RESULT 163  
AR040105/c  
LOCUS AR040105 18 bp DNA linear PAT 29-SEP-1999  
DEFINITION Sequence 953 from patent US 5807743.  
ACCESSION AR040105  
VERSION AR040105.1 GI:5959468  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
FEATURES  
source 1.18  
/organism="unknown"  
/mol\_type="unassigned DNA"

Query Match 0.9%; Score 14.8; DB 1; Length 18;  
Best Local Similarity 88.9%; Pred. No. 1.1e+02;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1121 GCTGGAGCAGCTGAACGA 1138  
|||||  
Db 18 GCAGGAGCAGCTGAAGGA 1

RESULT 164  
I18045/c  
LOCUS I18045 18 bp DNA linear PAT 07-OCT-1996  
DEFINITION Sequence 280 from patent US 5494807.  
ACCESSION I18045  
VERSION I18045.1 GI:1598400  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
FEATURES  
source 1.18  
/organism="unknown"  
/mol\_type="unassigned DNA"

Query Match 0.9%; Score 14.8; DB 1; Length 18;  
Best Local Similarity 88.9%; Pred. No. 1.1e+02;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 222 CTCATAGAAAAAACAAAC 239  
|||||  
Db 18 CTAATAGAAAAAACCAAC 1

RESULT 165  
AX115178  
LOCUS AX115178 18 bp DNA linear PAT 11-MAY-2001  
DEFINITION Sequence 301 from Patent WO0129262.  
ACCESSION AX115178  
VERSION AX115178.1 GI:14032120  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
FEATURES  
source 1  
/organism="unknown"  
/mol\_type="unassigned DNA"

Query Match 0.9%; Score 14.8; DB 1; Length 18;  
Best Local Similarity 88.9%; Pred. No. 1.1e+02;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 222 CTCATAGAAAAAACAAAC 239  
|||||  
Db 18 CTAATAGAAAAAACCAAC 1

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FEATURES
  source
    Location/Qualifiers
      1..18
        /organism="synthetic construct"
        /mol_type="unassigned DNA"
        /db_xref="taxon:32630"
        /note="Primer"

Query Match
  Best Local Similarity 88.9%; Score 14.8; DB 1; Length 18;
  Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1492 CCAAGTAACAGGCCCA 1509
Db 1 CCAGGTACAGGCCCA 18

RESULT 166
AX776586
LOCUS
  DEFINITION
    Sequence 11 from Patent WO03047611.
  ACCESSION
    AX776586
  VERSION
    AX776586.1 GI:32694120
  KEYWORDS
    synthetic construct
  SOURCE
    synthetic construct
    other sequences; artificial sequences.
  REFERENCE
    1
    AUTHORS
      Meise, M., Eulenberger, K., Fritsch, R., Haeder, T., Broenner, G. and
      Steuernagel, A.
    TITLE
      Ptp10d, tec protein tyrosine kinase and edtp homologous proteins
      involved in the regulation of energy homeostasis
    JOURNAL
      Patent: WO 03047611-A 11 12-JUN-2003;
      DeveloGen Aktiengesellschaft fuer entwicklungsbiologische Forschung
      (DE)
  FEATURES
    source
      Location/Qualifiers
        1..18
          /organism="synthetic construct"
          /mol_type="unassigned DNA"
          /db_xref="taxon:32630"
          /note="mouse PTPRB reverse primer"

Query Match
  Best Local Similarity 88.9%; Score 14.8; DB 1; Length 18;
  Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 764 CTTCCACGCCATCTTCCA 781
Db 1 CTTCCACGCCATCTTCCA 18

RESULT 167
AR173373
LOCUS
  DEFINITION
    Sequence 7 from patent US 6303847.
  ACCESSION
    AR173373
  VERSION
    AR173373.1 GI:17912864
  KEYWORDS
    Unknown.
  SOURCE
    Unknown.
  ORGANISM
    Unclassified.
  REFERENCE
    1 (bases 1 to 17)
    AUTHORS
      Kawaoka, A. and Ebina, H.
    TITLE
      DNA encoding a transcription factor controlling phenylpropanoid
      biosynthesis pathway
    JOURNAL
      Patent: US 6303847-A 7 16-OCT-2001;
  FEATURES
    source
      Location/Qualifiers
        1..17
          /organism="unknown"
          /mol_type="unassigned DNA"

Query Match
  Best Local Similarity 93.8%; Score 14.4; DB 1; Length 17;
  Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1104 CTCACACCTCTCTCT 1119
Db 2 CTCACACCTCTCTCT 17

RESULT 169
CQ623612/c
LOCUS
  DEFINITION
    Sequence 8352 from Patent WO0192524.
  ACCESSION
    CQ623612
  VERSION
    CQ623612.1 GI:41673830
  KEYWORDS
    Homo sapiens (human)
  SOURCE
    Homo sapiens
    Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
  REFERENCE
    1
    AUTHORS
      Gu, Y., Ji, Y., Penn, S.G., Hanzel, D.K., Rank, D.R., Chen, W. and
      Shannon, M.E.
    TITLE
      Myosin-like gene expressed in human heart and muscle
    JOURNAL
      Patent: WO 0192524-A 8352 06-DEC-2001;
      Aeomica, Inc. (US)
  FEATURES
    source
      Location/Qualifiers
        1..17
          /organism="Homo sapiens"
          /mol_type="unassigned DNA"
          /db_xref="taxon:9606"

Query Match
  Best Local Similarity 93.8%; Score 14.4; DB 1; Length 17;
  Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1109 CACCTCTCTCTCTCTG 1124
Db 17 CAGCTCTCTCTCTCTG 2

RESULT 169
CQ623613/c
LOCUS
  DEFINITION
    Sequence 8353 from Patent WO0192524.
  ACCESSION
    CQ623613
  VERSION
    CQ623613.1 GI:41673831
  KEYWORDS
    Homo sapiens (human)
  SOURCE
    Homo sapiens
    Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
  REFERENCE
    1
    AUTHORS
      Gu, Y., Ji, Y., Penn, S.G., Hanzel, D.K., Rank, D.R., Chen, W. and
      Shannon, M.E.
    TITLE
      Myosin-like gene expressed in human heart and muscle
    JOURNAL
      Patent: WO 0192524-A 8353 06-DEC-2001;
      Aeomica, Inc. (US)
  FEATURES
    source
      Location/Qualifiers
        1..17
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          /mol_type="unassigned DNA"
          /db_xref="taxon:9606"

Query Match
  Best Local Similarity 93.8%; Score 14.4; DB 1; Length 17;
  Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1109 CACCTCTCTCTCTCTG 1124
Db 16 CAGCTCTCTCTCTCTG 1

RESULT 170
CQ623925
LOCUS
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[illegible]





RESULT 182  
AX214729/C

REFERENCE  
AUTHORS Shannon, M., Gu, Y. and Nguyen, C.T.  
TITLE Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and mdz12  
JOURNAL Patent: EP 1281758-A 1452 05-FEB-2003;  
Acomica, Inc. (US)  
FEATURES  
source Location/Qualifiers  
1. .17  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"

Query Match 0.9%; Score 14.4; DB 1; Length 17;  
Best Local Similarity 93.8%; Pred. No. 1e+02;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 928 GCTGCTCGCGATGAA 943  
Db 16 GCTGCTCGCGCTGAA 1  
|||||

RESULT 185  
AX732888/c  
LOCUS AX732888 17 bp DNA linear PAT 08-MAY-2003  
DEFINITION Sequence 4522 from Patent WO03025175.  
ACCESSION AX732888  
VERSION AX732888.1 GI:30512231  
KEYWORDS Homo sapiens (human)  
SOURCE Homo sapiens  
ORGANISM Homo sapiens  
REFERENCE 1  
AUTHORS Telesman, A., Anson, R. and Tuijnder, M.  
TITLE Sequences involved in phenomena of tumour suppression, tumour reversion, apoptosis and/or virus resistance and their use as medicines  
JOURNAL Patent: WO 03025175-A 4522 27-MAR-2003;  
Molecular Engines Laboratories (FR)  
FEATURES  
source Location/Qualifiers  
1. .17  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"

Query Match 0.9%; Score 14.4; DB 1; Length 17;  
Best Local Similarity 93.8%; Pred. No. 1e+02;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 326 AAAGCTGAAGAGCTC 341  
Db 16 AAAGCTGAAGAGATC 1  
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RESULT 186  
AX760623  
LOCUS AX760623 17 bp DNA linear PAT 25-JUN-2003  
DEFINITION Sequence 3944 from Patent WO03040369.  
ACCESSION AX760623  
VERSION AX760623.1 GI:32255239  
KEYWORDS Homo sapiens (human)  
SOURCE Homo sapiens  
ORGANISM Homo sapiens  
REFERENCE 1  
AUTHORS Telesman, A., Anson, R. and Tuijnder, M.  
TITLE Sequences involved in tumoral suppression, tumoral reversion, apoptosis and/or viral resistance phenomena and their use as medicines  
JOURNAL Patent: WO 03040369-A 3944 15-MAY-2003;  
Molecular Engines Laboratories (FR)

REFERENCE  
AUTHORS Shannon, M., Gu, Y. and Nguyen, C.T.  
TITLE Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and mdz12  
JOURNAL Patent: EP 1281758-A 1452 05-FEB-2003;  
Acomica, Inc. (US)  
FEATURES  
source Location/Qualifiers  
1. .17  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"

Query Match 0.9%; Score 14.4; DB 1; Length 17;  
Best Local Similarity 93.8%; Pred. No. 1e+02;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 928 GCTGCTCGCGATGAA 943  
Db 16 GCTGCTCGCGCTGAA 1  
|||||

RESULT 185  
AX732888/c  
LOCUS AX732888 17 bp DNA linear PAT 08-MAY-2003  
DEFINITION Sequence 4522 from Patent WO03025175.  
ACCESSION AX732888  
VERSION AX732888.1 GI:30512231  
KEYWORDS Homo sapiens (human)  
SOURCE Homo sapiens  
ORGANISM Homo sapiens  
REFERENCE 1  
AUTHORS Telesman, A., Anson, R. and Tuijnder, M.  
TITLE Sequences involved in phenomena of tumour suppression, tumour reversion, apoptosis and/or virus resistance and their use as medicines  
JOURNAL Patent: WO 03025175-A 4522 27-MAR-2003;  
Molecular Engines Laboratories (FR)  
FEATURES  
source Location/Qualifiers  
1. .17  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"

Query Match 0.9%; Score 14.4; DB 1; Length 17;  
Best Local Similarity 93.8%; Pred. No. 1e+02;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 326 AAAGCTGAAGAGCTC 341  
Db 16 AAAGCTGAAGAGATC 1  
|||||

RESULT 186  
AX760623  
LOCUS AX760623 17 bp DNA linear PAT 25-JUN-2003  
DEFINITION Sequence 3944 from Patent WO03040369.  
ACCESSION AX760623  
VERSION AX760623.1 GI:32255239  
KEYWORDS Homo sapiens (human)  
SOURCE Homo sapiens  
ORGANISM Homo sapiens  
REFERENCE 1  
AUTHORS Telesman, A., Anson, R. and Tuijnder, M.  
TITLE Sequences involved in tumoral suppression, tumoral reversion, apoptosis and/or viral resistance phenomena and their use as medicines  
JOURNAL Patent: WO 03040369-A 3944 15-MAY-2003;  
Molecular Engines Laboratories (FR)

FEATURES  
source Location/Qualifiers  
1. .17  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"

Query Match 0.9%; Score 14.4; DB 1; Length 17;  
Best Local Similarity 93.8%; Pred. No. 1e+02;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 154 ATCAGGGAAGTAAGTA 169  
Db 2 ATCAGGGAAGTAAGTA 17  
|||||

RESULT 187  
AR067404/c  
LOCUS AR067404 18 bp DNA linear PAT 29-SEP-1999  
DEFINITION Sequence 797 from patent US 5851760.  
ACCESSION AR067404  
VERSION AR067404.1 GI:5998626  
KEYWORDS Unknown.  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 18)  
AUTHORS Evans, G.A. and Smith, M.W.  
TITLE Method for generation of sequence sampled maps of complex genomes  
JOURNAL Patent: US 5851760-A 797 22-DEC-1998;  
FEATURES  
source Location/Qualifiers  
1. .18  
/organism="unknown"  
/mol\_type="unassigned DNA"

Query Match 0.9%; Score 14.4; DB 1; Length 18;  
Best Local Similarity 93.8%; Pred. No. 1.2e+02;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1520 CCCCAACTCCGCCAG 1535  
Db 18 CCTTAATCCGCCAG 3  
|||||

RESULT 188  
AX837978  
LOCUS AX837978 18 bp DNA linear PAT 15-DEC-2003  
DEFINITION Sequence 5102 from Patent EP1347046.  
ACCESSION AX837978  
VERSION AX837978.1 GI:39921670  
KEYWORDS unidentified  
SOURCE unidentified  
ORGANISM unidentified  
REFERENCE 1  
AUTHORS Isogai, T., Sugiyama, T., Otsuka, T., Wakamatsu, A., Sato, H., Ishii, S., Yamamoto, J. I., Isono, Y., Hio, Y., Otsuka, K., Nagai, K., Irie, R., Tamechika, I., Seki, N., Yoshikawa, T., Otsuka, M., Nagahari, K. and Masuho, Y.  
TITLE Full-length cDNA sequences  
JOURNAL Patent: EP 1347046-A 5102 24-SEP-2003;  
Research Association for Biotechnology (JP)  
FEATURES  
source Location/Qualifiers  
1. .18  
/organism="unidentified"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32644"  
/note="Description of Artificial Sequence: an artificially synthesized primer se q"

Query Match 0.9%; Score 14.4; DB 1; Length 18;  
Best Local Similarity 93.8%; Pred. No. 1.2e+02;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1094 GTGGAAGATGCTCAAC 1109  
Db 1 GTGGAAGATGCTCGAC 16

RESULT 169  
AX324817/c  
LOCUS AX324817 17 bp DNA linear PAT 02-SEP-2002  
DEFINITION Sequence 955 from Patent WO0192512.  
ACCESSION AX324817  
VERSION AX324817.1 GI:18095570  
KEYWORDS  
SOURCE Eucalyptus camaldulensis (Murray red gum)  
ORGANISM Eucalyptus camaldulensis  
REFERENCE 1 Eucalyptus camaldulensis  
AUTHORS Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
TITLE Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
JOURNAL Rosids; Myrtales; Myrtaceae; Eucalyptus.  
FEATURES  
source 1  
Location/Qualifiers  
1..17  
/organism="Eucalyptus camaldulensis"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:34316"

Query Match 0.9%; Score 14; DB 1; Length 17;  
Best Local Similarity 100.0%; Pred. No. 1.2e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1202 GGTCAACCGGTGG 1215  
Db 14 GGTCAACCGGTGG 1

RESULT 190  
AX324818  
LOCUS AX324818 17 bp DNA linear PAT 02-SEP-2002  
DEFINITION Sequence 956 from Patent WO0192512.  
ACCESSION AX324818  
VERSION AX324818.1 GI:18095571  
KEYWORDS  
SOURCE Eucalyptus camaldulensis (Murray red gum)  
ORGANISM Eucalyptus camaldulensis  
REFERENCE 1 Eucalyptus camaldulensis  
AUTHORS Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
TITLE Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
JOURNAL Rosids; Myrtales; Myrtaceae; Eucalyptus.  
FEATURES  
source 1  
Location/Qualifiers  
1..17  
/organism="Eucalyptus camaldulensis"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:34316"

Query Match 0.9%; Score 14; DB 1; Length 17;  
Best Local Similarity 100.0%; Pred. No. 1.2e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1202 GGTCAACCGGTGG 1215  
Db 4 GGTCAACCGGTGG 17

RESULT 191  
AR039619

LOCUS AR039619 17 bp DNA linear PAT 29-SEP-1999  
DEFINITION Sequence 467 from patent US 5807743.  
ACCESSION AR039619  
VERSION AR039619.1 GI:5958982  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 17)  
AUTHORS Stinchcomb,D.T. and McSwiggen,J.A.  
TITLE Interleukin-2 receptor gamma-chain ribozymes  
JOURNAL Patent: US 5807743-A 467 15-SEP-1998;  
FEATURES  
source 1..17  
Location/Qualifiers  
/organism="unknown"  
/mol\_type="unassigned DNA"

Query Match 0.8%; Score 13.8; DB 1; Length 17;  
Best Local Similarity 88.2%; Pred. No. 1.3e+02;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 693 CCTCAGTCTCTTTC 709  
Db 1 CCTCCTCTCTCTTTC 17

RESULT 192  
AR081753  
LOCUS AR081753 17 bp DNA linear PAT 31-AUG-2000  
DEFINITION Sequence 25 from patent US 5972621.  
ACCESSION AR081753  
VERSION AR081753.1 GI:10008479  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 17)  
AUTHORS Tartaglia,L.A., Tepper,R.I. and Culpepper,J.A.  
TITLE Methods of identifying compounds that modulate body weight using the OB receptor  
JOURNAL Patent: US 5972621-A 25 26-OCT-1999;  
FEATURES  
source 1..17  
Location/Qualifiers  
/organism="unknown"  
/mol\_type="unassigned DNA"

Query Match 0.8%; Score 13.8; DB 1; Length 17;  
Best Local Similarity 88.2%; Pred. No. 1.3e+02;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 660 CACTACCTGCCCTTCAG 676  
Db 1 CACTATTGCCCTTCAG 17

RESULT 193  
AR081755  
LOCUS AR081755 17 bp DNA linear PAT 31-AUG-2000  
DEFINITION Sequence 27 from patent US 5972621.  
ACCESSION AR081755  
VERSION AR081755.1 GI:10008481  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 17)  
AUTHORS Tartaglia,L.A., Tepper,R.I. and Culpepper,J.A.  
TITLE Methods of identifying compounds that modulate body weight using the OB receptor  
JOURNAL Patent: US 5972621-A 27 26-OCT-1999;  
FEATURES  
source 1..17  
Location/Qualifiers  
/organism="unknown"

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/mol_type="unassigned DNA"

Query Match
Best Local Similarity 0.8%; Score 13.8; DB 1; Length 17;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 660 CACTACTGCGCCTTCAG 676
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Db 1 CACTATTGGCCTTCAG 17

RESULT 194
AR094983/C
LOCUS AR094983 17 bp DNA linear PAT 08-SEP-2000
DEFINITION Sequence 21 from patent US 6001990.
ACCESSION AR094983
VERSION AR094983.1 GI:10022419
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Wanda, J.R., Wakita, T. and Moradpour, D.
TITLE Antisense inhibition of hepatitis C virus
JOURNAL Patent: US 6001990-A 21 14-DEC-1999;
FEATURES
    source
        /organism="unknown"
        /mol_type="unassigned DNA"

Query Match
Best Local Similarity 0.8%; Score 13.8; DB 1; Length 17;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 222 CTCATGAGAAACAAA 238
    ||||| ||||| |||||
Db 17 CTCAGAGAAACCAA 1

RESULT 195
AR167985
LOCUS AR167985 17 bp DNA linear PAT 17-DEC-2001
DEFINITION Sequence 25 from patent US 6287782.
ACCESSION AR167985
VERSION AR167985.1 GI:17903799
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Tartaglia, L.A., Tepper, R.I., Culpepper, J.A. and White, D.W.
TITLE Methods of using the Ob receptor to identify therapeutic compounds
JOURNAL Patent: US 6287782-A 25 11-SEP-2001;
FEATURES
    source
        /organism="unknown"
        /mol_type="unassigned DNA"

Query Match
Best Local Similarity 0.8%; Score 13.8; DB 1; Length 17;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 660 CACTACTGCGCCTTCAG 676
    ||||| ||||| |||||
Db 1 CACTATTGGCCTTCAG 17

RESULT 196
AR167987
LOCUS AR167987 17 bp DNA linear PAT 17-DEC-2001
DEFINITION Sequence 27 from patent US 6287782.
ACCESSION AR167987
VERSION AR167987.1 GI:17903801

/mol_type="unassigned DNA"

Query Match
Best Local Similarity 0.8%; Score 13.8; DB 1; Length 17;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 660 CACTACTGCGCCTTCAG 676
    ||||| ||||| |||||
Db 1 CACTATTGGCCTTCAG 17

RESULT 197
BD254845 17 bp DNA linear PAT 17-JUL-2003
LOCUS BD254845
DEFINITION Regulation of repressor genes using nucleic acid molecules.
ACCESSION BD254845
VERSION BD254845.1 GI:33064615
KEYWORDS JP 2002541795-A/2638.
SOURCE unidentified.
ORGANISM unidentified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Blatt, L., Zwick, M., Pavco, P. and Mcswiggen, J.
TITLE Regulation of repressor genes using nucleic acid molecules
JOURNAL Patent: JP 2002541795-A 2638 10-DEC-2002;
COMMENT RIBOZYME PHARMACEUTICALS INC
    OS Eukaryote
    PN JP 2002541795-A/2638
    PD 10-DEC-2002
    PF 11-APR-2000 JP 2000611654
    PR 12-APR-1999 US 60/129390
    PI LAWRENCE BLATT, MICHAEL ZWICK, PAMELA PAVCO, JAMES MCSWIGGEN
    PC C12N15/09, A61K38/00, A61K48/00, A61P43/00, A61P43/00, C12N5/10, PC
    C12P21/02,
    PC
    C12P21/02, C12P21/02//A61K31/711, (C12N5/10, C12R1:91), (C12P21/02, PC
    C12R1:91),
    PC (C12P21/02, C12R1:91), (C12P21/02, C12R1:91), C12N15/00, C12N5/00,
    PC A61K37/02,
    PC (C12N5/00, C12R1:91)
    CC Regulation of repressor genes using nucleic acid molecules FH
    Key Location/Qualifiers
    FT source 1..17
    FT /organism='Eukaryote'.

FEATURES
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        Location/Qualifiers
        1..17
        /organism="unidentified"
        /mol_type="genomic DNA"
        /db_xref="taxon:32644"

Query Match
Best Local Similarity 0.8%; Score 13.8; DB 1; Length 17;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 116 CCAGACGGTCTCAGACA 132
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Db 1 CCAGACGTTCTCAGTCA 17

RESULT 198
CQ617155/C
LOCUS CQ617155 17 bp DNA linear PAT 02-FEB-2004
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DEFINITION      Sequence 1895 from Patent WO0192524.
ACCESSION       CQ617155
VERSION         CQ617155.1  GI:41667373
KEYWORDS        Homo sapiens (human)
SOURCE          Homo sapiens
ORGANISM        Homo sapiens
REFERENCE       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS        Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1
TITLE          Gu, Y., Ji, Y., Penn, S.G., Hanzel, D.K., Rank, D.R., Chen, W. and
JOURNAL        Shannon, M.E.
                Myosin-like gene expressed in human heart and muscle
                Patent: WO 0192524-A 1895 06-DEC-2001;
                Aeomica, Inc. (US)
FEATURES       Location/Qualifiers
source         1..17
               /organism="Homo sapiens"
               /mol_type="unassigned DNA"
               /db_xref="taxon:9606"

Query Match    0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.3e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 93 GAGAGTGGCGAGTCTCT 109
      ||||| ||||| |||||
Db 17 GAGAGAGGCCAGTCTCT 1

RESULT 199
CQ617903/c
LOCUS          CQ617903 17 bp DNA linear PAT 02-FEB-2004
DEFINITION     Sequence 2643 from Patent WO0192524.
ACCESSION      CQ617903
VERSION        CQ617903.1  GI:41668121
KEYWORDS       Homo sapiens (human)
SOURCE         Homo sapiens
ORGANISM       Homo sapiens
REFERENCE      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS        Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1
TITLE          Gu, Y., Ji, Y., Penn, S.G., Hanzel, D.K., Rank, D.R., Chen, W. and
JOURNAL        Shannon, M.E.
                Myosin-like gene expressed in human heart and muscle
                Patent: WO 0192524-A 2643 06-DEC-2001;
                Aeomica, Inc. (US)
FEATURES       Location/Qualifiers
source         1..17
               /organism="Homo sapiens"
               /mol_type="unassigned DNA"
               /db_xref="taxon:9606"

Query Match    0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.3e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 845 CTTCAGACCCGCGCAA 861
      ||||| ||||| |||||
Db 17 CTGCAGAGCCCGCAA 1

RESULT 200
CQ622615
LOCUS          CQ622615 17 bp DNA linear PAT 02-FEB-2004
DEFINITION     Sequence 7355 from Patent WO0192524.
ACCESSION      CQ622615
VERSION        CQ622615.1  GI:41672833
KEYWORDS       Homo sapiens (human)
SOURCE         Homo sapiens
ORGANISM       Homo sapiens
REFERENCE      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS        Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1
TITLE          Gu, Y., Ji, Y., Penn, S.G., Hanzel, D.K., Rank, D.R., Chen, W. and
JOURNAL        Shannon, M.E.
                Myosin-like gene expressed in human heart and muscle
                Patent: WO 0192524-A 7355 06-DEC-2001;
                Aeomica, Inc. (US)
FEATURES       Location/Qualifiers
source         1..17
               /organism="Homo sapiens"
               /mol_type="unassigned DNA"
               /db_xref="taxon:9606"

Query Match    0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.3e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1530 GCCCAGCCTCTCCCGC 1546
      ||||| ||||| |||||
Db 17 GTCCAGCCTCTCTCTCGC 1

RESULT 202
CQ623828
LOCUS          CQ623828 17 bp DNA linear PAT 02-FEB-2004
DEFINITION     Sequence 8568 from Patent WO0192524.
ACCESSION      CQ623828
VERSION        CQ623828.1  GI:41674046
KEYWORDS       Homo sapiens (human)
SOURCE         Homo sapiens
ORGANISM       Homo sapiens
REFERENCE      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS        Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1
TITLE          Gu, Y., Ji, Y., Penn, S.G., Hanzel, D.K., Rank, D.R., Chen, W. and
JOURNAL        Shannon, M.E.
                Myosin-like gene expressed in human heart and muscle
                Patent: WO 0192524-A 8568 06-DEC-2001;
                Aeomica, Inc. (US)
FEATURES       Location/Qualifiers
source         1..17
               /organism="Homo sapiens"
               /mol_type="unassigned DNA"
               /db_xref="taxon:9606"

Query Match    0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.3e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1530 GCCCAGCCTCTCCCGC 1546
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Db 17 GTCCAGCCTCTCTCTCGC 1

RESULT 203
CQ622745/c
LOCUS          CQ622745 17 bp DNA linear PAT 02-FEB-2004
DEFINITION     Sequence 7485 from Patent WO0192524.
ACCESSION      CQ622745
VERSION        CQ622745.1  GI:41672963
KEYWORDS       Homo sapiens (human)
SOURCE         Homo sapiens
ORGANISM       Homo sapiens
REFERENCE      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS        Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1
TITLE          Gu, Y., Ji, Y., Penn, S.G., Hanzel, D.K., Rank, D.R., Chen, W. and
JOURNAL        Shannon, M.E.
                Myosin-like gene expressed in human heart and muscle
                Patent: WO 0192524-A 7485 06-DEC-2001;
                Aeomica, Inc. (US)
FEATURES       Location/Qualifiers
source         1..17
               /organism="Homo sapiens"
               /mol_type="unassigned DNA"
               /db_xref="taxon:9606"

Query Match    0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.3e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 270 GAAGAAGCCCAAGAGAA 286
      ||||| ||||| |||||
Db 1 GAAGAAGCCCAAGAGAA 17

RESULT 204
CQ622745/c
LOCUS          CQ622745 17 bp DNA linear PAT 02-FEB-2004
DEFINITION     Sequence 7485 from Patent WO0192524.
ACCESSION      CQ622745
VERSION        CQ622745.1  GI:41672963
KEYWORDS       Homo sapiens (human)
SOURCE         Homo sapiens
ORGANISM       Homo sapiens
REFERENCE      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS        Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1
TITLE          Gu, Y., Ji, Y., Penn, S.G., Hanzel, D.K., Rank, D.R., Chen, W. and
JOURNAL        Shannon, M.E.
                Myosin-like gene expressed in human heart and muscle
                Patent: WO 0192524-A 7485 06-DEC-2001;
                Aeomica, Inc. (US)
FEATURES       Location/Qualifiers
source         1..17
               /organism="Homo sapiens"
               /mol_type="unassigned DNA"
               /db_xref="taxon:9606"

Query Match    0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.3e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 270 GAAGAAGCCCAAGAGAA 286
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Db 1 GAAGAAGCCCAAGAGAA 17
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/db\_xref="taxon:9606"

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Query Match      0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.3e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 292 AGGATGCCCTAAATGAG 308
||||| ||| |||||
Db 1 AGGATGACCTGAATGAG 17

RESULT 203
CQ623920
LOCUS      17 bp DNA linear PAT 02-FEB-2004
DEFINITION Sequence 8660 from Patent WO0192524.
ACCESSION CQ623920
VERSION CQ623920.1 GI:41674138
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Gu,Y., Ji,Y., Penn,S.G., Hanzel,D.K., Rank,D.R., Chen,W. and Shannon,M.E.
TITLE Myosin-like gene expressed in human heart and muscle
JOURNAL Patent: WO 0192524-A 8660 06-DEC-2001;
          Aeomica, Inc. (US)
FEATURES
source 1..17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match      0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.3e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 267 CTAGAAGAGCCCAAGAA 283
||||| ||| |||||
Db 1 CTGGAGAGCCCAAGAA 17

RESULT 204
CQ623921
LOCUS      17 bp DNA linear PAT 02-FEB-2004
DEFINITION Sequence 8661 from Patent WO0192524.
ACCESSION CQ623921
VERSION CQ623921.1 GI:41674139
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Gu,Y., Ji,Y., Penn,S.G., Hanzel,D.K., Rank,D.R., Chen,W. and Shannon,M.E.
TITLE Myosin-like gene expressed in human heart and muscle
JOURNAL Patent: WO 0192524-A 8661 06-DEC-2001;
          Aeomica, Inc. (US)
FEATURES
source 1..17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match      0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.3e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 268 TAGAAGAGCCCAAGAG 284
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Db 1 TGGAGGAGCCCAAGAG 17
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RESULT 205
CQ623923
LOCUS      17 bp DNA linear PAT 02-FEB-2004
DEFINITION Sequence 8663 from Patent WO0192524.
ACCESSION CQ623923
VERSION CQ623923.1 GI:41674141
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Gu,Y., Ji,Y., Penn,S.G., Hanzel,D.K., Rank,D.R., Chen,W. and Shannon,M.E.
TITLE Myosin-like gene expressed in human heart and muscle
JOURNAL Patent: WO 0192524-A 8663 06-DEC-2001;
          Aeomica, Inc. (US)
FEATURES
source 1..17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match      0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.3e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 270 GAAGAAGCCCAAGAGAA 286
||||| ||| |||||
Db 1 GAGGAGCCCAAGAGGA 17

RESULT 206
CQ623924
LOCUS      17 bp DNA linear PAT 02-FEB-2004
DEFINITION Sequence 8664 from Patent WO0192524.
ACCESSION CQ623924
VERSION CQ623924.1 GI:41674142
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Gu,Y., Ji,Y., Penn,S.G., Hanzel,D.K., Rank,D.R., Chen,W. and Shannon,M.E.
TITLE Myosin-like gene expressed in human heart and muscle
JOURNAL Patent: WO 0192524-A 8664 06-DEC-2001;
          Aeomica, Inc. (US)
FEATURES
source 1..17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match      0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.3e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 271 AAGAAGCCCAAGAGAGAG 287
||||| ||| |||||
Db 1 AGGAGCCCAAGAGGAG 17

RESULT 207
CQ624947/c
LOCUS      17 bp DNA linear PAT 02-FEB-2004
DEFINITION Sequence 9687 from Patent WO0192524.
ACCESSION CQ624947
VERSION CQ624947.1 GI:41675165
KEYWORDS
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SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE  
AUTHORS Gu,Y., Ji,Y., Penn,S.G., Hanzel,D.K., Rank,D.R., Chen,W. and  
Shannon,M.E.  
TITLE Myosin-like gene expressed in human heart and muscle  
JOURNAL Patent: WO 0192524-A 9687 06-DEC-2001;  
Aeomica, Inc. (US)  
FEATURES  
source Location/Qualifiers  
1..17  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"  
Query Match 0.8%; Score 13.8; DB 1; Length 17;  
Best Local Similarity 88.2%; Pred. No. 1.3e+02;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 93 GGAGTGGGCGAGTCCT 109  
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Db 17 GGAGTGGGCGAGTCCT 1  
RESULT 208  
CO624948/c  
LOCUS 17 bp DNA linear PAT 02-FEB-2004  
DEFINITION Sequence 9688 from Patent WO0192524.  
ACCESSION CO624948  
VERSION CO624948.1 GI:41675166  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE  
AUTHORS Gu,Y., Ji,Y., Penn,S.G., Hanzel,D.K., Rank,D.R., Chen,W. and  
Shannon,M.E.  
TITLE Myosin-like gene expressed in human heart and muscle  
JOURNAL Patent: WO 0192524-A 9688 06-DEC-2001;  
Aeomica, Inc. (US)  
FEATURES  
source Location/Qualifiers  
1..17  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"  
Query Match 0.8%; Score 13.8; DB 1; Length 17;  
Best Local Similarity 88.2%; Pred. No. 1.3e+02;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 92 GGAGTGGGCGAGTCCT 108  
|||||  
Db 17 GGAGTGGGCGAGTCCT 1  
RESULT 209  
CO624949/c  
LOCUS 17 bp DNA linear PAT 02-FEB-2004  
DEFINITION Sequence 9689 from Patent WO0192524.  
ACCESSION CO624949  
VERSION CO624949.1 GI:41675167  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE  
AUTHORS Gu,Y., Ji,Y., Penn,S.G., Hanzel,D.K., Rank,D.R., Chen,W. and  
Shannon,M.E.  
TITLE Myosin-like gene expressed in human heart and muscle  
JOURNAL Patent: WO 0192524-A 9689 06-DEC-2001;

FEATURES  
source Location/Qualifiers  
1..17  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"  
Query Match 0.8%; Score 13.8; DB 1; Length 17;  
Best Local Similarity 88.2%; Pred. No. 1.3e+02;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 91 GGAGAGTGGGCGAGTC 107  
|||||  
Db 17 GGGAGAGTGGGCGAGTC 1  
RESULT 210  
E65210/c  
LOCUS 17 bp DNA linear PAT 18-JUN-2001  
DEFINITION Method for analyzing oligonucleotide.  
ACCESSION E65210  
VERSION E65210.1 GI:13025986  
KEYWORDS JP 1999046800-A/4.  
SOURCE synthetic construct  
ORGANISM other sequences; artificial sequences.  
REFERENCE  
AUTHORS Leroy,E.H., Michael,W.H., Lloyd,M.S. and Tim,J.H.  
TITLE Method for analyzing oligonucleotide  
JOURNAL Patent: JP 1999046800-A 4 23-FEB-1999;  
CALIFORNIA INSTITUTE OF TECHNOLOGY  
COMMENT OS Artificial Sequence  
PN JP 1999046800-A/4  
PD 23-FEB-1999  
PF 12-FEB-1998 JP 1998030272  
PI 16-JAN-1984 US 570973  
PC C12Q1/68, G01N21/76, G01N27/447, G01N33/50, G01N33/58//C12N15/09  
CC Leroy,E.H., Michael,W.H., Lloyd,M.S. and Tim,J.H.  
FH Key Location/Qualifiers  
FT source 1..17  
/organism="Artificial Sequence".  
FEATURES  
source Location/Qualifiers  
1..17  
/organism="synthetic construct"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:32630"  
Query Match 0.8%; Score 13.8; DB 1; Length 17;  
Best Local Similarity 88.2%; Pred. No. 1.3e+02;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 1357 AAGCGCTGCAGGATAC 1373  
|||||  
Db 17 ATGCTCTGCAGGATAC 1  
RESULT 211  
AR192271  
LOCUS 17 bp DNA linear PAT 20-APR-2002  
DEFINITION Sequence 7759 from patent US 6346398.  
ACCESSION AR192271  
VERSION AR192271.1 GI:20238236  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE  
AUTHORS Pavco,P., McSwiggen,J., Stinchcomb,D. and Escobedo,J.  
TITLE Method and reagent for the treatment of diseases or conditions  
related to levels of vascular endothelial growth factor receptor  
JOURNAL Patent: US 6346398-A 7759 12-FEB-2002;  
FEATURES  
source Location/Qualifiers



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source 1. .17
/organism="unknown"
/mol_type="unassigned DNA"

Query Match
Best Local Similarity 0.8%; Score 13.8; DB 1; Length 17;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1112 CTCCTCTTCTGTCGAGC 1128
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Db 1 CTCCTCTTCTGTCGAGC 17

RESULT 212
AR196222/c
LOCUS AR196222 17 bp DNA linear PAT 20-APR-2002
DEFINITION Sequence 687 from patent US 6350934.
ACCESSION AR196222
VERSION AR196222.1 GI:20245659
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS Zwick,M.G., Edington,B.E., McSwiggen,J.A., Merlo,P.Ann.Owens.,
TITLE Nucleic acid encoding delta-9 desaturase
JOURNAL Patent: US 6350934-A 687 26-FEB-2002;
FEATURES
source 1. .17
/organism="unknown"
/mol_type="unassigned DNA"

Query Match
Best Local Similarity 0.8%; Score 13.8; DB 1; Length 17;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1213 TGGCTTCCCACTTCT 1229
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Db 17 TGGCTGCAACTTCT 1

RESULT 213
AR213316
LOCUS AR213316 17 bp DNA linear PAT 25-SEP-2002
DEFINITION Sequence 25 from patent US 6403552.
ACCESSION AR213316
VERSION AR213316.1 GI:23310499
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS Tartaglia,L.A., Tepper,R.I., Culpepper,J.A. and White,D.W.
TITLE Ob receptor and methods for the diagnosis and treatment of body
weight disorders
JOURNAL Patent: US 6403552-A 25 11-JUN-2002;
FEATURES
source 1. .17
/organism="unknown"
/mol_type="genomic DNA"

Query Match
Best Local Similarity 0.8%; Score 13.8; DB 1; Length 17;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 660 CACTACTGCGCTTCAG 676
|||||
Db 1 CACTATTGCGCTTCAG 17

RESULT 214
AR213318
LOCUS AR213318 17 bp DNA linear PAT 20-DEC-2002
DEFINITION Sequence 27 from patent US 6482927.
ACCESSION AR213318
VERSION AR213318.1 GI:27305557
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS Tartaglia,L.A., Tepper,R.I., Culpepper,J.A. and White,D.W.
TITLE Chimeric proteins comprising the extracellular domain of murine Ob
receptor
JOURNAL Patent: US 6482927-A 27 19-NOV-2002;
FEATURES
source 1. .17
/organism="genomic DNA"

LOCUS AR213318 17 bp DNA linear PAT 25-SEP-2002
DEFINITION Sequence 27 from patent US 6403552.
ACCESSION AR213318
VERSION AR213318.1 GI:23310501
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS Tartaglia,L.A., Tepper,R.I., Culpepper,J.A. and White,D.W.
TITLE Ob receptor and methods for the diagnosis and treatment of body
weight disorders
JOURNAL Patent: US 6403552-A 27 11-JUN-2002;
FEATURES
source 1. .17
/organism="unknown"
/mol_type="genomic DNA"

Query Match
Best Local Similarity 0.8%; Score 13.8; DB 1; Length 17;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 660 CACTACTGCGCTTCAG 676
|||||
Db 1 CACTATTGCGCTTCAG 17

RESULT 215
AR256153
LOCUS AR256153 17 bp DNA linear PAT 20-DEC-2002
DEFINITION Sequence 25 from patent US 6482927.
ACCESSION AR256153
VERSION AR256153.1 GI:27305555
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS Tartaglia,L.A., Tepper,R.I., Culpepper,J.A. and White,D.W.
TITLE Chimeric proteins comprising the extracellular domain of murine Ob
receptor
JOURNAL Patent: US 6482927-A 25 19-NOV-2002;
FEATURES
source 1. .17
/organism="unknown"
/mol_type="genomic DNA"

Query Match
Best Local Similarity 0.8%; Score 13.8; DB 1; Length 17;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 660 CACTACTGCGCTTCAG 676
|||||
Db 1 CACTATTGCGCTTCAG 17

RESULT 216
AR256155
LOCUS AR256155 17 bp DNA linear PAT 20-DEC-2002
DEFINITION Sequence 27 from patent US 6482927.
ACCESSION AR256155
VERSION AR256155.1 GI:27305557
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS Tartaglia,L.A., Tepper,R.I., Culpepper,J.A. and White,D.W.
TITLE Chimeric proteins comprising the extracellular domain of murine Ob
receptor
JOURNAL Patent: US 6482927-A 27 19-NOV-2002;
FEATURES
source 1. .17
/organism="genomic DNA"

Query Match
Best Local Similarity 0.8%; Score 13.8; DB 1; Length 17;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 660 CACTACTGCGCTTCAG 676
|||||
Db 1 CACTATTGCGCTTCAG 17
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/organism="unknown"
/mol_type="genomic DNA"

Query Match
Best Local Similarity 0.8%; Score 13.8; DB 1; Length 17;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 660 CACTACCTGCCCTTCAG 676
||||| |||||||
Db 1 CACTATTGGCCCTTCAG 17

RESULT 217
AR275110 17 bp DNA linear PAT 10-APR-2003
LOCUS
DEFINITION Sequence 25 from patent US 6506877.
ACCESSION AR275110
VERSION AR275110.1 GI:29708051
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 17)
AUTHORS Tartaglia,L.A., Tepper,R.I. and Culpepper,J.A.
TITLE Ob receptor
JOURNAL Patent: US 6506877-A 25 14-JAN-2003;
FEATURES
source
/organism="unknown"
/mol_type="genomic DNA"

Query Match
Best Local Similarity 0.8%; Score 13.8; DB 1; Length 17;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 660 CACTACCTGCCCTTCAG 676
||||| |||||||
Db 1 CACTATTGGCCCTTCAG 17

RESULT 218
AR275112 17 bp DNA linear PAT 10-APR-2003
LOCUS
DEFINITION Sequence 27 from patent US 6506877.
ACCESSION AR275112
VERSION AR275112.1 GI:29708053
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 17)
AUTHORS Tartaglia,L.A., Tepper,R.I. and Culpepper,J.A.
TITLE Ob receptor
JOURNAL Patent: US 6506877-A 27 14-JAN-2003;
FEATURES
source
/organism="unknown"
/mol_type="genomic DNA"

Query Match
Best Local Similarity 0.8%; Score 13.8; DB 1; Length 17;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 660 CACTACCTGCCCTTCAG 676
||||| |||||||
Db 1 CACTATTGGCCCTTCAG 17

RESULT 219
AR306243 17 bp DNA linear PAT 12-JUN-2003
LOCUS
DEFINITION Sequence 25 from patent US 6548269.
ACCESSION AR306243
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VERSION AR306243.1 GI:31695966
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 17)
AUTHORS Tartaglia,L.A., Tepper,R.I. and Culpepper,J.A.
TITLE Ob receptor and methods for the diagnosis and treatment of body
weight disorders, including obesity and cachexia
JOURNAL Patent: US 6548269-A 25 15-APR-2003;
FEATURES
source
/organism="unknown"
/mol_type="genomic DNA"

Query Match
Best Local Similarity 0.8%; Score 13.8; DB 1; Length 17;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 660 CACTACCTGCCCTTCAG 676
||||| |||||||
Db 1 CACTATTGGCCCTTCAG 17

RESULT 220
AR306245 17 bp DNA linear PAT 12-JUN-2003
LOCUS
DEFINITION Sequence 27 from patent US 6548269.
ACCESSION AR306245
VERSION AR306245.1 GI:31695968
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 17)
AUTHORS Tartaglia,L.A., Tepper,R.I. and Culpepper,J.A.
TITLE Ob receptor and methods for the diagnosis and treatment of body
weight disorders, including obesity and cachexia
JOURNAL Patent: US 6548269-A 27 15-APR-2003;
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source
/organism="unknown"
/mol_type="genomic DNA"

Query Match
Best Local Similarity 0.8%; Score 13.8; DB 1; Length 17;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 660 CACTACCTGCCCTTCAG 676
||||| |||||||
Db 1 CACTATTGGCCCTTCAG 17

RESULT 221
AR326141 17 bp RNA linear PAT 17-AUG-2003
LOCUS
DEFINITION Sequence 3543 from patent US 6566127.
ACCESSION AR326141
VERSION AR326141.1 GI:33711949
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 17)
AUTHORS Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.
TITLE Method and reagent for the treatment of diseases or conditions
related to levels of vascular endothelial growth factor receptor
JOURNAL Patent: US 6566127-A 3543 20-MAY-2003;
FEATURES
source
/organism="unknown"
/mol_type="unassigned RNA"
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Query Match      0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.3e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1112 CTCCTCGCTGCTGAGC 1128
Db 1 CTCCTCGCTGCTGAGC 17

RESULT 222
AR326780
LOCUS AR326780 17 bp RNA linear PAT 17-AUG-2003
DEFINITION Sequence 4182 from patent US 6566127.
ACCESSION AR326780
VERSION AR326780.1 GI:33712588
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Pavco, P., McSwiggen, J.A., Stinchcomb, D.T. and Escobedo, J.
TITLE Method and reagent for the treatment of diseases or conditions
related to levels of vascular endothelial growth factor receptor
JOURNAL Patent: US 6566127-A 4182 20-MAY-2003;
FEATURES
source Location/Qualifiers
1..17
/mol_type="unassigned RNA"

Query Match      0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.3e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1115 CTCCTGCTGCTGAGCAGC 1131
Db 1 CTCCTGCTGCTGAGCCGC 17

RESULT 223
AR371631
LOCUS AR371631 17 bp DNA linear PAT 12-SEP-2003
DEFINITION Sequence 25 from patent US 6395498.
ACCESSION AR371631
VERSION AR371631.1 GI:34608616
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Tartaglia, L.A., Tepper, R.I., Culppepper, J.A. and White, D.W.
TITLE Methods of identifying compounds that modulate body weight using
the OB receptor
JOURNAL Patent: US 6395498-A 25 28-MAY-2002;
FEATURES
source Location/Qualifiers
1..17
/mol_type="genomic DNA"

Query Match      0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.3e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 660 CACTACTGCGCCTTCAG 676
Db 1 CACTATTGCGCCTTCAG 17

RESULT 224
AR371633
LOCUS AR371633 17 bp DNA linear PAT 12-SEP-2003
DEFINITION Sequence 27 from patent US 6395498.
ACCESSION AR371633
VERSION AR371633.1 GI:34608618

Query Match      0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.3e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 660 CACTACTGCGCCTTCAG 676
Db 1 CACTATTGCGCCTTCAG 17

Query Match      0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.3e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 93 GAGAGTGGCGCAGTCTCT 109
Db 17 GAGAGAGCGCCAGTCTCT 1

RESULT 226
AR458966/c
LOCUS AR458966 17 bp DNA linear PAT 20-FEB-2004
DEFINITION Sequence 2643 from patent US 6686188.
ACCESSION AR458966
VERSION AR458966.1 GI:42694023
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Gu, Y., Ji, Y., Penn, S.G., Hanzel, D.K., Rank, D.R., Chen, W. and
Shannon, M.E.
TITLE Polynucleotide encoding a human myosin-like polypeptide expressed
predominantly in heart and muscle
JOURNAL Patent: US 6686188-A 2643 03-FEB-2004;
FEATURES
source Location/Qualifiers
1..17
/mol_type="genomic DNA"
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RESULT	LOCUS	bp	DNA	linear	PAT	JOURNAL	TITLE
229	AR464891	17	DNA	linear	PAT 20-FEB-2004		
	AR464891						Polynucleotide encoding a human myosin-like polypeptide expressed predominantly in heart and muscle
							Shannon; et al.
							Patent: US 6696188-A 8661 03-FEB-2004;

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FEATURES
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Query Match      0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.3e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 268 TAGAAGAGCCAGAG 284
Db 1 TCGAGGAGCCAGAG 17

RESULT 232
AR464986
LOCUS      17 bp DNA linear PAT 20-FEB-2004
DEFINITION Sequence 8663 from patent US 6686188.
ACCESSION AR464986
VERSION AR464986.1 GI:42700043
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS Gu, Y., Ji, Y., Penn, S.G., Hanzel, D.K., Rank, D.R., Chen, W. and Shannon, M.E.
TITLE Polynucleotide encoding a human myosin-like polypeptide expressed predominantly in heart and muscle
JOURNAL Patent: US 6686188-A 9687 03-FEB-2004;
FEATURES Location/Qualifiers
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Query Match      0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.3e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 93 GAGAGTGGCGAGGTCTCT 109
Db 17 GAGAGTGGCGAGGTCTCT 1

RESULT 235
AR466011/c
LOCUS      17 bp DNA linear PAT 20-FEB-2004
DEFINITION Sequence 9688 from patent US 6686188.
ACCESSION AR466011
VERSION AR466011.1 GI:42701068
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS Gu, Y., Ji, Y., Penn, S.G., Hanzel, D.K., Rank, D.R., Chen, W. and Shannon, M.E.
TITLE Polynucleotide encoding a human myosin-like polypeptide expressed predominantly in heart and muscle
JOURNAL Patent: US 6686188-A 9688 03-FEB-2004;
FEATURES Location/Qualifiers
  source      1..17
    /organism="unknown"
    /mol_type="genomic DNA"

Query Match      0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.3e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 92 GGAGAGTGGCGAGGTCTC 108
Db 17 GGAGAGTGGCGAGGTCTC 1

RESULT 236
AR466012/c
LOCUS      17 bp DNA linear PAT 20-FEB-2004
DEFINITION Sequence 9689 from patent US 6686188.
ACCESSION AR466012
VERSION AR466012.1 GI:42701069
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS Gu, Y., Ji, Y., Penn, S.G., Hanzel, D.K., Rank, D.R., Chen, W. and Shannon, M.E.

FEATURES
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Query Match      0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.3e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 270 GAGGAGCCAGAGAG 286
Db 1 GAGGAGCCAGAGAG 17

RESULT 233
AR464987
LOCUS      17 bp DNA linear PAT 20-FEB-2004
DEFINITION Sequence 8664 from patent US 6686188.
ACCESSION AR464987
VERSION AR464987.1 GI:42700044
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS Gu, Y., Ji, Y., Penn, S.G., Hanzel, D.K., Rank, D.R., Chen, W. and Shannon, M.E.
TITLE Polynucleotide encoding a human myosin-like polypeptide expressed predominantly in heart and muscle
JOURNAL Patent: US 6686188-A 8664 03-FEB-2004;
FEATURES Location/Qualifiers
  source      1..17
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    /mol_type="genomic DNA"

Query Match      0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.3e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 271 AAGAAGCCAGAGAG 287
Db 1 AGGAAGCCAGAGAG 17
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Shannon, M.S.
Polynucleotide encoding a human myosin-like polypeptide expressed
predominantly in heart and muscle
JOURNAL Patent: US 6686188-A 9689 03-FEB-2004;
FEATURES Location/Qualifiers
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            /mol_type="genomic DNA"

Query Match      0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.3e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 91 GGGAGAGTGGCAGGTC 107
Db 17 GGGAGAGTGGCAGGTC 1

RESULT 237
AX215611/c
LOCUS AX215611 17 bp RNA linear PAT 07-SEP-2001
DEFINITION Sequence 1053 from Patent WO0159103.
ACCESSION AX215611
VERSION AX215611.1 GI:15525654
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1
AUTHORS Blatt, L., McSwiggen, J. and Chowrira, B.M.
TITLE Method and reagent for the modulation and diagnosis of cd20 and
JOURNAL nogo gene expression
PATENT: WO 0159103-A 1053 16-AUG-2001;
RIBOZYME PHARMACEUTICALS, INC. (US) ; Blatt, Lawrence (US) ;
McSwiggen, James (US) ; Chowrira, Bharat M. (US)
FEATURES Location/Qualifiers
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            /mol_type="unassigned RNA"
            /db_xref="taxon:32630"
            /note="Nucleic Acid"

Query Match      0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.3e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1622 AATAAACTGCTTTGTG 1638
Db 17 AATAAACTGCTTTGTG 1

RESULT 238
AX216443/c
LOCUS AX216443 17 bp RNA linear PAT 07-SEP-2001
DEFINITION Sequence 1895 from Patent WO0159103.
ACCESSION AX216443
VERSION AX216443.1 GI:15526504
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1
AUTHORS Blatt, L., McSwiggen, J. and Chowrira, B.M.
TITLE Method and reagent for the modulation and diagnosis of cd20 and
JOURNAL nogo gene expression
PATENT: WO 0159103-A 1895 16-AUG-2001;
RIBOZYME PHARMACEUTICALS, INC. (US) ; Blatt, Lawrence (US) ;
McSwiggen, James (US) ; Chowrira, Bharat M. (US)
FEATURES Location/Qualifiers
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            /mol_type="unassigned RNA"
            /db_xref="taxon:32630"

Shannon, M.S.
Polynucleotide encoding a human myosin-like polypeptide expressed
predominantly in heart and muscle
JOURNAL Patent: US 6686188-A 9689 03-FEB-2004;
FEATURES Location/Qualifiers
    source
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            /mol_type="genomic DNA"

Query Match      0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.3e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1621 CAATAAACTGCTTTGT 1637
Db 17 CATTAATACTGCTTTT 1

RESULT 239
AX272871/c
LOCUS AX272871 17 bp RNA linear PAT 29-OCT-2001
DEFINITION Sequence 440 from Patent WO0162911.
ACCESSION AX272871
VERSION AX272871.1 GI:16545608
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Jarvis, T., von Carlowitz, I., McSwiggen, J.A., Hamblin, P.A. and
TITLE Method and reagent for the inhibition of grid
JOURNAL Patent: WO 0162911-A 440 30-AUG-2001;
RIBOZYME PHARMACEUTICALS, INC. (US) ; GLAXO GROUP LIMITED (GB)
FEATURES Location/Qualifiers
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            /mol_type="unassigned RNA"
            /db_xref="taxon:9606"

Query Match      0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.3e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1539 CTCCCCGCTCTGGATCC 1555
Db 17 CTCCCCGCTGTGAACC 1

RESULT 240
AX422540
LOCUS AX422540 17 bp RNA linear PAT 18-JUN-2002
DEFINITION Sequence 876 from Patent WO0188124.
ACCESSION AX422540
VERSION AX422540.1 GI:21525922
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Jarvis, T., von Carlowitz, I., McSwiggen, J.A., McLaughlin, F.G. and
TITLE Method and reagent for the inhibition of erg
JOURNAL Patent: WO 0188124-A 876 22-NOV-2001;
RIBOZYME PHARMACEUTICALS, INC. (US) ; GLAXO GROUP LIMITED (GB)
FEATURES Location/Qualifiers
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            /mol_type="unassigned RNA"
            /db_xref="taxon:9606"

Query Match      0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.3e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1504 GCCCCAGCCTCCAGGCC 1520
Db 1 GCCCCACCTCCAGGCC 17
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RESULT 241
AX423446
LOCUS AX423446 17 bp RNA linear PAT 18-JUN-2002
DEFINITION Sequence 1782 from Patent WO0180124.
ACCESSION AX423446
VERSION AX423446.1 GI:21526828
FEATURES
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1
AUTHORS Jarvis, T., von Carlwitz, I., Mcswiggen, J.A., McLaughlin, F.G. and
Randi, A.M.
TITLE Method and reagent for the inhibition of erg
JOURNAL Patent: WO 0180124-A 1782 22-NOV-2001;
RIBOSYME PHARMACEUTICALS, INC. (US); GLAXO GROUP LIMITED (GB)
FEATURES
source
1. .17
/organism="Homo sapiens"
/mol_type="unassigned RNA"
/db_xref="taxon:9606"
Query Match 0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.3e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 218 GACTCTCATGAAAAA 234
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DB 1 GACTCAGAGAAAAA 17
||||| ||||| |||||
RESULT 242
AX475287
LOCUS AX475287 17 bp DNA linear PAT 12-AUG-2002
DEFINITION Sequence 508 from Patent WO0224750.
ACCESSION AX475287
VERSION AX475287.1 GI:22214572
FEATURES
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1
AUTHORS Zhang, J.
TITLE Human kidney tumor overexpressed membrane protein 1
JOURNAL Patent: WO 0224750-A 508 28-MAR-2002;
Aeomica, Inc. (US)
FEATURES
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1. .17
/organism="Homo sapiens"
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Best Local Similarity 88.2%; Pred. No. 1.3e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 520 GCATCGACTCCCTGCTG 536
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DB 1 GCATCTACTCCAGCTG 17
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RESULT 243
AX475288
LOCUS AX475288 17 bp DNA linear PAT 12-AUG-2002
DEFINITION Sequence 509 from Patent WO0224750.
ACCESSION AX475288
VERSION AX475288.1 GI:22214573
FEATURES
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1
AUTHORS Zhang, J.
TITLE Human kidney tumor overexpressed membrane protein 1
JOURNAL Patent: WO 0224750-A 511 28-MAR-2002;
Aeomica, Inc. (US)
FEATURES
source
1. .17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
Query Match 0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.3e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 522 ATCGACTCCCTGCTGGA 538
||||| ||||| |||||
DB 1 ATCTACTCCAGCTGGA 17
||||| ||||| |||||
RESULT 245
AX475290
LOCUS AX475290 17 bp DNA linear PAT 12-AUG-2002
DEFINITION Sequence 511 from Patent WO0224750.
ACCESSION AX475290
VERSION AX475290.1 GI:22214575
FEATURES
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1
AUTHORS Zhang, J.
TITLE Human kidney tumor overexpressed membrane protein 1
JOURNAL Patent: WO 0224750-A 511 28-MAR-2002;
Aeomica, Inc. (US)
FEATURES
source
1. .17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
Query Match 0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.3e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 522 ATCGACTCCCTGCTGGA 538
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DB 1 ATCTACTCCAGCTGGA 17
||||| ||||| |||||
RESULT 247
AX475292
LOCUS AX475292 17 bp DNA linear PAT 12-AUG-2002
DEFINITION Sequence 513 from Patent WO0224750.
ACCESSION AX475292
VERSION AX475292.1 GI:22214577
FEATURES
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1
AUTHORS Zhang, J.
TITLE Human kidney tumor overexpressed membrane protein 1
JOURNAL Patent: WO 0224750-A 513 28-MAR-2002;
Aeomica, Inc. (US)
FEATURES
source
1. .17
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"
Query Match 0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.3e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 524 ATCGACTCCCTGCTGGA 540
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DB 1 ATCTACTCCAGCTGGA 17
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Query Match      0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.3e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 523 TCGACTCCCTGCTGGAG 539
      |||||||
Db 1 TCTACTCCAGCTGGAG 17

RESULT 246
AX475291
LOCUS      17 bp DNA linear PAT 12-AUG-2002
DEFINITION Sequence 512 from Patent WO0224750.
ACCESSION AX475291
VERSION AX475291.1 GI:22214576
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Zhang, J.
TITLE Human kidney tumor overexpressed membrane protein 1
JOURNAL Patent: WO 0224750-A 512 28-MAR-2002;
          Aeomica, Inc. (US)
FEATURES
source      Location/Qualifiers
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            /mol_type="unassigned DNA"
            /db_xref="taxon:9606"

Query Match      0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.3e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 524 CGACTCCCTGCTGGAGA 540
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Db 1 CTACTCCAGCTGGAGA 17

RESULT 247
AX475293
LOCUS      17 bp DNA linear PAT 12-AUG-2002
DEFINITION Sequence 514 from Patent WO0224750.
ACCESSION AX475293
VERSION AX475293.1 GI:22214578
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Zhang, J.
TITLE Human kidney tumor overexpressed membrane protein 1
JOURNAL Patent: WO 0224750-A 514 28-MAR-2002;
          Aeomica, Inc. (US)
FEATURES
source      Location/Qualifiers
            1..17
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            /mol_type="unassigned DNA"
            /db_xref="taxon:9606"

Query Match      0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.3e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 526 ACTCCCTGCTGGAGAAC 542
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Db 1 ACTCCGAGCTGGAGACC 17

/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match      0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.3e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 523 TCGACTCCCTGCTGGAG 539
      |||||||
Db 1 TCTACTCCAGCTGGAG 17

RESULT 248
AX475720
LOCUS      17 bp DNA linear PAT 12-AUG-2002
DEFINITION Sequence 941 from Patent WO0224750.
ACCESSION AX475720
VERSION AX475720.1 GI:22215005
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Zhang, J.
TITLE Human kidney tumor overexpressed membrane protein 1
JOURNAL Patent: WO 0224750-A 941 28-MAR-2002;
          Aeomica, Inc. (US)
FEATURES
source      Location/Qualifiers
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            /mol_type="unassigned DNA"
            /db_xref="taxon:9606"

Query Match      0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.3e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1203 GTCACACAGGTGGCTTC 1219
      |||||||
Db 1 GTCACCACTGTGGCTGC 17

RESULT 249
AX499441
LOCUS      17 bp DNA linear PAT 27-SEP-2002
DEFINITION Sequence 748 from Patent EP1229046.
ACCESSION AX499441
VERSION AX499441.1 GI:23381734
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Zhan, J.
TITLE Human testis expressed patched like protein
JOURNAL Patent: EP 1229046-A 748 07-AUG-2002;
          Aeomica, Inc. (US)
FEATURES
source      Location/Qualifiers
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Query Match      0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.3e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 521 CATCGACTCCCTGCTGG 537
      |||||||
Db 1 CAGCGACTCACTGCTGG 17

RESULT 250
AX499442
LOCUS      17 bp DNA linear PAT 27-SEP-2002
DEFINITION Sequence 749 from Patent EP1229046.
ACCESSION AX499442
VERSION AX499442.1 GI:23381735
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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AUTHORS Telerman,A., Anson,R. and Tuijnder,M.  
TITLE Sequences involved in tumoral suppression, tumoral reversion, apoptosis and/or viral resistance phenomena and their use as medicines  
JOURNAL Patent: WO 03040369-A 50 15-MAY-2003;  
Molecular Engines Laboratories (FR)  
FEATURES  
source 1. .17  
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/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"  
Query Match 0.8%; Score 13.8; DB 1; Length 17;  
Best Local Similarity 88.2%; Pred. No. 1.3e+02;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 91 GCGAGAGCTGGCAGGTC 107  
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Db 17 GCGAGGTTGGCAGATC 1  
RESULT 260  
I61606  
LOCUS I61606 15 bp DNA linear PAT 07-OCT-1997  
DEFINITION Sequence 160 from patent US 5658780.  
ACCESSION I61606  
VERSION I61606.1 GI:2479554  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 15)  
AUTHORS Stinchcomb,D.T., Draper,K.G. and McSwiggen,J.  
TITLE Rel a targeted ribozymes  
JOURNAL Patent: US 5658780-A 160 19-AUG-1997;  
FEATURES  
source 1. .15  
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/mol\_type="unassigned DNA"  
Query Match 0.8%; Score 13.4; DB 1; Length 15;  
Best Local Similarity 93.3%; Pred. No. 1e+02;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1507 CCAGCTCCAGGCC 1521  
|||||  
Db 1 CCAGCTCCAGGTC 15  
RESULT 261  
AR180106/c  
LOCUS AR180106 15 bp DNA linear PAT 20-APR-2002  
DEFINITION Sequence 174 from patent US 6333152.  
ACCESSION AR180106  
VERSION AR180106.1 GI:20222139  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 15)  
AUTHORS Vogelstein,B., Kinzler,K.W., Zhang,L. and Zhou,W.  
TITLE Gene expression profiles in normal and cancer cells  
JOURNAL Patent: US 6333152-A 174 25-DEC-2001;  
FEATURES  
source 1. .15  
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/mol\_type="unassigned DNA"  
Query Match 0.8%; Score 13.4; DB 1; Length 15;  
Best Local Similarity 93.3%; Pred. No. 1e+02;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 807 GCTCAGCAGGCCATG 821

Db 15 GCCCAGCAGGCCATG 1  
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RESULT 262  
AR180715/c  
LOCUS AR180715 15 bp DNA linear PAT 20-APR-2002  
DEFINITION Sequence 783 from patent US 6333152.  
ACCESSION AR180715  
VERSION AR180715.1 GI:20222748  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 15)  
AUTHORS Vogelstein,B., Kinzler,K.W., Zhang,L. and Zhou,W.  
TITLE Gene expression profiles in normal and cancer cells  
JOURNAL Patent: US 6333152-A 783 25-DEC-2001;  
FEATURES  
source 1. .15  
/organism="unknown"  
/mol\_type="unassigned DNA"  
Query Match 0.8%; Score 13.4; DB 1; Length 15;  
Best Local Similarity 93.3%; Pred. No. 1e+02;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 807 GCTCAGCAGGCCATG 821  
|||||  
Db 15 GCCCAGCAGGCCATG 1  
RESULT 263  
AR532147/c  
LOCUS AR532147 15 bp DNA linear PAT 08-OCT-2004  
DEFINITION Sequence 75 from patent US 6727085.  
ACCESSION AR532147  
VERSION AR532147.1 GI:53920820  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 15)  
AUTHORS Fano,T.S. and Mikkelsen,F.  
TITLE Subtilase variants having an improved wash performance on egg stains  
JOURNAL Patent: US 6727085-A 75 27-APR-2004;  
FEATURES  
source 1. .15  
/organism="unknown"  
/mol\_type="genomic DNA"  
Query Match 0.8%; Score 13.4; DB 1; Length 15;  
Best Local Similarity 93.3%; Pred. No. 1e+02;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1076 GCTGCTAAAGTCCTA 1090  
|||||  
Db 15 GCTGTTAAAGTCCTA 1  
RESULT 264  
AX167089/c  
LOCUS AX167089 15 bp DNA linear PAT 03-JUL-2001  
DEFINITION Sequence 75 from Patent WO0144452.  
ACCESSION AX167089  
VERSION AX167089.1 GI:14596577  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM synthetic construct  
REFERENCE 1  
AUTHORS Fan,T.S. and Mikkelsen,F.F.

TITLE Subtilase variants having an improved wash performance on egg stains  
JOURNAL Patent: WO 0144452-A 75 21-JUN-2001;  
Novozymes A/S (DK)  
FEATURES Location/Qualifiers  
source  
1..15  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="Antisense primer"

Query Match 0.8%; Score 13.4; DB 1; Length 15;  
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Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1076 GCTGCTAAAGTCTTA 1090  
Db 15 GCTGTTAAAGTCTTA 1

RESULT 265  
AX635964  
LOCUS AX635964 15 bp RNA linear PAT 21-FEB-2003  
DEFINITION Sequence 3103 from Patent EP1260586.  
ACCESSION AX635964  
VERSION AX635964.1 GI:28471578  
KEYWORDS  
SOURCE unidentified  
ORGANISM unidentified  
unclassified.

REFERENCE 1  
AUTHORS Stinchcomb,D.T., Dudycz,L.W., Chowrira,B., Grimm,S., Drenzo,A., Karpeisky,A., Draper,K.G., Kisich,K., Matulic-Adamic,J., Mcswiggin,J.A., Modak,A., Pavco,P., Beigelman,L., Sullivan,S.M., Svedler,D., Thompson,J.D., Tracz,D., Usman,N., Wincott,F.E. and Woolf,I.  
TITLE Method and reagent for inhibiting the expression of disease related genes  
JOURNAL Patent: EP 1260586-A 3103 27-NOV-2002;  
RIBOZYME PHARMACEUTICALS, INC. (US)  
FEATURES Location/Qualifiers  
source  
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/organism="unidentified"  
/mol\_type="unassigned RNA"  
/db\_xref="taxon:32644"

Query Match 0.8%; Score 13.4; DB 1; Length 15;  
Best Local Similarity 93.3%; Pred. No. 1e+02; 1; Indels 0; Gaps 0;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1507 CCAGCCTCCAGGCC 1521  
Db 1 CCAGCCTCCAGGCTC 15

RESULT 266  
AR029843/c  
LOCUS AR029843 16 bp DNA linear PAT 29-SEP-1999  
DEFINITION Sequence 32 from patent US 5861244.  
ACCESSION AR029843  
VERSION AR029843.1 GI:5943057  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
unclassified.

REFERENCE 1 (bases 1 to 16)  
AUTHORS Wang,C.-G. and Hepburn,A.G.  
TITLE Genetic assay using DNA triple strand formation  
JOURNAL Patent: US 5861244-A 32 19-JAN-1999;  
FEATURES Location/Qualifiers  
source  
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/organism="unknown"  
/mol\_type="unassigned DNA"

TITLE Subtilase variants having an improved wash performance on egg stains  
JOURNAL Patent: WO 0144452-A 75 21-JUN-2001;  
Novozymes A/S (DK)  
FEATURES Location/Qualifiers  
source  
1..15  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="Antisense primer"

Query Match 0.8%; Score 13.4; DB 1; Length 15;  
Best Local Similarity 93.3%; Pred. No. 1e+02;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1076 GCTGCTAAAGTCTTA 1090  
Db 15 GCTGTTAAAGTCTTA 1

RESULT 265  
AX635964  
LOCUS AX635964 15 bp RNA linear PAT 21-FEB-2003  
DEFINITION Sequence 3103 from Patent EP1260586.  
ACCESSION AX635964  
VERSION AX635964.1 GI:28471578  
KEYWORDS  
SOURCE unidentified  
ORGANISM unidentified  
unclassified.

REFERENCE 1  
AUTHORS Stinchcomb,D.T., Dudycz,L.W., Chowrira,B., Grimm,S., Drenzo,A., Karpeisky,A., Draper,K.G., Kisich,K., Matulic-Adamic,J., Mcswiggin,J.A., Modak,A., Pavco,P., Beigelman,L., Sullivan,S.M., Svedler,D., Thompson,J.D., Tracz,D., Usman,N., Wincott,F.E. and Woolf,I.  
TITLE Method and reagent for inhibiting the expression of disease related genes  
JOURNAL Patent: EP 1260586-A 3103 27-NOV-2002;  
RIBOZYME PHARMACEUTICALS, INC. (US)  
FEATURES Location/Qualifiers  
source  
1..15  
/organism="unidentified"  
/mol\_type="unassigned RNA"  
/db\_xref="taxon:32644"

Query Match 0.8%; Score 13.4; DB 1; Length 15;  
Best Local Similarity 93.3%; Pred. No. 1e+02; 1; Indels 0; Gaps 0;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1507 CCAGCCTCCAGGCC 1521  
Db 1 CCAGCCTCCAGGCTC 15

RESULT 266  
AR029843/c  
LOCUS AR029843 16 bp DNA linear PAT 29-SEP-1999  
DEFINITION Sequence 32 from patent US 5861244.  
ACCESSION AR029843  
VERSION AR029843.1 GI:5943057  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
unclassified.

REFERENCE 1 (bases 1 to 16)  
AUTHORS Wang,C.-G. and Hepburn,A.G.  
TITLE Genetic assay using DNA triple strand formation  
JOURNAL Patent: US 5861244-A 32 19-JAN-1999;  
FEATURES Location/Qualifiers  
source  
1..16  
/organism="unknown"  
/mol\_type="unassigned DNA"

Query Match 0.8%; Score 13.4; DB 1; Length 16;  
Best Local Similarity 93.3%; Pred. No. 1.2e+02;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 271 AAGAAGCCAGCAAGA 285  
Db 15 AAGAAGCAAGAGAGA 1

RESULT 267  
AR131574  
LOCUS AR131574 16 bp DNA linear PAT 16-MAY-2001  
DEFINITION Sequence 67 from patent US 6194149.  
ACCESSION AR131574  
VERSION AR131574.1 GI:14120477  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
unclassified.

REFERENCE 1 (bases 1 to 16)  
AUTHORS Neri,B., Dong,F., Lyamichev,V., Brow,M,Ann.D. and Fors,L.  
TITLE Target-dependent reactions using structure-bridging oligonucleotides  
JOURNAL Patent: US 6194149-A 67 27-FEB-2001;  
FEATURES Location/Qualifiers  
source  
1..16  
/organism="unknown"  
/mol\_type="unassigned DNA"

Query Match 0.8%; Score 13.4; DB 1; Length 16;  
Best Local Similarity 93.3%; Pred. No. 1.2e+02;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1508 CAGCCTCCAGGCC 1522  
Db 2 CAGCCTCCAGGACCC 16

RESULT 268  
AR131575  
LOCUS AR131575 16 bp DNA linear PAT 16-MAY-2001  
DEFINITION Sequence 68 from patent US 6194149.  
ACCESSION AR131575  
VERSION AR131575.1 GI:14120478  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
unclassified.

REFERENCE 1 (bases 1 to 16)  
AUTHORS Neri,B., Dong,F., Lyamichev,V., Brow,M,Ann.D. and Fors,L.  
TITLE Target-dependent reactions using structure-bridging oligonucleotides  
JOURNAL Patent: US 6194149-A 68 27-FEB-2001;  
FEATURES Location/Qualifiers  
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1..16  
/organism="unknown"  
/mol\_type="unassigned DNA"

Query Match 0.8%; Score 13.4; DB 1; Length 16;  
Best Local Similarity 93.3%; Pred. No. 1.2e+02;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1508 CAGCCTCCAGGCC 1522  
Db 2 CAGCCTCCAGGACCC 16

RESULT 269  
CQ796994/c  
LOCUS CQ796994 16 bp DNA linear PAT 19-APR-2004  
DEFINITION Sequence 11 from Patent WO2004027066.  
ACCESSION CQ796994

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VERSION CQ796994.1 GI:46408576
KEYWORDS
SOURCE unidentified
ORGANISM unidentified
unclassified.
REFERENCE 1
AUTHORS Letourneur, O.
TITLE ChimERIC recombinant protein and in vitro diagnosis
JOURNAL Patent: WO 2004027066-A 11 01-APR-2004;
Biomerieux (FR)
FEATURES
source Location/Qualifiers
1..16
/organism="unidentified"
/mol_type="unassigned DNA"
/db_xref="taxon:32644"
/notes="artificial sequence"
Query Match 0.8%; Score 13.4; DB 1; Length 16;
Best Local Similarity 93.3%; Pred. No. 1.2e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 476 CCTGAACCGAGCTC 490
Db 15 CCTGAACCGAGCTC 1
RESULT 270
LOCUS CQ858546/c
DEFINITION Sequence 8 from Patent WO2004069991.
ACCESSION CQ858546
VERSION CQ858546.1 GI:51852513
KEYWORDS Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Hansen, B., Thru, C.A., Petersen, K.D., Westergaard, M. and
Wissenbach, M.
TITLE Oligomeric compounds for the modulation of survivin expression
JOURNAL Patent: WO 2004069991-A 8 19-AUG-2004;
Santaris Pharma A/S (DK)
FEATURES
source Location/Qualifiers
1..16
/organism="Homo sapiens"
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/db_xref="taxon:9606"
Query Match 0.8%; Score 13.4; DB 1; Length 16;
Best Local Similarity 93.3%; Pred. No. 1.2e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 278 CAAGAGAGAGAAAGA 292
Db 16 CAATAGAGAGAAAGA 2
RESULT 271
LOCUS AR199508
DEFINITION Sequence 67 from patent US 6355437.
ACCESSION AR199508
VERSION AR199508.1 GI:20249582
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 16)
AUTHORS Neri, B., Dong, F., Lyamichev, V., Brow, M. Ann. D. and Fors, L.
TITLE Target-dependent reactions using structure-bridging
oligonucleotides
JOURNAL Patent: US 6355437-A 67 12-MAR-2002;
FEATURES
source Location/Qualifiers
1..16
/organism="unassigned DNA"
/mol_type="unassigned DNA"
Query Match 0.8%; Score 13.4; DB 1; Length 16;
Best Local Similarity 93.3%; Pred. No. 1.2e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1508 CAGCCTCCAGGACCC 1522
Db 2 CAGCCTCCAGGACCC 16
RESULT 272
LOCUS AR199509
DEFINITION Sequence 68 from patent US 6355437.
ACCESSION AR199509
VERSION AR199509.1 GI:20249583
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 16)
AUTHORS Neri, B., Dong, F., Lyamichev, V., Brow, M. Ann. D. and Fors, L.
TITLE Target-dependent reactions using structure-bridging
oligonucleotides
JOURNAL Patent: US 6355437-A 68 12-MAR-2002;
FEATURES
source Location/Qualifiers
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/organism="unassigned DNA"
/mol_type="unassigned DNA"
Query Match 0.8%; Score 13.4; DB 1; Length 16;
Best Local Similarity 93.3%; Pred. No. 1.2e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1508 CAGCCTCCAGGACCC 1522
Db 2 CAGCCTCCAGGACCC 16
RESULT 273
LOCUS AR200979
DEFINITION Sequence 67 from patent US 6358691.
ACCESSION AR200979
VERSION AR200979.1 GI:20251867
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 16)
AUTHORS Neri, B., Dong, F., Lyamichev, V., Brow, M. Ann. D. and Fors, L.
TITLE Target-dependent reactions using structure-bridging
oligonucleotides
JOURNAL Patent: US 6358691-A 67 19-MAR-2002;
FEATURES
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Query Match 0.8%; Score 13.4; DB 1; Length 16;
Best Local Similarity 93.3%; Pred. No. 1.2e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1508 CAGCCTCCAGGACCC 1522
Db 2 CAGCCTCCAGGACCC 16
RESULT 274
LOCUS AR200979
DEFINITION Sequence 67 from patent US 6358691.
ACCESSION AR200979
VERSION AR200979.1 GI:20251867
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 16)
AUTHORS Neri, B., Dong, F., Lyamichev, V., Brow, M. Ann. D. and Fors, L.
TITLE Target-dependent reactions using structure-bridging
oligonucleotides
JOURNAL Patent: US 6358691-A 67 19-MAR-2002;
FEATURES
source Location/Qualifiers
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/mol_type="unassigned DNA"
Query Match 0.8%; Score 13.4; DB 1; Length 16;
Best Local Similarity 93.3%; Pred. No. 1.2e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1508 CAGCCTCCAGGACCC 1522
Db 2 CAGCCTCCAGGACCC 16
RESULT 274
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AR200980  
LOCUS AR200980 16 bp DNA linear PAT 20-APR-2002  
DEFINITION Sequence 68 from patent US 6358691.  
ACCESSION AR200980  
VERSION AR200980.1 GI:20251868  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE  
1 (bases 1 to 16)  
Neri,B., Dong,F., Lyamichev,V., Brow,M.Ann.D. and Fors,L.  
Target-dependent reactions using structure-bridging  
oligonucleotides  
JOURNAL Patent: US 6358691-A 68 19-MAR-2002;  
FEATURES  
source  
Location/Qualifiers  
1..16  
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/mol\_type="unassigned DNA"

Query Match 0.8%; Score 13.4; DB 1; Length 16;  
Best Local Similarity 93.3%; Pred. No. 1.2e+02;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1508 CAGCCTCCAGGCC 1522  
|||||  
Db 2 CAGCCTCCAGGACCC 16

RESULT 275  
LOCUS AR488738 16 bp DNA linear PAT 15-MAY-2004  
DEFINITION Sequence 67 from patent US 6709815.  
ACCESSION AR488738  
VERSION AR488738.1 GI:47254936  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE  
1 (bases 1 to 16)  
Dong,F., Lyamichev,V.I., Prudent,J.R., Fors,L., Neri,B.P.,  
Brow,M.A.D., Anderson,T.A. and Dahlberg,J.E.  
Target-dependent reactions using structure-bridging  
oligonucleotides  
JOURNAL Patent: US 6709815-A 67 23-MAR-2004;  
FEATURES  
source  
Location/Qualifiers  
1..16  
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/mol\_type="genomic DNA"

Query Match 0.8%; Score 13.4; DB 1; Length 16;  
Best Local Similarity 93.3%; Pred. No. 1.2e+02;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1508 CAGCCTCCAGGCC 1522  
|||||  
Db 2 CAGCCTCCAGGACCC 16

RESULT 276  
LOCUS AR488739 16 bp DNA linear PAT 15-MAY-2004  
DEFINITION Sequence 68 from patent US 6709815.  
ACCESSION AR488739  
VERSION AR488739.1 GI:47254937  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE  
1 (bases 1 to 16)  
Dong,F., Lyamichev,V.I., Prudent,J.R., Fors,L., Neri,B.P.,  
Brow,M.A.D., Anderson,T.A. and Dahlberg,J.E.  
Target-dependent reactions using structure-bridging  
oligonucleotides

JOURNAL Patent: US 6709815-A 68 23-MAR-2004;  
FEATURES  
source  
Location/Qualifiers  
1..16  
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/mol\_type="genomic DNA"

Query Match 0.8%; Score 13.4; DB 1; Length 16;  
Best Local Similarity 93.3%; Pred. No. 1.2e+02;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1508 CAGCCTCCAGGCC 1522  
|||||  
Db 2 CAGCCTCCAGGACCC 16

RESULT 277  
LOCUS AX419730 16 bp DNA linear PAT 18-JUN-2002  
DEFINITION Sequence 67 from Patent WO0198537.  
ACCESSION AX419730  
VERSION AX419730.1 GI:21524097  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM synthetic construct  
other sequences; artificial sequences.  
REFERENCE  
1  
Lyamichev,V., Allawi,H., Dong,F., Neri,B.P. and Vener,I.T.  
Nucleic acid accessible hybridization sites  
Patent: WO 0198537-A 67 27-DEC-2001;  
JOURNAL THIRD WAVE TECHNOLOGIES, INC. (US)  
FEATURES  
source  
Location/Qualifiers  
1..16  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"

Query Match 0.8%; Score 13.4; DB 1; Length 16;  
Best Local Similarity 93.3%; Pred. No. 1.2e+02;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1508 CAGCCTCCAGGCC 1522  
|||||  
Db 2 CAGCCTCCAGGACCC 16

RESULT 278  
LOCUS AX419731 16 bp DNA linear PAT 18-JUN-2002  
DEFINITION Sequence 68 from Patent WO0198537.  
ACCESSION AX419731  
VERSION AX419731.1 GI:21524098  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM synthetic construct  
other sequences; artificial sequences.  
REFERENCE  
1  
Lyamichev,V., Allawi,H., Dong,F., Neri,B.P. and Vener,I.T.  
Nucleic acid accessible hybridization sites  
Patent: WO 0198537-A 68 27-DEC-2001;  
JOURNAL THIRD WAVE TECHNOLOGIES, INC. (US)  
FEATURES  
source  
Location/Qualifiers  
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/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"

Query Match 0.8%; Score 13.4; DB 1; Length 16;  
Best Local Similarity 93.3%; Pred. No. 1.2e+02;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1508 CAGCCTCCAGGCC 1522  
|||||  
Db 2 CAGCCTCCAGGACCC 16

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PR 05-MAY-1997 US 08/851588,19-SEP-1997 US 08/934097 PR
03-MAR-1998 US 09/034205
PI FANG DONG,VICTOR I LYANICHEV,JAMES R PRUDENT,LANCE FORS,BRUCE
PI P NERI,
PI MARY ANN D BROW,TODD A ANDERSON,JAMES E DAHLBERG PC
C07H21/04,C07H21/02,C12Q1/68
CC Strandedness: Single;
CC Topology: Linear;
CC /desc = 'DNA'
FH Key
FT source
FT Location/Qualifiers
FT Location/Qualifiers
1..16
/organism='Unidentified'.
/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"

Query Match 0.8%; Score 13.4; DB 1; Length 16;
Best Local Similarity 93.3%; Pred. No. 1.2e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1508 CAGCTCCAGGCCCC 1522
DB |||||||
2 CAGCTCCAGGACCC 16

RESULT 281
S81287/c
LOCUS S81287 16 bp DNA linear PRI 07-MAY-1993
DEFINITION Mitochondrial acetoacetyl-coenzyme A thiolase [human, Genomic
Mutant, 16 nt].
ACCESSION S81287
VERSION S81287.1 GI:245359
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 16)
Fukao,T., Yamauchi,S., Orii,T., Schutgens,R.B., Osumi,T. and
Hashimoto,T.
Identification of three mutant alleles of the gene for
mitochondrial acetoacetyl-coenzyme A thiolase. A complete analysis
of two generations of a family with 3-ketothiolase deficiency
J. Clin Invest. 89 (2), 474-479 (1992)
92147861
MEDLINE 1346617
PUBMED
REMARK GenBank staff at the National Library of Medicine created this
entry [NCBI gibbsq 81287] from the original journal article.
A->C mutation at 3'splice site intron 10.
COMMENT
FEATURES
source
1..16
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
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/gene="mitochondrial acetoacetyl-coenzyme A thiolase"

Query Match 0.8%; Score 13.4; DB 1; Length 16;
Best Local Similarity 93.3%; Pred. No. 1.2e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1323 AGAACCCCTAAATTT 1337
DB |||||||
15 AGAACCCGTAATTT 1

RESULT 282
AR066302/c
LOCUS AR066302 14 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 1 from patent US 5849903.
ACCESSION AR066302

```

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JOURNAL
MEDLINE
PUBMED
REFERENCE
2 (bases 1 to 15)
AUTHORS
Balzerque,S.
TITLE
Direct Submission
JOURNAL
Submitted (21-NOV-2002) Balzerque S., UMRGV, INRA/CNRS, 2 rue
COMMENT
Gaston Cremieux, 91057 Evry cedex, FRANCE
PCR was performed on DNA from transformants of Arabidopsis thaliana
plants from INRA (Versailles). The DNA fragment(s) resulting from
the PCR were directly sequenced from the left or the right border
to determine the genomic sequence flanking the insertion. T-DNA
derived sequences were removed. Information to order the
corresponding mutant line and a link to a database providing a
graphical display of the insertion site are available at
http://dbsgap.versailles.inra.fr/publiclines/. This sequence has
been generated in the framework of the French plant genomics
program 'Genoplante' (http://www.genoplante.com and
http://genoplante-info.infobiogen.fr).

FEATURES
source
1. .15
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/cultivar="Wassillewskija"
/db_xref="taxon:3702"
/clone="282G05"
/clone_lib="Arabidopsis thaliana T-DNA insertion lines"
misc_feature
1. .15
/notes="T-DNA flanking sequence
left border"

Query Match 0.8%; Score 13; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 229 AAAAAACAACGA 241
Db 14 AAAAAACAACGA 2

RESULT 285
LOCUS
CQ806753 16 bp DNA linear PAT 10-MAY-2004
DEFINITION
Sequence 203 from Patent WO2004035803.
ACCESSION
CQ806753
VERSION
CQ806753.1 GI:47112135
KEYWORDS
Homo sapiens (human)
SOURCE
Homo sapiens
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1
AUTHORS
Foekens,J., Harbeck,N., Koenig,T., Maier,S., Martens,J., Model,F.,
Nimmrich,I., Rujan,T., Schmitt,A., Schmitt,M., Look,M.P. and
Marx,A.
TITLE
Method and nucleic acids for the improved treatment of breast cell
proliferative disorders
JOURNAL
Patent: WO 2004035803-A 203 29-APR-2004;
Epigenomics AG (DE)
FEATURES
source
1. .16
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 0.8%; Score 13; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1345 CCGTGGCGGAGAA 1357
Db 3 CCGTGGCGGAGAA 15

JOURNAL
MEDLINE
PUBMED
REFERENCE
1 (bases 1 to 14)
AUTHORS
Pietrzkowski,Z., Cieslak,D. and Olbina,G.
TITLE
Antisense oligonucleotides for IL-8 and IL-8 receptor
JOURNAL
Patent: US 5849903-A 1 15-DEC-1998;
FEATURES
Location/Qualifiers
1. .14
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.8%; Score 13; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 95;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1239 GTTCTTCGGTG 1251
Db 13 GTTCTTCGGTG 1

RESULT 283
AX377347/c
LOCUS
AX377347 15 bp DNA linear PAT 18-MAR-2002
DEFINITION
Sequence 11 from Patent WO0212499.
ACCESSION
AX377347
VERSION
AX377347.1 GI:19573633
KEYWORDS
Homo sapiens (human)
SOURCE
Homo sapiens
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1
AUTHORS
Kliem,S.E., Koshy,B. and Lanz,E.M.
TITLE
Haplotypes of the ntfs gene
JOURNAL
Patent: WO 0212499-A 11 14-FEB-2002;
Genaisance Pharmaceuticals, Inc. (US)
FEATURES
Location/Qualifiers
1. .15
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

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Best Local Similarity 86.7%; Pred. No. 1.2e+02;
Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1537 CTCTCCCGCTCTCG 1551
Db 15 CYCTCCCGCTCCGG 1

RESULT 284
ATH551605/c
LOCUS
ATH551605 15 bp DNA linear PLN 29-MAR-2003
DEFINITION
Arabidopsis thaliana T-DNA flanking sequence, left border, clone
282G05.
ACCESSION
AJ551605
AJ551605.1 GI:29367738
VERSION
AJ551605.1
KEYWORDS
left border; T-DNA flanking sequence.
SOURCE
Arabidopsis thaliana (thale cress)
ORGANISM
Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE
1
AUTHORS
Brunaud,V., Balzerque,S., Dubreucq,B., Aubourg,S., Samson,F.,
Chauvin,S., Bechtold,N., Cruaud,C., Dekose,R., Pelletier,G.,
Lepiniec,L., Caboche,M. and Lecharny,A.
TITLE
T-DNA integration into the Arabidopsis genome depends on sequences
of pre-insertion sites

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RESULT 286
A88141
LOCUS       A88141                16 bp    DNA    linear    PAT 22-JAN-2000
DEFINITION  Sequence 289 from Patent WO9833904.
ACCESSION   A88141
VERSION     A88141.1  GI:6736711
KEYWORDS    .
SOURCE      unidentified
            unclassified
REFERENCE   1 (bases 1 to 16)
AUTHORS    Brysch,W. and Schlingensiepen,K.
TITLE      AN ANTISENSE OLIGONUCLEOTIDE PREPARATION METHOD
JOURNAL    PATENT: WO 9833904-A 289 06-AUG-1998;
          BIOGNOSTIK GES (DE); BRYSCH WOLFGANG (DE)
FEATURES    Location/Qualifiers
             source
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               /organism="unidentified"
               /mol_type="unassigned DNA"
               /db_xref="taxon:32644"

Query Match      0.8%; Score 12.8; DB 1; Length 16;
Best Local Similarity 87.5%; Pred. No. 1.5e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      456  GGCGCCGACGCTTGAGG 471
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          1  GGCGCGCACCTTGGGG 16
          Db

RESULT 287
A89435
LOCUS       A89435                16 bp    DNA    linear    PAT 22-JAN-2000
DEFINITION  Sequence 1583 from Patent WO9833904.
ACCESSION   A89435
VERSION     A89435.1  GI:6738005
KEYWORDS    .
SOURCE      unidentified
            unclassified
REFERENCE   1 (bases 1 to 16)
AUTHORS    Brysch,W. and Schlingensiepen,K.
TITLE      AN ANTISENSE OLIGONUCLEOTIDE PREPARATION METHOD
JOURNAL    PATENT: WO 9833904-A 1583 06-AUG-1998;
          BIOGNOSTIK GES (DE); BRYSCH WOLFGANG (DE)
FEATURES    Location/Qualifiers
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Query Match      0.8%; Score 12.8; DB 1; Length 16;
Best Local Similarity 87.5%; Pred. No. 1.5e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      456  GGCGCCGACGCTTGAGG 471
          ||||| ||||| |||||
          1  GGCGCGCACCTTGGGG 16
          Db

RESULT 288
A90108
LOCUS       A90108                16 bp    DNA    linear    PAT 22-JAN-2000
DEFINITION  Sequence 289 from Patent EP0856579.
ACCESSION   A90108
VERSION     A90108.1  GI:6738622
KEYWORDS    .
SOURCE      unidentified
            unclassified
REFERENCE   1 (bases 1 to 16)
AUTHORS    Brysch,W.D. and Schlingensiepen,K.D.
TITLE      .
JOURNAL    .
FEATURES    .
             source
               1..16
               /organism="unidentified"
               /mol_type="unassigned DNA"
               /db_xref="taxon:32644"

Query Match      0.8%; Score 12.8; DB 1; Length 16;
Best Local Similarity 87.5%; Pred. No. 1.5e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      630  TTCTTCACCCGGGAGC 645
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          1  TTCTTCATCCGGAGC 16
          Db

RESULT 289
A90108
LOCUS       A90108                16 bp    DNA    linear    PAT 24-MAR-2004
DEFINITION  Sequence 146 from Patent WO2004020668.
ACCESSION   CQ786338
VERSION     CQ786338.1  GI:45721440
KEYWORDS    .
SOURCE      synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
AUTHORS    Nakamura,Y. and Katagiri,T.
TITLE      Method for treating synovial sarcoma
JOURNAL    Patent: WO 2004020668-A 146 11-MAR-2004;
          Oncotherapy Science, Inc. (JP); The University of Tokyo (JP)
FEATURES    Location/Qualifiers
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Query Match      0.8%; Score 12.8; DB 1; Length 16;
Best Local Similarity 87.5%; Pred. No. 1.5e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

TITLE      An antisense oligonucleotide preparation method
JOURNAL    Patent: EP 0856579-A 289 05-AUG-1998;
          BIOGNOSTIK GES (DE)
FEATURES    Location/Qualifiers
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RESULT 289
AR104209/c
LOCUS       AR104209                16 bp    DNA    linear    PAT 14-FEB-2001
DEFINITION  Sequence 25 from patent US 6093545.
ACCESSION   AR104209
VERSION     AR104209.1  GI:12816917
KEYWORDS    .
SOURCE      Unknown.
            Unclassified.
REFERENCE   1 (bases 1 to 16)
AUTHORS    Goodearl,A.D.J. and Glucksmann,M.Alexandra.
TITLE      Methods for detecting nucleic acid molecules encoding a member of
          the muscarinic family of receptors
JOURNAL    Patent: US 6093545-A 25 25-JUL-2000;
          Location/Qualifiers
FEATURES    Location/Qualifiers
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               1..16
               /organism="unknown"
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Query Match      0.8%; Score 12.8; DB 1; Length 16;
Best Local Similarity 87.5%; Pred. No. 1.5e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      72  GTGGGGCTGCTGCTGA 87
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          16  GTGGGGCAGCTGCTCA 1
          Db

RESULT 290
CQ786338/c
LOCUS       CQ786338                16 bp    DNA    linear    PAT 24-MAR-2004
DEFINITION  Sequence 146 from Patent WO2004020668.
ACCESSION   CQ786338
VERSION     CQ786338.1  GI:45721440
KEYWORDS    .
SOURCE      synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
AUTHORS    Nakamura,Y. and Katagiri,T.
TITLE      Method for treating synovial sarcoma
JOURNAL    Patent: WO 2004020668-A 146 11-MAR-2004;
          Oncotherapy Science, Inc. (JP); The University of Tokyo (JP)
FEATURES    Location/Qualifiers
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               1..16
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               /mol_type="unassigned DNA"
               /db_xref="taxon:32630"
               /note="Description of Artificial Sequence: synthetic
               oligonucleotide"

Query Match      0.8%; Score 12.8; DB 1; Length 16;
Best Local Similarity 87.5%; Pred. No. 1.5e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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Query Match 0.8%; Score 12.8; DB 1; Length 16;
Best Local Similarity 87.5%; Pred. No. 1.5e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 669 CCCTTCAGCCTGCCCC 684
Db 1 CCCACCAGCCTGCCCC 16

RESULT 296
BD065654
LOCUS 16 bp DNA linear PAT 27-AUG-2002
DEFINITION An antisense oligonucleotide preparation method.
ACCESSION BD065654
VERSION BD065654.1 GI:22611257
KEYWORDS JP 2001511000-A/289.
SOURCE unidentified
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 16)
AUTHORS Schlingensiepen,K.H. and Brysch,W.
TITLE An antisense oligonucleotide preparation method
JOURNAL Patent: JP 2001511000-A 289 07-AUG-2001;
COMMENT BIOGHOSTIK GESELLSCHAFT FUR BIOMOLEKULARE DIAGNOSTIK MBH
OS Unknown
PN JP 2001511000-A/289
PD 07-AUG-2001
PF 30-JAN-1998 JP 1998532533
PR 31-JAN-1997 EP 97101531.8
PI KARL HERMANN SCHLINGENSIEPEN,WOLFGANG BRYSCH
PC C12N15/11,C07H21/04,A61K31/70
CC An antisense oligonucleotide preparation method FH Key
FT source 1. .16
FT Location/Qualifiers
/organism="Unknown"

Query Match 0.8%; Score 12.8; DB 1; Length 16;
Best Local Similarity 87.5%; Pred. No. 1.5e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 630 TTCTTCACCCGGGAGC 645
Db 1 TTCTTCATCCCGGAGC 16

RESULT 298
BD086293/c
LOCUS 16 bp DNA linear PAT 27-AUG-2002
DEFINITION G protein-coupled receptor and utilization thereof.
ACCESSION BD086293
VERSION BD086293.1 GI:22631903
KEYWORDS JP 2001525174-A/9.
SOURCE unidentified
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 16)
AUTHORS Goodearl,A.D.J., Glucksmann,A.M., Xie,M. and Distefano,P.
TITLE G protein-coupled receptor and utilization thereof
JOURNAL Patent: JP 2001525174-A 9 11-DEC-2001;
COMMENT MILLENNIUM PHARMACEUTICALS INC
OS Unidentified
PN JP 2001525174-A/9
PD 11-DEC-2001
PF 04-DEC-1998 JP 2000523346
PR 04-DEC-1997 US 08/985090,17-MAR-1998 US 09/042780 PT
ANDREW D J GOODEARL,ALEXANDRA M GLUCKSMANN,MICHAEL XIE,PETER PI
DISTEFANO
PC C12N15/09,C07K14/705,C07K16/28,C12N5/10,C12P21/02,C12Q1/68//
CC (C12P21/02,C12R1:91),C12N15/00,C12N5/00
CC Strandedness: Single;
CC Topology: Linear;
CC G protein-coupled receptor and utilization thereof FH Key
FT source 1. .16
FT Location/Qualifiers
/organism="Unidentified"

FEATURES
source
Location/Qualifiers
1. .16
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/db_xref="taxon:32644"

Query Match 0.8%; Score 12.8; DB 1; Length 16;
Best Local Similarity 87.5%; Pred. No. 1.5e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 72 GTGGGGCTGCTGCTGA 87
Db 16 GTGGGGCAGCTGCTCA 1

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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: September 13, 2005, 10:42:36 ; Search time 8 Seconds

(without alignments)  
3.180 Million cell updates/sec

Title: us-10-828-394-1

Perfect score: 1643

Sequence: 1 Gaattccgcgctgaccgag.....taaaactgtctgtgagctg 1643

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 0.5

Searched: 411 seqs, 7741 residues

Total number of hits satisfying chosen parameters: 822

Minimum DB seq length: 8

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 411 summaries

Database : rngdb:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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6	25	1.5	25	1	ADP14578
7	25	1.5	25	1	ADP14583
8	25	1.5	25	1	ADP14580
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11	25	1.5	25	1	ADP14587
12	25	1.5	25	1	ADP14582
13	25	1.5	25	1	ADP14584
14	25	1.5	25	1	ADP14586
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16	25	1.5	25	1	ADP14592
17	25	1.5	25	1	ADP14579
18	25	1.5	25	1	ADP14581
19	25	1.5	25	1	ADP14591
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21	23	1.4	23	1	ACF36411
22	23	1.4	23	1	ACF36410
23	23	1.4	23	1	ADM83082
24	23	1.4	23	1	ADM83081
25	23	1.4	23	1	ADL70521
26	23	1.4	23	1	ADL70512
27	23	1.4	23	1	ADL70515
28	23	1.4	23	1	ADL70518
29	21	1.3	21	1	AAT39500
30	21	1.3	21	1	AA52783
31	21	1.3	21	1	AAA94227
32	21	1.3	21	1	AAA94231
33	21	1.3	21	1	AAA94230

Human testosterone	21	1.3	21	1	AAA94232	Human testosterone
Human testosterone	21	1.3	21	1	AAA94233	Human testosterone
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Human gene single	21	1.3	21	1	AAF97657	Human gene single
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TRPM-2 antisense o	21	1.3	21	1	ACF36397	TRPM-2 antisense o
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RNAi for human clu	21	1.3	21	1	ADL70520	RNAi for human clu
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Antisense oligonuc	21	1.3	21	1	ADL70412	Antisense oligonuc
RNAi for human clu	21	1.3	21	1	ADL70425	RNAi for human clu
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RNAi for human clu	21	1.3	21	1	ADL70423	RNAi for human clu
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RNAi for human clu	21	1.3	21	1	ADL70443	RNAi for human clu
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RNAi for human clu	21	1.3	21	1	ADL70439	RNAi for human clu
RNAi for human clu	21	1.3	21	1	ADL70438	RNAi for human clu
Antisense oligonuc	21	1.3	21	1	ADL70414	Antisense oligonuc
Antisense oligonuc	21	1.3	21	1	ADL70409	Antisense oligonuc
RNAi for human clu	21	1.3	21	1	ADL70427	RNAi for human clu
Antisense oligonuc	21	1.3	21	1	ADL70405	Antisense oligonuc
Antisense oligonuc	21	1.3	21	1	ADL70407	Antisense oligonuc
RNAi for human clu	21	1.3	21	1	ADL70424	RNAi for human clu
Dog genomic marker	20.8	1.3	24	1	AAA66325	Dog genomic marker
Human clusterin in	20	1.2	20	1	ABN99680	Human clusterin in
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C 108	20	1.2	20	1	ABN99718	Human clusterin in
C 109	20	1.2	20	1	ABN99677	Human clusterin in
C 110	20	1.2	20	1	ABN99681	Human clusterin in
C 111	20	1.2	20	1	ABN99688	Human clusterin in
C 112	20	1.2	20	1	ABN99675	Human clusterin in
C 113	20	1.2	20	1	ABN99695	Human clusterin in
C 114	20	1.2	20	1	ABN99697	Human clusterin in
C 115	20	1.2	20	1	ABN99701	Human clusterin in
C 116	20	1.2	20	1	ABN99702	Human clusterin in
C 117	20	1.2	20	1	ABN99704	Human clusterin in
C 118	20	1.2	20	1	ABN99716	Human clusterin in
C 119	20	1.2	20	1	ABN99726	Human clusterin in
C 120	20	1.2	20	1	ABN99727	Human clusterin in
C 121	20	1.2	20	1	ABN99670	Human clusterin in
C 122	20	1.2	20	1	ABN99683	Human clusterin in
C 123	20	1.2	20	1	ABN99722	Human clusterin in
C 124	20	1.2	20	1	ABN99667	Human clusterin in
C 125	20	1.2	20	1	ABN99687	Human clusterin in
C 126	20	1.2	20	1	ABN99712	Human clusterin in
C 127	20	1.2	20	1	ABN99725	Human clusterin in
C 128	20	1.2	20	1	ABN99671	Human clusterin in
C 129	20	1.2	20	1	ABN99678	Human clusterin in
C 130	20	1.2	20	1	ABN99694	Human clusterin in
C 131	20	1.2	20	1	ABN99700	Human clusterin in
C 132	20	1.2	20	1	ABN99721	Human clusterin in
C 133	20	1.2	20	1	ABN99669	Human clusterin in
C 134	20	1.2	20	1	ABN99685	Human clusterin in
C 135	20	1.2	20	1	ABN99689	Human clusterin in
C 136	20	1.2	20	1	ABN99703	Human clusterin in
C 137	20	1.2	20	1	ABN99720	Human clusterin in
C 138	20	1.2	20	1	ABN99691	Human clusterin in
C 139	20	1.2	20	1	ABN99713	Human clusterin in
C 140	20	1.2	20	1	ABN99724	Human clusterin in
C 141	20	1.2	20	1	ABN99690	Human clusterin in
C 142	20	1.2	20	1	ABN99708	Human clusterin in
C 143	20	1.2	20	1	ABN99672	Human clusterin in
C 144	20	1.2	20	1	ABN99693	Human clusterin in
C 145	20	1.2	20	1	ABN99698	Human clusterin in
C 146	20	1.2	20	1	ABN99679	Human clusterin in
C 147	20	1.2	20	1	ABN99715	Human clusterin in
C 148	20	1.2	20	1	ABN99728	Human clusterin in
C 149	20	1.2	20	1	ABN99733	Human clusterin in
C 150	20	1.2	20	1	ABN99673	Human clusterin in
C 151	20	1.2	20	1	ABN99673	Human clusterin in
C 152	20	1.2	20	1	ABN99679	Human clusterin in
C 153	20	1.2	20	1	ABN99696	Human clusterin in
C 154	20	1.2	20	1	ABN99705	Human clusterin in
C 155	20	1.2	20	1	ABN99706	Human clusterin in
C 156	20	1.2	20	1	ABN99723	Human clusterin in
C 157	20	1.2	20	1	ABN99731	Human clusterin in
C 158	20	1.2	20	1	ABN99699	Human clusterin in
C 159	20	1.2	20	1	ABN99714	Human clusterin in
C 160	20	1.2	20	1	ABN99674	Human clusterin in
C 161	20	1.2	20	1	ABN99688	Human clusterin in
C 162	20	1.2	20	1	ABN99710	Human clusterin in
C 163	20	1.2	20	1	ABN99676	Human clusterin in
C 164	20	1.2	20	1	ABN99692	Human clusterin in
C 165	20	1.2	20	1	ABN99707	Human clusterin in
C 166	20	1.2	20	1	ADO07105	CLU gene forward p
C 167	20	1.2	20	1	ADO07106	CLU gene reverse p
C 168	20	1.2	21	1	ADL70464	RNAi for human clu
C 169	20	1.2	21	1	ADL70430	RNAi for human clu
C 170	19.4	1.2	21	1	AAAS2782	Murine clusterin p
C 171	19	1.2	19	1	ADL70522	RNAi for human clu
C 172	19	1.2	19	1	ADL70523	RNAi for human clu
C 173	19	1.2	19	1	ADL70444	RNAi for human clu
C 174	19	1.2	19	1	ADL70445	RNAi for human clu
C 175	19	1.2	21	1	ADL70465	RNAi for human clu
C 176	19	1.2	21	1	ADL70431	RNAi for human clu
C 177	18.8	1.1	22	1	ADCI0398	Human NOVX polypep
C 178	18	1.1	18	1	AAT41539	Human apolipoprote
C 179	18	1.1	18	1	AAT41527	Human apolipoprote

C 180	18	1.1	18	1	AAT39501	Chromosome 8p clus
C 181	18	1.1	18	1	ABN99657	Human clusterin PC
C 182	17.8	1.1	21	1	ACF36409	DNA sequence of a
C 183	17.8	1.1	21	1	ADM83080	Control TRPM-2 mis
C 184	17	1.0	17	1	AAT41526	Human apolipoprote
C 185	17	1.0	17	1	AAT41542	Human apolipoprote
C 186	17	1.0	17	1	AAT34616	Tumour suppression
C 187	17	1.0	17	1	ADB45708	Tumour suppression
C 188	16.8	1.0	20	1	AAQ58405	Antisense oligonuc
C 189	16.8	1.0	20	1	ADN02449	Western equine enc
C 190	16	1.0	20	1	AAQ68062	Antisense probe 15
C 191	16	1.0	17	1	AXA14650	Triple helix formi
C 192	16	1.0	19	1	ADS00161	Duchenne muscular
C 193	16	1.0	19	1	ADS73873	DMD gene specific
C 194	16	1.0	20	1	ADI19217	Human PCTAIRE prot
C 195	16	1.0	20	1	ADI19270	Human PCTAIRE prot
C 196	15.8	1.0	19	1	ABN98070	Caenorhabditis ele
C 197	15.8	1.0	19	1	ADD00110	HCV coding region-
C 198	15.8	1.0	19	1	ADD00259	HCV coding region-
C 199	15.8	1.0	19	1	ADFS1715	Hepatitis C virus
C 200	15.8	1.0	19	1	ADFS2411	Hepatitis C virus
C 201	15.8	1.0	19	1	ADL70462	RNAi for human clu
C 202	15.8	1.0	19	1	ADL70463	RNAi for human clu
C 203	15.8	1.0	19	1	ADL70429	RNAi for human clu
C 204	15.8	1.0	19	1	ADL70426	RNAi for human clu
C 205	15.8	1.0	19	1	ADL70428	Human apolipoprote
C 206	15.4	0.9	17	1	AAT41543	Human apolipoprote
C 207	15.4	0.9	17	1	AAT41525	Rabbit stromelysin
C 208	15.4	0.9	17	1	AXA63903	Human NOGO Hammer
C 209	15.4	0.9	17	1	ABK00170	Human NOGO Hammer
C 210	15.4	0.9	17	1	ABN08674	Human MD23 scannin
C 211	15.4	0.9	17	1	ADB00465	HCV minus strand D
C 212	15.4	0.9	17	1	ACD62817	HCV DNzyme subst
C 213	15.4	0.9	17	1	ACD59852	Tumour suppression
C 214	15.4	0.9	17	1	ADB45503	HCV DNzyme subst
C 215	15.4	0.9	17	1	ADI84296	Human GDMPL-1 prob
C 216	15.4	0.9	18	1	ACN71764	PCR primer for DNA
C 217	15.4	0.9	18	1	AXA85604	Allele specific pr
C 218	15.4	0.9	18	1	ADR74784	Peptide nucleic ac
C 219	15	0.9	15	1	AAV31968	HCV minus strand D
C 220	15	0.9	17	1	ACD62818	HCV DNzyme subst
C 221	15	0.9	17	1	ADI85768	HCV DNzyme subst
C 222	15	0.9	17	1	ADO79635	EIV primer EIVAIP7
C 223	14.8	0.9	18	1	AAQ35721	Mouse IL-2 recepto
C 224	14.8	0.9	18	1	AAV95047	SNP specific upper
C 225	14.8	0.9	18	1	AAH37505	Mouse PTPRB revers
C 226	14.6	0.9	18	1	ACC79773	Hepatitis C virus
C 227	14.6	0.9	17	1	AXA63904	Rabbit stromelysin
C 228	14.4	0.9	17	1	AAV93469	Human B-raf substr
C 229	14.4	0.9	17	1	ABK00171	Human NOGO Hammer
C 230	14.4	0.9	17	1	ABN08360	Human GDMPL-1 17-m
C 231	14.4	0.9	17	1	ABN08675	Human GDMPL-1 17-m
C 232	14.4	0.9	17	1	ABN08361	Human GDMPL-1 17-m
C 233	14.4	0.9	17	1	ABN10046	Human GDMPL-1 17-m
C 234	14.4	0.9	17	1	ABN08673	Human GDMPL-1 17-m
C 235	14.4	0.9	17	1	ABN10045	Human GDMPL-1 17-m
C 236	14.4	0.9	17	1	ACN07604	WNV minus strand H
C 237	14.4	0.9	17	1	ACN07604	WNV minus strand I
C 238	14.4	0.9	17	1	ACN09975	WNV Amberyze subs
C 239	14.4	0.9	17	1	ACN07053	WNV Amberyze subs
C 240	14.4	0.9	17	1	ACN07193	WNV Zinzyme subst
C 241	14.4	0.9	17	1	ACN04500	WNV minus strand H
C 242	14.4	0.9	17	1	ACN07603	Tumour suppression
C 243	14.4	0.9	17	1	ABT38885	Human MD23 scannin
C 244	14.4	0.9	17	1	ABE00466	Human MD23 scannin
C 245	14.4	0.9	17	1	ABE00464	Human MD23 scannin
C 246	14.4	0.9	17	1	ABZ61479	Human H-Ras DNazym
C 247	14.4	0.9	17	1	ACD59853	HCV DNzyme subst
C 248	14.4	0.9	17	1	ADB43621	HBV zinzyme subst
C 249	14.4	0.9	17	1	AD53920	Tumour suppression
C 250	14.4	0.9	17	1	AD303979	Cholesterol homeos
C 251	14.4	0.9	17	1	ABX95832	Human Phe311leu mu
C 252	14.4	0.9	17	1	ABX95833	Human Phe311leu mu

Chromosome 8p clus	Chromosome 9p clus	Human clusterin PC	DNA sequence of a	Control TRPM-2 mis	Human apolipoprote	Human apolipoprote	Tumour suppression	Tumour suppression	Antisense oligonuc	Western equine enc	Antisense probe 15	Triple helix formi	Duchenne muscular	DMD gene specific	Human PCTAIRE prot	Human PCTAIRE prot	Caenorhabditis ele	HCV coding region-	HCV coding region-	Hepatitis C virus	Hepatitis C virus	RNAi for human clu	RNAi for human clu	RNAi for human clu	RNAi for human clu	Human apolipoprote	Human apolipoprote	Rabbit stromelysin	Human NOGO Hammer	Human NOGO Hammer	Human MD23 scannin	HCV minus strand D	HCV DNzyme subst	Tumour suppression	HCV DNzyme subst	Human GDMPL-1 prob	PCR primer for DNAP	Allele specific pr	Peptide nucleic ac	HCV minus strand D	HCV DNzyme subst	KIAA0783 extend pri	EIV primer EIVAIP7	Mouse IL-2 recepto	SNP specific upper	Mouse PTPB3 revers	Hepatitis C virus	Rabbit stromelysin	Human B-raf subst	Human NOGO Hammer	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1 17-w	Human GDMPL-1
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253	14.4	0.9	17	1	ADL18587	RT-PCR primer HP6.	326	13.8	0.8	17	1	ABK18229	Human ERG hammerhe
c 254	14.4	0.9	17	1	ADM59611	Hepatitis B virus	327	13.8	0.8	17	1	ABK19135	Human ERG hammerhe
255	14.4	0.9	17	1	ADI84297	HCV DNzyme subutr	328	13.8	0.8	17	1	AAK18269	Mouse Ob receptor
c 256	14.4	0.9	17	1	ADI85767	HCV DNzyme subutr	329	13.8	0.8	17	1	AAK18271	Mouse Ob receptor
257	14.4	0.9	17	1	ACN17163	Human GMPLP-1 prob	c 330	13.8	0.8	17	1	ACN05936	WNV Amberzyme subs
c 258	14.4	0.9	17	1	ACN73136	Human GMPLP-1 prob	331	13.8	0.8	17	1	ACN08391	WNV minus strand H
c 259	14.4	0.9	17	1	ACN73135	Human GMPLP-1 prob	332	13.8	0.8	17	1	ACN05008	WNV minus strand A
c 260	14.4	0.9	17	1	ACN71450	Human GMPLP-1 prob	c 333	13.8	0.8	17	1	ACN00398	WNV Hammerhead Rib
c 261	14.4	0.9	17	1	ACN71451	Human GMPLP-1 prob	334	13.8	0.8	17	1	ACN14016	WNV minus strand D
c 262	14.4	0.9	17	1	ACN71451	Human GMPLP-1 prob	335	13.8	0.8	17	1	ACN15009	WNV minus strand A
c 263	14.4	0.9	18	1	AAQ080949	PCR primer to gene	c 336	13.8	0.8	17	1	ACN06460	WNV Amberzyme subs
c 264	14.4	0.9	18	1	ADM06417	Human PCR primer S	c 337	13.8	0.8	17	1	ACN01953	WNV inozyme subutr
c 265	14.4	0.9	18	1	ADM92954	SNP-containing car	338	13.8	0.8	17	1	ACN01953	WNV minus strand H
c 266	14.4	0.9	18	1	ADH71057	Human Vbeta point	c 339	13.8	0.8	17	1	ACN01835	WNV minus strand I
c 267	14.4	0.9	15	1	AAK47085	IGFBP3 oligonucleo	c 340	13.8	0.8	17	1	ACN05385	WNV DNzyme subutr
c 268	14.4	0.9	15	1	AAK47084	IGFBP3 oligonucleo	341	13.8	0.8	17	1	ACN08973	WNV minus strand H
c 269	14.4	0.9	17	1	ABK25595	Stress tolerance c	c 342	13.8	0.8	17	1	ABT34420	Tumour suppression
c 270	14.4	0.9	17	1	ABK25596	Stress tolerance c	343	13.8	0.8	17	1	ABT37717	Tumour suppression
c 271	14.4	0.9	17	1	ACD59851	HCV DNzyme subutr	344	13.8	0.8	17	1	ACA06296	NFKB sub-unit modu
c 272	14.4	0.9	17	1	ADI84295	HCV DNzyme subutr	345	13.8	0.8	17	1	ACA07700	NFKB sub-unit modu
c 273	14.4	0.9	17	1	ADN44286	Mutant cell identi	346	13.8	0.8	17	1	ACA07701	NFKB sub-unit modu
c 274	14.4	0.9	17	1	ADN44287	Mutant cell identi	347	13.8	0.8	17	1	ACA08217	NFKB sub-unit modu
c 275	13.8	0.8	17	1	AAK05231	Hepatitis C virus	348	13.8	0.8	17	1	ACA06298	NFKB sub-unit modu
c 276	13.8	0.8	17	1	AAK55009	Mouse fit-1 VEGF r	349	13.8	0.8	17	1	ACA06394	NFKB sub-unit modu
c 277	13.8	0.8	17	1	AAK52812	Delta-9 desaturase	350	13.8	0.8	17	1	ACA06396	NFKB sub-unit modu
c 278	13.8	0.8	17	1	AAK69614	Murine obr gene fo	351	13.8	0.8	17	1	ACA06517	NFKB sub-unit modu
c 279	13.8	0.8	17	1	AAV61074	Synthetic DNA frag	352	13.8	0.8	17	1	ADA99701	Human MD23 scannin
c 280	13.8	0.8	17	1	AAV47411	Antisense oligonuc	c 353	13.8	0.8	17	1	ADB00467	Human MD24 scannin
c 281	13.8	0.8	17	1	AAV46535	Antisense oligonuc	354	13.8	0.8	17	1	ADB02413	HCV DNzyme subutr
c 282	13.8	0.8	17	1	AAV94804	Human IL-2 recepto	355	13.8	0.8	17	1	ACD58046	HCV DNzyme subutr
c 283	13.8	0.8	17	1	AAV92651	Human A-Raf subutr	356	13.8	0.8	17	1	ACD61087	HCV DNzyme subutr
c 284	13.8	0.8	17	1	AAK53788	Human adenosine A1	c 357	13.8	0.8	17	1	ACD62816	HCV minus strand D
c 285	13.8	0.8	17	1	AAK52912	Human adenosine A1	358	13.8	0.8	17	1	ACC67637	Murine oligonucleo
c 286	13.8	0.8	17	1	AAA33231	Low adenosine anti	c 359	13.8	0.8	17	1	ADB39727	Tumour suppression
c 287	13.8	0.8	17	1	AAA32356	Low adenosine anti	360	13.8	0.8	17	1	ADI47981	Human tumour suppr
c 288	13.8	0.8	17	1	AAZ57766	Hepatitis C virus	c 361	13.8	0.8	17	1	ABZ94171	Human adenosine A1
c 289	13.8	0.8	17	1	AAA03590	Human adenosine A1	c 362	13.8	0.8	17	1	ABZ95047	Human adenosine A1
c 290	13.8	0.8	17	1	AAK03660	Human adenosine A1	363	13.8	0.8	17	1	ADL48005	Human IKK-gamma su
c 291	13.8	0.8	17	1	AAK19353	Human adenosine A1	c 364	13.8	0.8	17	1	ADL50256	Human PKR subutr
c 292	13.8	0.8	17	1	AAK18477	Human adenosine A1	365	13.8	0.8	17	1	ADL48380	Human IKK-gamma su
c 293	13.8	0.8	17	1	AAK02647	Hammerhead ribozym	366	13.8	0.8	17	1	ADM09485	Human NOD recepto
c 294	13.8	0.8	17	1	ABK01885	Human NOD Zinzyme	c 367	13.8	0.8	17	1	ADM54165	Human GRID mRNA su
c 295	13.8	0.8	17	1	ABK01053	Human NOD inozyme	c 368	13.8	0.8	17	1	ABD18019	Human adenosine A1
c 296	13.8	0.8	17	1	AAD20527	Mouse OBR genomic	c 369	13.8	0.8	17	1	ABD18895	Human adenosine A1
c 297	13.8	0.8	17	1	AAK05292	Mouse famj5312 Obr	370	13.8	0.8	17	1	ADG63002	Mouse genomic DNA
c 298	13.8	0.8	17	1	AAK79852	DNA sequencing met	371	13.8	0.8	17	1	ADG63000	Mouse genomic DNA
c 299	13.8	0.8	17	1	ABL46807	Human GRID NCH rib	c 372	13.8	0.8	17	1	ADK98279	Primer of the inve
300	13.8	0.8	17	1	AAK41482	Mouse Ob receptor	373	13.8	0.8	17	1	ADI84915	HCV DNzyme subutr
301	13.8	0.8	17	1	AAK41484	Mouse Ob receptor	374	13.8	0.8	17	1	ADI83386	HCV DNzyme subutr
302	13.8	0.8	17	1	AAK42341	Mouse obesity rece	c 375	13.8	0.8	17	1	ACN64993	Human GMPLP-1 prob
303	13.8	0.8	17	1	AAK42339	Mouse obesity rece	376	13.8	0.8	17	1	ACN71759	Human GMPLP-1 prob
c 304	13.8	0.8	17	1	ABN01903	Human GMPLP-1 17-m	c 377	13.8	0.8	17	1	ACN72785	Human GMPLP-1 prob
c 305	13.8	0.8	17	1	ABN07493	Human GMPLP-1 17-m	c 378	13.8	0.8	17	1	ACN72787	Human GMPLP-1 prob
c 306	13.8	0.8	17	1	ABN08576	Human GMPLP-1 17-m	379	13.8	0.8	17	1	ACN71758	Human GMPLP-1 prob
c 307	13.8	0.8	17	1	ABN09695	Human GMPLP-1 17-m	c 380	13.8	0.8	17	1	ACN71761	Human GMPLP-1 prob
c 308	13.8	0.8	17	1	ABN08671	Human GMPLP-1 17-m	c 381	13.8	0.8	17	1	ACN65741	Human GMPLP-1 prob
c 309	13.8	0.8	17	1	ABN09696	Human GMPLP-1 17-m	c 382	13.8	0.8	17	1	ACN70453	Human GMPLP-1 prob
c 310	13.8	0.8	17	1	ABN09697	Human GMPLP-1 17-m	c 383	13.8	0.8	17	1	ACN70583	Human GMPLP-1 prob
311	13.8	0.8	17	1	ABN07363	Human GMPLP-1 17-m	384	13.8	0.8	17	1	ACN71762	Human GMPLP-1 prob
312	13.8	0.8	17	1	ABN08672	Human GMPLP-1 17-m	385	13.8	0.8	17	1	ACN71686	Human GMPLP-1 prob
313	13.8	0.8	17	1	ABN08669	Human GMPLP-1 17-m	c 386	13.8	0.8	17	1	ACN72786	Human GMPLP-1 prob
c 314	13.8	0.8	17	1	ABN02651	Human GMPLP-1 17-m	c 387	13.6	0.8	15	1	ABL52123	Human PER1 allele
315	13.8	0.8	17	1	ABN08668	Human GMPLP-1 17-m	c 388	13.6	0.8	15	1	AAK595535	Human IL8RB gene a
316	13.8	0.8	17	1	ABQ63736	Human KTM1a porti	389	13.4	0.8	15	1	AAK54903	Mouse rela hammerh
317	13.8	0.8	17	1	ABQ63734	Human KTM1a porti	c 390	13.4	0.8	15	1	AAV31969	Peptide nucleic ac
318	13.8	0.8	17	1	ABQ63732	Human KTM1a porti	c 391	13.4	0.8	15	1	AAV31970	Peptide nucleic ac
319	13.8	0.8	17	1	ABQ63733	Human KTM1a porti	c 392	13.4	0.8	15	1	AAV31967	Peptide nucleic ac
320	13.8	0.8	17	1	ABQ63735	Human KTM1a porti	c 393	13.4	0.8	15	1	AAK31120	Tag sequence of a
321	13.8	0.8	17	1	ABQ63738	Human KTM1a porti	c 394	13.4	0.8	15	1	AAK31728	Transcript tag seq
322	13.8	0.8	17	1	ABQ64165	Human KTM1a porti	395	13.4	0.8	15	1	AAK50848	IGF-1 oligonucleot
323	13.8	0.8	17	1	ABV79503	Human HTPL scannin	c 396	13.4	0.8	15	1	ABK32682	Human colorectal a
324	13.8	0.8	17	1	ABV79592	Human HTPL scannin	c 397	13.4	0.8	15	1	ABK32073	Human colon cancer
325	13.8	0.8	17	1	ABV79502	Human HTPL scannin	398	13.4	0.8	15	1	ABK01805	Hepatitis C virus

399 13.4 0.8 15 1 AEX01804 Hepatitis C virus  
400 13.4 0.8 16 1 AAV70490 Sequence ID# 68 fr  
401 13.4 0.8 16 1 AAV70489 Sequence ID# 67 fr  
c 402 13.4 0.8 16 1 AAX14645 Triple helix third  
403 13.4 0.8 16 1 AEL46101 Hepatitis C virus  
404 13.4 0.8 16 1 ABL46100 Hepatitis C virus  
405 13.4 0.8 16 1 ADR82290 Nucleic acid analy  
406 13.4 0.8 16 1 ADR82291 Nucleic acid analy  
c 407 13.4 0.8 16 1 ADM80152 Linker peptide enc  
408 13.4 0.8 16 1 ADR32381 E. coli nicking ag  
409 13.4 0.8 16 1 ADR32430 E. coli fingerprin  
410 13.4 0.8 16 1 ADR33575 E. coli strain K12  
c 411 13.4 0.8 16 1 ADR69939 Human survivin gen

## ALIGNMENTS

RESULT 1  
AAQ11501  
ID AAQ11501 standard; DNA; 32 BP.  
AC AAQ11501;  
XX  
DT 20-JUN-1991 (first entry)  
XX  
DE Probe based on amino acids 6-15 of the Cytolysis Inhibitor A-chain.  
XX  
KW cytolysis inhibitor; perforin; immunological effector molecule;  
KW infertility; ss.  
XX  
OS Homo sapiens.  
XX  
PN DE3933850-A.  
XX  
PD 18-APR-1991.  
XX  
PF 06-OCT-1989; 89DE-03933850.  
XX  
PR 06-OCT-1989; 89DE-03933850.  
XX  
PA (SCHD ) SCHERING AG.  
XX  
PI Tachopp J, Jenne D;  
XX  
PS WPI; 1991-118338/17.  
XX  
PT DNA sequence coding for cytolysis inhibitor - is strong inhibitor of  
PT terminal complement protein, e.g. perforin secreted by killer cells.  
XX  
PS Example 1; Page 4; 15pp; German.  
XX  
CC The partial amino acid sequences of both chains of the Cytolysis  
CC Inhibitor were known. This probe is one of two which were prepared based  
CC on the N-terminal sequences of the inhibitor. It corresponds to the  
CC sequence DNELQMSMQG. Both probes were radioactively labelled and used to  
CC screen a liver-specific cDNA library. One clone which hybridised  
CC positively to both probes was found to contain a 1.7kb BamHI-KpnI  
CC fragment. This was inserted into plasmid pGEM4, to give DSM 5269, and  
CC sequenced. See also AAQ11502 and AAQ11503  
XX  
SQ Sequence 32 BP; 10 A; 7 C; 11 G; 4 T; 0 U; 0 Other;

Query Match 1.7%; Score 27.2; DB 1; Length 32;  
Best Local Similarity 90.6%; Pred. No. 23;  
Matches 29; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 129 GACAATGAGCTCCAGGAATGTCCATCAGG 160  
|||||  
DB 1 GACAATGAGCTCGAGGAGATGTCCAACAGGG 32  
|||||  
RESULT 2

ABK66659  
ID ABK66659 standard; DNA; 26 BP.  
XX  
AC ABK66659;  
XX  
DT 02-JUL-2002 (first entry)  
XX  
DE Human gene specific PCR primer #747.  
XX  
KW Primer; ss; DNA microarray; differential expression analysis; human.  
XX  
OS Homo sapiens.  
XX  
PN US6352829-B1.  
XX  
PD 05-MAR-2002.  
XX  
PF 05-JAN-1999; 99US-00225928.  
XX  
PR 21-MAY-1997; 97US-00859998.  
XX  
PA (CLON-) CLONTECH LAB INC.  
XX  
PI Chenchik A, Jokhadze G, Bibilashvili R;  
XX  
PS WPI; 2002-314699/35.  
XX  
PT Producing sub-population of labeled nucleic acids, useful for analyzing  
PT differences in RNA profiles between several different physiological  
PT sources, using set of distinct gene specific primers.  
XX  
PS Example 3; SEQ ID NO 747; 11pp; English.  
XX  
CC The invention relates to producing a sub-population of labeled nucleic  
CC acids (NAs) comprising contacting a NA sample from a physiological  
CC source, with a pool of 50 distinct gene specific primers under suitable  
CC conditions to enzymatically generate sub-population of NAs, where each  
CC gene specific primer has a sequence complementary to a distinct mRNA, and  
CC each labeled NA is generated using a single gene specific primer. The  
CC method is useful for producing a sub-population of labeled NAs which is  
CC useful for analysing the differences in the RNA profiles between several  
CC different physiological sources, where the method comprises producing  
CC subpopulation of labeled NAs for the different physiological sources,  
CC comprising the populations for each physiological source to identify  
CC differences in the population, where the comparison is preferably  
CC performed by hybridising the labeled NAs for each of the distinct  
CC physiological sources to an array of probe NAs stably associated with the  
CC surface of a substrate to produce a hybridisation pattern for each of the  
CC sources, and comparing the patterns for each of the sources, where  
CC differential gene expression assays are utilised in differential  
CC expression analysis of diseased a normal tissue e.g. neoplastic a normal  
CC tissue, or different tissue or subtypes. The present sequence is a  
CC human gene specific PCR primer used in the method of the invention. Note:  
CC The sequence data for this patent did not form part of the printed  
CC specification, but was obtained in electronic format directly from USPTO  
CC at http.wipo.segdata.uspto.gov/sequence.html?DocID=6352829B1  
XX  
SQ Sequence 26 BP; 8 A; 4 C; 10 G; 4 T; 0 U; 0 Other;

Query Match 1.6%; Score 26; DB 1; Length 26;  
Best Local Similarity 100.0%; Pred. No. 16;  
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 934 TCCGGATGAGGACCAAGTGTGACAG 959  
|||||  
DB 1 TCCGGATGAGGACCAAGTGTGACAG 26  
|||||  
RESULT 3  
ABK66660/c  
ID ABK66660 standard; DNA; 25 BP.  
XX  
AC ABK66660;



XX 02-JUL-2002 (first entry)  
DT Human gene specific PCR primer #748.  
DE  
XX Primer; ss; DNA microarray; differential expression analysis; human.  
XX Homo sapiens.  
OS  
XX US6352829-B1.  
PN  
XX 05-MAR-2002.  
PD  
XX 05-JAN-1999; 99US-00225928.  
PF  
XX 21-MAY-1997; 97US-00859998.  
PR  
XX (CLON-) CLONTECH LAB INC.  
PA  
XX Chenchik A, Jokhadze G, Bibilashvili R;  
PI WPI; 2002-314699/35.  
XX  
XX Producing sub-population of labeled nucleic acids, useful for analyzing  
PT differences in RNA profiles between several different physiological  
PT sources, using set of distinct gene specific primers.  
XX  
XX Example 3; SEQ ID NO 748; 11pp; English.  
PS  
XX  
XX The invention relates to producing a sub-population of labeled nucleic  
CC acids (NAs) comprising contacting a NA sample from a physiological  
CC source, with a pool of 50 distinct gene specific primers under suitable  
CC conditions to enzymatically generate sub-population of NAs, where each  
CC gene specific primer has a sequence complementary to a distinct mRNA, and  
CC each labeled NA is generated using a single gene specific primer. The  
CC method is useful for producing a sub-population of labeled NAs which is  
CC useful for analysing the differences in the RNA profiles between several  
CC different physiological sources, where the method comprises producing  
CC subpopulation of labeled NAs for the different physiological sources,  
CC comprising the populations for each physiological source to identify  
CC differences in the population, where the comparison is preferably  
CC performed by hybridising the labeled NAs for each of the distinct  
CC physiological sources to an array of probe NAs stably associated with the  
CC surface of a substrate to produce a hybridisation pattern for each of the  
CC sources, and comparing the patterns for each of the sources, where  
CC differential gene expression assays are utilised in differential  
CC expression analysis of diseased a normal tissue e.g. neoplastic a normal  
CC tissue, or different tissue or subtype types. The present sequence is a  
CC human gene specific PCR primer used in the method of the invention. Note:  
CC The sequence data for this patent did not form part of the printed  
CC specification, but was obtained in electronic format directly from USPTO  
CC at <http://wipo.seqdata.uspto.gov/sequence.html?docID=6352829B1>  
XX  
SQ Sequence 25 BP; 6 A; 8 C; 7 G; 4 T; 0 U; 0 Other;  
Query Match 1.5%; Score 25; DB 1; Length 25;  
Best Local Similarity 100.0%; Pred. No. 19;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1190 GTACTATCTCGGGGTCCACCGGTG 1214  
|||||  
Db 25 GTACTATCTCGGGGTCCACCGGTG 1  
RESULT 4  
ID ADP14589 standard; DNA; 25 BP.  
XX  
AC ADP14589;  
XX  
XX 26-AUG-2004 (first entry)  
DT  
XX Renal cell carcinoma differentially expressed gene probe #994.  
DE

XX ss; diagnosis; non-blood disease; solid tumor; gene expression;  
KW peripheral blood mononuclear cell; renal cell carcinoma; prostate cancer;  
KW head/neck cancer; differential expression; probe.  
XX Homo sapiens.  
OS  
XX WO2004048933-A2.  
PN  
XX 10-JUN-2004.  
PD  
XX 21-NOV-2003; 2003WO-US037481.  
PF  
XX 21-NOV-2002; 2002US-0427982P.  
PR  
XX 03-APR-2003; 2003US-0459782P.  
XX (AMHP ) WYETH.  
PA (TWIN/) TWINE N C.  
PA (BURC/) BURCZYNSKI M E.  
PA (TREP/) TREPICCHIO W L.  
PA (DORN/) DORNER A.  
PA (STOV/) STOVER J A.  
PA (SLON/) SLONI D K.  
XX  
XX Twine NC, Burczynski ME, Trepicchio WL, Dorner A, Stover JA;  
PI Sloni DK;  
XX  
XX WPI; 2004-460799/43.  
DR  
XX  
XX Diagnosing non-blood disease such as solid tumor, involves comparing  
PT differential expression profile of specific genes in peripheral blood  
PT sample of subject with reference expression profile of specific genes.  
XX  
XX Disclosure; SEQ ID NO 1325; 350pp; English.  
XX  
XX The invention relate to a method of diagnosing (M1) non-blood disease  
CC such as solid tumor by providing peripheral blood sample of human having  
CC non-blood disease, and comparing an expression profile of specific genes  
CC in the peripheral blood sample to reference expression profile of the  
CC genes, where each of the genes is differentially expressed in peripheral  
CC blood mononuclear cells (PBMCs) of patients having the disease as  
CC compared to PBMCs of normal humans. The method is useful for diagnosing  
CC renal cell carcinoma (RCC), prostate cancer and head/neck cancer. The  
CC peripheral blood sample comprises enriched PBMCs. The peripheral blood  
CC sample is a whole blood sample (claimed). (M1) is useful for identifying  
CC genes that are differentially expressed in peripheral blood samples  
CC isolated at different stages of progression, development or treatment of  
CC RCC and/or other solid tumors. This sequence corresponds to a probe to  
CC detect a gene that is differentially expressed and detected by the method  
CC of the invention.  
XX  
SQ Sequence 25 BP; 6 A; 9 C; 4 G; 6 T; 0 U; 0 Other;  
Query Match 1.5%; Score 25; DB 1; Length 25;  
Best Local Similarity 100.0%; Pred. No. 19;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1550 GGATCCTGCACCTTAACACTCGACT 1574  
|||||  
Db 1 GGATCCTGCACCTTAACACTCGACT 25  
RESULT 5  
ID ADP14593  
XX ADP14593 standard; DNA; 25 BP.  
XX  
AC ADP14593;  
XX  
XX 26-AUG-2004 (first entry)  
DT  
XX Renal cell carcinoma differentially expressed gene probe #998.  
DE  
XX

KW ss; diagnosis; non-blood disease; solid tumor; gene expression;  
KW peripheral blood mononuclear cell; renal cell carcinoma; prostate cancer;  
XX head/neck cancer; differential expression; probe.

OS Homo sapiens.

FN WO2004048933-A2.

PD 10-JUN-2004.

XX 21-NOV-2003; 2003WO-US037481.

PF 21-NOV-2002; 2002US-0427982P.

PR 03-APR-2003; 2003US-0459782P.

XX (AMHP ) WYETH.

PA (TWIN/) TWINE N C.

PA (BURC/) BURCZYNSKI M E.

PA (TREP/) TREPICCHIO W L.

PA (DORN/) DORNER A.

PA (STOV/) STOVER J A.

PA (SLON/) SLONI D K.

XX Twine NC, Burczynski ME, Trepicchio WL, Dorner A, Stover JA;

PI Sloni DK;

XX WPI; 2004-460799/43.

XX Diagnosing non-blood disease such as solid tumor, involves comparing

PT differential expression profile of specific genes in peripheral blood

PT sample of subject with reference expression profile of specific genes.

XX Disclosure; SEQ ID NO 1329; 350pp; English.

XX The invention relate to a method of diagnosing (M1) non-blood disease  
CC such as solid tumor by providing peripheral blood sample of human having  
CC non-blood disease, and comparing an expression profile of specific genes  
CC in the peripheral blood sample to reference expression profile of the  
CC genes, where each of the genes is differentially expressed in peripheral  
CC blood mononuclear cells (PBMCs) of patients having the disease as  
CC compared to PBMCs of normal humans. The method is useful for diagnosing  
CC non-blood disease such as solid tumor. The solid tumor is chosen from  
CC renal cell carcinoma (RCC), prostate cancer and head/neck cancer. The  
CC peripheral blood sample comprises enriched PBMCs. The peripheral blood  
CC sample is a whole blood sample (claimed). (M1) is useful for identifying  
CC genes that are differentially expressed in peripheral blood samples  
CC isolated at different stages of progression, development or treatment of  
CC RCC and/or other solid tumors. This sequence corresponds to a probe to  
CC detect a gene that is differentially expressed and detected by the method  
CC of the invention.

XX SQ Sequence 25 BP; 5 A; 8 C; 6 G; 6 T; 0 U; 0 Other;

Query Match 1.5%; Score 25; DB 1; Length 25;  
Best Local Similarity 100.0%; Pred. No. 19;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1564 AACACTCGACTCTGCTGCTCATGGG 1588

DB 1 AACACTCGACTCTGCTGCTCATGGG 25

RESULT 6

ID ADP14578

XX ADP14578 standard; DNA; 25 BP.

AC ADP14578;

XX 26-AUG-2004 (first entry)

DE Renal cell carcinoma differentially expressed gene probe #983.

XX ss; diagnosis; non-blood disease; solid tumor; gene expression;

KW peripheral blood mononuclear cell; renal cell carcinoma; prostate cancer;

KW peripheral blood mononuclear cell; renal cell carcinoma; prostate cancer;  
KW head/neck cancer; differential expression; probe.

XX Homo sapiens.

FN WO2004048933-A2.

XX 10-JUN-2004.

XX 21-NOV-2003; 2003WO-US037481.

PF 21-NOV-2002; 2002US-0427982P.

PR 03-APR-2003; 2003US-0459782P.

XX (AMHP ) WYETH.

PA (TWIN/) TWINE N C.

PA (BURC/) BURCZYNSKI M E.

PA (TREP/) TREPICCHIO W L.

PA (DORN/) DORNER A.

PA (STOV/) STOVER J A.

PA (SLON/) SLONI D K.

XX Twine NC, Burczynski ME, Trepicchio WL, Dorner A, Stover JA;

PI Sloni DK;

XX WPI; 2004-460799/43.

XX Diagnosing non-blood disease such as solid tumor, involves comparing  
PT differential expression profile of specific genes in peripheral blood  
PT sample of subject with reference expression profile of specific genes.

XX Disclosure; SEQ ID NO 1314; 350pp; English.

XX The invention relate to a method of diagnosing (M1) non-blood disease  
CC such as solid tumor by providing peripheral blood sample of human having  
CC non-blood disease, and comparing an expression profile of specific genes  
CC in the peripheral blood sample to reference expression profile of the  
CC genes, where each of the genes is differentially expressed in peripheral  
CC blood mononuclear cells (PBMCs) of patients having the disease as  
CC compared to PBMCs of normal humans. The method is useful for diagnosing  
CC non-blood disease such as solid tumor. The solid tumor is chosen from  
CC renal cell carcinoma (RCC), prostate cancer and head/neck cancer. The  
CC peripheral blood sample comprises enriched PBMCs. The peripheral blood  
CC sample is a whole blood sample (claimed). (M1) is useful for identifying  
CC genes that are differentially expressed in peripheral blood samples  
CC isolated at different stages of progression, development or treatment of  
CC RCC and/or other solid tumors. This sequence corresponds to a probe to  
CC detect a gene that is differentially expressed and detected by the method  
CC of the invention.

XX SQ Sequence 25 BP; 8 A; 8 C; 5 G; 4 T; 0 U; 0 Other;

Query Match 1.5%; Score 25; DB 1; Length 25;  
Best Local Similarity 100.0%; Pred. No. 19;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1088 CTACCAGTGGAGATGCTCAACACC 1112

DB 1 CTACCAGTGGAGATGCTCAACACC 25

RESULT 7

ID ADP14583

XX ADP14583 standard; DNA; 25 BP.

AC ADP14583;

XX 26-AUG-2004 (first entry)

DE Renal cell carcinoma differentially expressed gene probe #988.

XX ss; diagnosis; non-blood disease; solid tumor; gene expression;

KW peripheral blood mononuclear cell; renal cell carcinoma; prostate cancer;

KW head/neck cancer; differential expression; probe.

XX Homo sapiens.

XX WO2004048933-A2.

XX 10-JUN-2004.

XX 21-NOV-2003; 2003WO-US037481.

XX 21-NOV-2002; 2002US-0427982P.

XX 03-APR-2003; 2003US-0459782P.

XX (AMHP ) WYETH.

XX (TWIN/) TWINE N C.

XX (BURC/) BURCZYNSKI M E.

XX (TREP/) TREPICCHIO W L.

XX (DORN/) DORNER A.

XX (STOV/) STOVER J A.

XX (SLON/) SLONI D K.

XX Twine NC, Burczynski ME, Trepicchio WL, Dorner A, Stover JA;  
PI Sloni DK;

XX WPI; 2004-460799/43.

XX Diagnosing non-blood disease such as solid tumor, involves comparing  
PT differential expression profile of specific genes in peripheral blood  
PT sample of subject with reference expression profile of specific genes.

XX Disclosure; SEQ ID NO 1319; 350pp; English.

XX The invention relate to a method of diagnosing (M1) non-blood disease  
CC such as solid tumor by providing peripheral blood sample of human having  
CC non-blood disease, and comparing an expression profile of specific genes  
CC in the peripheral blood sample to reference expression profile of the  
CC genes, where each of the genes is differentially expressed in peripheral  
CC blood mononuclear cells (PBMCs) of patients having the disease as  
CC compared to PBMCs of normal humans. The method is useful for diagnosing  
CC non-blood disease such as solid tumor. The solid tumor is chosen from  
CC renal cell carcinoma (RCC), prostate cancer and head/neck cancer. The  
CC peripheral blood sample comprises enriched PBMCs. The peripheral blood  
CC sample is a whole blood sample (claimed). (M1) is useful for identifying  
CC genes that are differentially expressed in peripheral blood samples  
CC isolated at different stages of progression, development or treatment of  
CC RCC and/or other solid tumors. This sequence corresponds to a probe to  
CC detect a gene that is differentially expressed and detected by the method  
CC of the invention.

XX SQ Sequence 25 BP; 5 A; 8 C; 4 G; 8 T; 0 U; 0 Other;

Query Match 1.5%; Score 25; DB 1; Length 25;  
Best Local Similarity 100.0%; Pred. No. 19;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1268 GAAGCTCTTTGACTCTGATCCCATC 1292

Db 1 GAAGCTCTTTGACTCTGATCCCATC 25

RESULT 8

ID ADP14580

ADP14580 standard; DNA; 25 BP.

XX AC ADP14580;

XX 26-AUG-2004 (first entry)

XX Renal cell carcinoma differentially expressed gene probe #985.

XX ss; diagnosis; non-blood disease; solid tumor; gene expression;

KW peripheral blood mononuclear cell; renal cell carcinoma; prostate cancer;

KW head/neck cancer; differential expression; probe.

XX Homo sapiens.

XX WO2004048933-A2.

XX 10-JUN-2004.

XX 21-NOV-2003; 2003WO-US037481.

XX 21-NOV-2002; 2002US-0427982P.

XX 03-APR-2003; 2003US-0459782P.

XX (AMHP ) WYETH.

XX (TWIN/) TWINE N C.

XX (BURC/) BURCZYNSKI M E.

XX (TREP/) TREPICCHIO W L.

XX (DORN/) DORNER A.

XX (STOV/) STOVER J A.

XX (SLON/) SLONI D K.

XX Twine NC, Burczynski ME, Trepicchio WL, Dorner A, Stover JA;  
PI Sloni DK;

XX WPI; 2004-460799/43.

XX Diagnosing non-blood disease such as solid tumor, involves comparing  
PT differential expression profile of specific genes in peripheral blood  
PT sample of subject with reference expression profile of specific genes.

XX Disclosure; SEQ ID NO 1316; 350pp; English.

XX The invention relate to a method of diagnosing (M1) non-blood disease  
CC such as solid tumor by providing peripheral blood sample of human having  
CC non-blood disease, and comparing an expression profile of specific genes  
CC in the peripheral blood sample to reference expression profile of the  
CC genes, where each of the genes is differentially expressed in peripheral  
CC blood mononuclear cells (PBMCs) of patients having the disease as  
CC compared to PBMCs of normal humans. The method is useful for diagnosing  
CC non-blood disease such as solid tumor. The solid tumor is chosen from  
CC renal cell carcinoma (RCC), prostate cancer and head/neck cancer. The  
CC peripheral blood sample comprises enriched PBMCs. The peripheral blood  
CC sample is a whole blood sample (claimed). (M1) is useful for identifying  
CC genes that are differentially expressed in peripheral blood samples  
CC isolated at different stages of progression, development or treatment of  
CC RCC and/or other solid tumors. This sequence corresponds to a probe to  
CC detect a gene that is differentially expressed and detected by the method  
CC of the invention.

XX SQ Sequence 25 BP; 2 A; 9 C; 8 G; 6 T; 0 U; 0 Other;

Query Match 1.5%; Score 25; DB 1; Length 25;  
Best Local Similarity 100.0%; Pred. No. 19;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1196 TCTGGGGTTCACACGGTGGCTTCC 1220

Db 1 TCTGGGGTTCACACGGTGGCTTCC 25

RESULT 9

ADP14590

ID ADP14590 standard; DNA; 25 BP.

XX AC ADP14590;

XX 26-AUG-2004 (first entry)

XX Renal cell carcinoma differentially expressed gene probe #995.

XX ss; diagnosis; non-blood disease; solid tumor; gene expression;

KW peripheral blood mononuclear cell; renal cell carcinoma; prostate cancer;

KW head/neck cancer; differential expression; probe.

XX

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OS Homo sapiens.
XX WO2004048933-A2.
XX PD 10-JUN-2004.
XX PF 21-NOV-2003; 2003WO-US037481.
XX PR 21-NOV-2002; 2002US-0427982P.
XX PR 03-APR-2003; 2003US-0459782P.
XX (AMHP ) WYETH.
XX (TWIN/) TWINE N C.
XX (BURC/) BURCZYNSKI M E.
XX (TREP/) TREPICCHIO W L.
XX (DORN/) DORNER A.
XX (STOV/) STOVER J A.
XX (SLON/) SLONI D K.
XX Twine NC, Burczynski ME, Trepicchio WL, Dorner A, Stover JA;
PI Sloni DK;
XX WPI; 2004-460799/43.
XX Diagnosing non-blood disease such as solid tumor, involves comparing
PT differential expression profile of specific genes in peripheral blood
PT sample of subject with reference expression profile of specific genes.
XX Disclosure; SEQ ID NO 1326; 350pp; English.
XX The invention relate to a method of diagnosing (M1) non-blood disease
CC such as solid tumor by providing peripheral blood sample of human having
CC non-blood disease, and comparing an expression profile of specific genes
CC in the peripheral blood sample to reference expression profile of the
CC genes, where each of the genes is differentially expressed in peripheral
CC blood mononuclear cells (PBMCs) of patients having the disease as
CC compared to PBMCs of normal humans. The method is useful for diagnosing
CC non-blood disease such as solid tumor. The solid tumor is chosen from
CC renal cell carcinoma (RCC), prostate cancer and head/neck cancer. The
CC peripheral blood sample comprises enriched PBMCs. The peripheral blood
CC sample is a whole blood sample (claimed). (M1) is useful for identifying
CC genes that are differentially expressed in peripheral blood samples
CC isolated at different stages of progression, development or treatment of
CC RCC and/or other solid tumors. This sequence corresponds to a probe to
CC detect a gene that is differentially expressed and detected by the method
CC of the invention.
XX Sequence 25 BP; 5 A; 9 C; 4 G; 7 T; 0 U; 0 Other;
SQ
Query Match 1.5%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1556 TGCACCTTAACACTCGACTCTGCTG 1580
Db 1 TGCACCTTAACACTCGACTCTGCTG 25
RESULT 10
ADP14585
ID ADP14585 standard; DNA; 25 BP.
XX AC ADP14585;
XX DT 26-AUG-2004 (first entry)
XX Renal cell carcinoma differentially expressed gene probe #990.
DE ss; diagnosis; non-blood disease; solid tumor; gene expression;
KW peripheral blood mononuclear cell; renal cell carcinoma; prostate cancer;
KW head/neck cancer; differential expression; probe.
XX Homo sapiens.
XX

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XX WO2004048933-A2.
XX PD 10-JUN-2004.
XX PF 21-NOV-2003; 2003WO-US037481.
XX PR 21-NOV-2002; 2002US-0427982P.
XX PR 03-APR-2003; 2003US-0459782P.
XX (AMHP ) WYETH.
XX (TWIN/) TWINE N C.
XX (BURC/) BURCZYNSKI M E.
XX (TREP/) TREPICCHIO W L.
XX (DORN/) DORNER A.
XX (STOV/) STOVER J A.
XX (SLON/) SLONI D K.
XX Twine NC, Burczynski ME, Trepicchio WL, Dorner A, Stover JA;
PI Sloni DK;
XX WPI; 2004-460799/43.
XX Diagnosing non-blood disease such as solid tumor, involves comparing
PT differential expression profile of specific genes in peripheral blood
PT sample of subject with reference expression profile of specific genes.
XX Disclosure; SEQ ID NO 1321; 350pp; English.
XX The invention relate to a method of diagnosing (M1) non-blood disease
CC such as solid tumor by providing peripheral blood sample of human having
CC non-blood disease, and comparing an expression profile of specific genes
CC in the peripheral blood sample to reference expression profile of the
CC genes, where each of the genes is differentially expressed in peripheral
CC blood mononuclear cells (PBMCs) of patients having the disease as
CC compared to PBMCs of normal humans. The method is useful for diagnosing
CC non-blood disease such as solid tumor. The solid tumor is chosen from
CC renal cell carcinoma (RCC), prostate cancer and head/neck cancer. The
CC peripheral blood sample comprises enriched PBMCs. The peripheral blood
CC sample is a whole blood sample (claimed). (M1) is useful for identifying
CC genes that are differentially expressed in peripheral blood samples
CC isolated at different stages of progression, development or treatment of
CC RCC and/or other solid tumors. This sequence corresponds to a probe to
CC detect a gene that is differentially expressed and detected by the method
CC of the invention.
XX Sequence 25 BP; 4 A; 4 C; 7 G; 10 T; 0 U; 0 Other;
SQ
Query Match 1.5%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1397 AGATGTGATGTTGCTTTTGACCT 1421
Db 1 AGATGTGATGTTGCTTTTGACCT 25
RESULT 11
ADP14587
ID ADP14587 standard; DNA; 25 BP.
XX AC ADP14587;
XX DT 26-AUG-2004 (first entry)
XX Renal cell carcinoma differentially expressed gene probe #992.
DE ss; diagnosis; non-blood disease; solid tumor; gene expression;
KW peripheral blood mononuclear cell; renal cell carcinoma; prostate cancer;
KW head/neck cancer; differential expression; probe.
XX Homo sapiens.
XX

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PN WO2004048933-A2.
XX 10-JUN-2004.
XX 21-NOV-2003; 2003WO-US037481.
XX 21-NOV-2002; 2002US-0427982P.
XX 03-APR-2003; 2003US-0459782P.
XX (AMHP ) WYETH.
XX (TWIN/) TWINE N C.
XX (BURC/) BURCZYNSKI M E.
XX (TREP/) TREPICCHIO W L.
XX (DORN/) DORNER A.
XX (STOV/) STOVER J A.
XX (SLON/) SLONI D K.
XX Twine NC, Burczynski ME, Trepicchio WL, Dorner A, Stover JA;
PI Sloni DK;
XX WPI; 2004-460799/43.
XX Diagnosing non-blood disease such as solid tumor, involves comparing
PT differential expression profile of specific genes in peripheral blood
PT sample of subject with reference expression profile of specific genes.
XX Disclosure; SEQ ID NO 1323; 350pp; English.
XX The invention relate to a method of diagnosing (M1) non-blood disease
CC such as solid tumor by providing peripheral blood sample of human having
CC non-blood disease, and comparing an expression profile of specific genes
CC in the peripheral blood sample to reference expression profile of the
CC genes, where each of the genes is differentially expressed in peripheral
CC blood mononuclear cells (PBMCs) of patients having the disease as
CC compared to PBMCs of normal humans. The method is useful for diagnosing
CC non-blood disease such as solid tumor. The solid tumor is chosen from
CC renal cell carcinoma (RCC), prostate cancer and head/neck cancer. The
CC peripheral blood sample comprises enriched PBMCs. The peripheral blood
CC sample is a whole blood sample (claimed). (M1) is useful for identifying
CC genes that are differentially expressed in peripheral blood samples
CC isolated at different stages of progression, development or treatment of
CC RCC and/or other solid tumors. This sequence corresponds to a probe to
CC detect a gene that is differentially expressed and detected by the method
CC of the invention.
XX Sequence 25 BP; 8 A; 7 C; 6 G; 4 T; 0 U; 0 Other;
SQ Query Match 1.5%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1474 AGAGAGCTCTGCACGTCACCAAGTA 1498
DB 1 AGAGAGCTCTGCACGTCACCAAGTA 25
RESULT 12
ADP14582
ID ADP14582 standard; DNA; 25 BP.
XX ADP14582;
XX 26-AUG-2004 (first entry)
XX Renal cell carcinoma differentially expressed gene probe #987.
XX ss; diagnosis; non-blood disease; solid tumor; gene expression;
KW peripheral blood mononuclear cell; renal cell carcinoma; prostate cancer;
KW head/neck cancer; differential expression; probe.
XX Homo sapiens.
XX WO2004048933-A2.
PN
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XX 10-JUN-2004.
XX 21-NOV-2003; 2003WO-US037481.
XX 21-NOV-2002; 2002US-0427982P.
XX 03-APR-2003; 2003US-0459782P.
XX (AMHP ) WYETH.
XX (TWIN/) TWINE N C.
XX (BURC/) BURCZYNSKI M E.
XX (TREP/) TREPICCHIO W L.
XX (DORN/) DORNER A.
XX (STOV/) STOVER J A.
XX (SLON/) SLONI D K.
XX Twine NC, Burczynski ME, Trepicchio WL, Dorner A, Stover JA;
PI Sloni DK;
XX WPI; 2004-460799/43.
XX Diagnosing non-blood disease such as solid tumor, involves comparing
PT differential expression profile of specific genes in peripheral blood
PT sample of subject with reference expression profile of specific genes.
XX Disclosure; SEQ ID NO 1318; 350pp; English.
XX The invention relate to a method of diagnosing (M1) non-blood disease
CC such as solid tumor by providing peripheral blood sample of human having
CC non-blood disease, and comparing an expression profile of specific genes
CC in the peripheral blood sample to reference expression profile of the
CC genes, where each of the genes is differentially expressed in peripheral
CC blood mononuclear cells (PBMCs) of patients having the disease as
CC compared to PBMCs of normal humans. The method is useful for diagnosing
CC non-blood disease such as solid tumor. The solid tumor is chosen from
CC renal cell carcinoma (RCC), prostate cancer and head/neck cancer. The
CC peripheral blood sample comprises enriched PBMCs. The peripheral blood
CC sample is a whole blood sample (claimed). (M1) is useful for identifying
CC genes that are differentially expressed in peripheral blood samples
CC isolated at different stages of progression, development or treatment of
CC RCC and/or other solid tumors. This sequence corresponds to a probe to
CC detect a gene that is differentially expressed and detected by the method
CC of the invention.
XX Sequence 25 BP; 4 A; 5 C; 7 G; 9 T; 0 U; 0 Other;
SQ Query Match 1.5%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1262 GGTCGTGAAGCTCTTTGACTCTGAT 1286
DB 1 GGTCGTGAAGCTCTTTGACTCTGAT 25
RESULT 13
ADP14584
ID ADP14584 standard; DNA; 25 BP.
XX ADP14584;
XX 26-AUG-2004 (first entry)
XX Renal cell carcinoma differentially expressed gene probe #989.
XX ss; diagnosis; non-blood disease; solid tumor; gene expression;
KW peripheral blood mononuclear cell; renal cell carcinoma; prostate cancer;
KW head/neck cancer; differential expression; probe.
XX Homo sapiens.
XX WO2004048933-A2.
PN
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PD 10-JUN-2004.
XX
XX 21-NOV-2003; 2003WO-US037481.
XX
XX 21-NOV-2002; 2002US-0427982P.
XX
XX 03-APR-2003; 2003US-0459782P.
XX
XX (AMHP ) WYETH.
PA (TWIN/) TWINE N C.
PA (BURC/) BURCZYNSKI M E.
PA (TREP/) TREPICCHIO W L.
PA (DORN/) DORNER A.
PA (STOV/) STOVER J A.
PA (SLON/) SLONI D K.
XX
XX Twine NC, Burczynski ME, Trepicchio WL, Dorner A, Stover JA;
PI Sloni DK;
XX
XX WPI; 2004-460799/43.
XX
XX Diagnosing non-blood disease such as solid tumor, involves comparing
PT differential expression profile of specific genes in peripheral blood
PT sample of subject with reference expression profile of specific genes.
XX
XX Disclosure; SEQ ID NO 1320; 350pp; English.
XX
XX The invention relate to a method of diagnosing (M1) non-blood disease
CC such as solid tumor by providing peripheral blood sample of human having
CC non-blood disease, and comparing an expression profile of specific genes
CC in the peripheral blood sample to reference expression profile of the
CC genes, where each of the genes is differentially expressed in peripheral
CC blood mononuclear cells (PBMCs) of patients having the disease as
CC compared to PBMCs of normal humans. The method is useful for diagnosing
CC non-blood disease such as solid tumor. The solid tumor is chosen from
CC renal cell carcinoma (RCC), prostate cancer and head/neck cancer. The
CC peripheral blood sample comprises enriched PBMCs. The peripheral blood
CC sample is a whole blood sample (claimed). (M1) is useful for identifying
CC genes that are differentially expressed in peripheral blood samples
CC isolated at different stages of progression, development or treatment of
CC RCC and/or other solid tumors. This sequence corresponds to a probe to
CC detect a gene that is differentially expressed and detected by the method
CC of the invention.
XX
XX Sequence 25 BP; 4 A; 8 C; 4 G; 9 T; 0 U; 0 Other;
SQ
Query Match 1.5%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1274 CTTTGACTCTGATCCCATCACTGTG 1298
Db 1 CTTTGACTCTGATCCCATCACTGTG 25
RESULT 14
ADP14586
ID ADP14586 standard; DNA; 25 BP.
XX
XX ADP14586;
AC
XX
XX 26-AUG-2004 (first entry)
DT
XX
XX Renal cell carcinoma differentially expressed gene probe #991.
DE
XX
XX ss; diagnosis; non-blood disease; solid tumor; gene expression;
KW peripheral blood mononuclear cell; renal cell carcinoma; prostate cancer;
KW head/neck cancer; differential expression; probe.
XX
XX Homo sapiens.
OS
XX
XX WO2004048933-A2.
PN
XX
XX 10-JUN-2004.
PD

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XX 21-NOV-2003; 2003WO-US037481.
XX
XX 21-NOV-2002; 2002US-0427982P.
XX
XX 03-APR-2003; 2003US-0459782P.
XX
XX (AMHP ) WYETH.
PA (TWIN/) TWINE N C.
PA (BURC/) BURCZYNSKI M E.
PA (TREP/) TREPICCHIO W L.
PA (DORN/) DORNER A.
PA (STOV/) STOVER J A.
PA (SLON/) SLONI D K.
XX
XX Twine NC, Burczynski ME, Trepicchio WL, Dorner A, Stover JA;
PI Sloni DK;
XX
XX WPI; 2004-460799/43.
XX
XX Diagnosing non-blood disease such as solid tumor, involves comparing
PT differential expression profile of specific genes in peripheral blood
PT sample of subject with reference expression profile of specific genes.
XX
XX Disclosure; SEQ ID NO 1322; 350pp; English.
XX
XX The invention relate to a method of diagnosing (M1) non-blood disease
CC such as solid tumor by providing peripheral blood sample of human having
CC non-blood disease, and comparing an expression profile of specific genes
CC in the peripheral blood sample to reference expression profile of the
CC genes, where each of the genes is differentially expressed in peripheral
CC blood mononuclear cells (PBMCs) of patients having the disease as
CC compared to PBMCs of normal humans. The method is useful for diagnosing
CC non-blood disease such as solid tumor. The solid tumor is chosen from
CC renal cell carcinoma (RCC), prostate cancer and head/neck cancer. The
CC peripheral blood sample comprises enriched PBMCs. The peripheral blood
CC sample is a whole blood sample (claimed). (M1) is useful for identifying
CC genes that are differentially expressed in peripheral blood samples
CC isolated at different stages of progression, development or treatment of
CC RCC and/or other solid tumors. This sequence corresponds to a probe to
CC detect a gene that is differentially expressed and detected by the method
CC of the invention.
XX
XX Sequence 25 BP; 7 A; 9 C; 6 G; 3 T; 0 U; 0 Other;
SQ
Query Match 1.5%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1470 CCAGAGAGAGCTCTGCAGTCACCA 1494
Db 1 CCAGAGAGAGCTCTGCAGTCACCA 25
RESULT 15
ADP14588
ID ADP14588 standard; DNA; 25 BP.
XX
XX ADP14588;
AC
XX
XX 26-AUG-2004 (first entry)
DT
XX
XX Renal cell carcinoma differentially expressed gene probe #993.
DE
XX
XX ss; diagnosis; non-blood disease; solid tumor; gene expression;
KW peripheral blood mononuclear cell; renal cell carcinoma; prostate cancer;
KW head/neck cancer; differential expression; probe.
XX
XX Homo sapiens.
OS
XX
XX WO2004048933-A2.
PN
XX
XX 10-JUN-2004.
PD

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PF 21-NOV-2003; 2003WO-US037481.
XX
PR 21-NOV-2002; 2002US-0427982P.
PR 03-APR-2003; 2003US-0459782P.
XX
XX (AMHP ) WYETH.
PA (TWIN/) TWINE N C.
PA (BURC/) BURCZYNSKI M E.
PA (TREP/) TREPICCHIO W L.
PA (DORN/) DORNER A.
PA (STOV/) STOVER J A.
PA (SLOW/) SLONI D K.
XX
XX Twine NC, Burczynski ME, Trepicchio WL, Dorner A, Stover JA;
PI Sloni DK;
XX
XX WPI; 2004-460799/43.
XX
XX Diagnosing non-blood disease such as solid tumor, involves comparing
PT differential expression profile of specific genes in peripheral blood
PT sample of subject with reference expression profile of specific genes.
XX
XX Disclosure; SEQ ID NO 1324; 350pp; English.
XX
XX The invention relate to a method of diagnosing (M1) non-blood disease
CC such as solid tumor by providing peripheral blood sample of human having
CC non-blood disease, and comparing an expression profile of specific genes
CC in the peripheral blood sample to reference expression profile of the
CC genes, where each of the genes is differentially expressed in peripheral
CC blood mononuclear cells (PBMCs) of patients having the disease as
CC compared to PBMCs of normal humans. The method is useful for diagnosing
CC non-blood disease such as solid tumor. The solid tumor is chosen from
CC renal cell carcinoma (RCC), prostate cancer and head/neck cancer. The
CC peripheral blood sample comprises enriched PBMCs. The peripheral blood
CC sample is a whole blood sample (claimed). (M1) is useful for identifying
CC genes that are differentially expressed in peripheral blood samples
CC isolated at different stages of progression, development or treatment of
CC RCC and/or other solid tumors. This sequence corresponds to a probe to
CC detect a gene that is differentially expressed and detected by the method
CC of the invention.
XX
XX Sequence 25 BP; 7 A; 9 C; 5 G; 4 T; 0 U; 0 Other;
SQ
Query Match 1.5%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1480 CTCTGCACGTCCACCAAGTACCAGG 1504
DB 1 CTCTGCACGTCCACCAAGTACCAGG 25
RESULT 16
ADP14592
ID ADP14592 standard; DNA; 25 BP.
AC ADP14592;
XX
XX 26-AUG-2004 (first entry)
DT
XX Renal cell carcinoma differentially expressed gene probe #997.
DE
XX ss; diagnosis; non-blood disease; solid tumor; gene expression;
KW peripheral blood mononuclear cell; renal cell carcinoma; prostate cancer;
KW head/neck cancer; differential expression; probe.
XX
XX Homo sapiens.
OS
XX WO2004048933-A2.
PN
XX 10-JUN-2004.
PD
XX 21-NOV-2003; 2003WO-US037481.
PF

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XX 21-NOV-2002; 2002US-0427982P.
PR 03-APR-2003; 2003US-0459782P.
XX
XX (AMHP ) WYETH.
PA (TWIN/) TWINE N C.
PA (BURC/) BURCZYNSKI M E.
PA (TREP/) TREPICCHIO W L.
PA (DORN/) DORNER A.
PA (STOV/) STOVER J A.
PA (SLOW/) SLONI D K.
XX
XX Twine NC, Burczynski ME, Trepicchio WL, Dorner A, Stover JA;
PI Sloni DK;
XX
XX WPI; 2004-460799/43.
XX
XX Diagnosing non-blood disease such as solid tumor, involves comparing
PT differential expression profile of specific genes in peripheral blood
PT sample of subject with reference expression profile of specific genes.
XX
XX Disclosure; SEQ ID NO 1328; 350pp; English.
XX
XX The invention relate to a method of diagnosing (M1) non-blood disease
CC such as solid tumor by providing peripheral blood sample of human having
CC non-blood disease, and comparing an expression profile of specific genes
CC in the peripheral blood sample to reference expression profile of the
CC genes, where each of the genes is differentially expressed in peripheral
CC blood mononuclear cells (PBMCs) of patients having the disease as
CC compared to PBMCs of normal humans. The method is useful for diagnosing
CC non-blood disease such as solid tumor. The solid tumor is chosen from
CC renal cell carcinoma (RCC), prostate cancer and head/neck cancer. The
CC peripheral blood sample comprises enriched PBMCs. The peripheral blood
CC sample is a whole blood sample (claimed). (M1) is useful for identifying
CC genes that are differentially expressed in peripheral blood samples
CC isolated at different stages of progression, development or treatment of
CC RCC and/or other solid tumors. This sequence corresponds to a probe to
CC detect a gene that is differentially expressed and detected by the method
CC of the invention.
XX
XX Sequence 25 BP; 5 A; 8 C; 5 G; 7 T; 0 U; 0 Other;
SQ
Query Match 1.5%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1563 TAACACTCGACTCTGCTGCTCATGG 1587
DB 1 TAACACTCGACTCTGCTGCTCATGG 25
RESULT 17
ADP14579
ID ADP14579 standard; DNA; 25 BP.
XX
XX ADP14579;
XX
XX 26-AUG-2004 (first entry)
DT
XX Renal cell carcinoma differentially expressed gene probe #984.
DE
XX ss; diagnosis; non-blood disease; solid tumor; gene expression;
KW peripheral blood mononuclear cell; renal cell carcinoma; prostate cancer;
KW head/neck cancer; differential expression; probe.
XX
XX Homo sapiens.
OS
XX WO2004048933-A2.
PN
XX 10-JUN-2004.
PD
XX 21-NOV-2003; 2003WO-US037481.
PF

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```
PR 21-NOV-2002; 2002US-0427982P.
PR 03-APR-2003; 2003US-0459782P.
XX (AMHP ) WYETH.
PA (TWIN/) TWINE N C.
PA (BURC/) BURCZYNSKI M E.
PA (TREP/) TREPICCHIO W L.
PA (DORN/) DORNER A.
PA (STOV/) STOVER J A.
PA (SLON/) SLONI D K.
XX Twine NC, Burczynski ME, Trepicchio WL, Dornier A, Stover JA;
PI Sloni DK;
XX WPI; 2004-460799/43.
XX Diagnosing non-blood disease such as solid tumor, involves comparing
PT differential expression profile of specific genes in peripheral blood
PT sample of subject with reference expression profile of specific genes.
XX Disclosure; SEQ ID NO 1315; 350pp; English.
XX The invention relate to a method of diagnosing (M1) non-blood disease
CC such as solid tumor by providing peripheral blood sample of human having
CC non-blood disease, and comparing an expression profile of specific genes
CC in the peripheral blood sample to reference expression profile of the
CC genes, where each of the genes is differentially expressed in peripheral
CC blood mononuclear cells (PBMCs) of patients having the disease as
CC compared to PBMCs of normal humans. The method is useful for diagnosing
CC non-blood disease such as solid tumor. The solid tumor is chosen from
CC renal cell carcinoma (RCC), prostate cancer and head/neck cancer. The
CC peripheral blood sample comprises enriched PBMCs. The peripheral blood
CC sample is a whole blood sample (claimed). (M1) is useful for identifying
CC genes that are differentially expressed in peripheral blood samples
CC isolated at different stages of progression, development or treatment of
CC RCC and/or other solid tumors. This sequence corresponds to a probe to
CC detect a gene that is differentially expressed and detected by the method
CC of the invention.
XX SQ Sequence 25 BP; 8 A; 6 C; 7 G; 4 T; 0 U; 0 Other;
Query Match 1.5%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1177 AAGGCGAAGACCAGTACTATCTGCG 1201
| | | | | | | | | | | | | | | | | | | | |
Db 1 AAGGCGAAGACCAGTACTATCTGCG 25
RESULT 18
ADP14581
ID ADP14581 standard; DNA; 25 BP.
AC ADP14581;
XX 26-AUG-2004 (first entry)
XX Renal cell carcinoma differentially expressed gene probe #986.
XX ss; diagnosis; non-blood disease; solid tumor; gene expression;
KW peripheral blood mononuclear cell; renal cell carcinoma; prostate cancer;
KW head/neck cancer; differential expression; probe.
XX Homo sapiens.
XX OS
XX WO2004048933-A2.
XX 10-JUN-2004.
XX 21-NOV-2003; 2003WO-US037481.
XX 21-NOV-2002; 2002US-0427982P.
PR
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PR 03-APR-2003; 2003US-0459782P.
XX (AMHP ) WYETH.
PA (TWIN/) TWINE N C.
PA (BURC/) BURCZYNSKI M E.
PA (TREP/) TREPICCHIO W L.
PA (DORN/) DORNER A.
PA (STOV/) STOVER J A.
PA (SLON/) SLONI D K.
XX Twine NC, Burczynski ME, Trepicchio WL, Dornier A, Stover JA;
PI Sloni DK;
XX WPI; 2004-460799/43.
XX Diagnosing non-blood disease such as solid tumor, involves comparing
PT differential expression profile of specific genes in peripheral blood
PT sample of subject with reference expression profile of specific genes.
XX Disclosure; SEQ ID NO 1317; 350pp; English.
XX The invention relate to a method of diagnosing (M1) non-blood disease
CC such as solid tumor by providing peripheral blood sample of human having
CC non-blood disease, and comparing an expression profile of specific genes
CC in the peripheral blood sample to reference expression profile of the
CC genes, where each of the genes is differentially expressed in peripheral
CC blood mononuclear cells (PBMCs) of patients having the disease as
CC compared to PBMCs of normal humans. The method is useful for diagnosing
CC non-blood disease such as solid tumor. The solid tumor is chosen from
CC renal cell carcinoma (RCC), prostate cancer and head/neck cancer. The
CC peripheral blood sample comprises enriched PBMCs. The peripheral blood
CC sample is a whole blood sample (claimed). (M1) is useful for identifying
CC genes that are differentially expressed in peripheral blood samples
CC isolated at different stages of progression, development or treatment of
CC RCC and/or other solid tumors. This sequence corresponds to a probe to
CC detect a gene that is differentially expressed and detected by the method
CC of the invention.
XX SQ Sequence 25 BP; 4 A; 4 C; 9 G; 8 T; 0 U; 0 Other;
Query Match 1.5%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1256 TGAGGTGCTCGTGAAGCTCTTTGAC 1280
| | | | | | | | | | | | | | | | | | | | |
Db 1 TGAGGTGCTCGTGAAGCTCTTTGAC 25
RESULT 19
ADP14591
ID ADP14591 standard; DNA; 25 BP.
AC ADP14591;
XX 26-AUG-2004 (first entry)
XX Renal cell carcinoma differentially expressed gene probe #996.
XX ss; diagnosis; non-blood disease; solid tumor; gene expression;
KW peripheral blood mononuclear cell; renal cell carcinoma; prostate cancer;
KW head/neck cancer; differential expression; probe.
XX Homo sapiens.
XX OS
XX WO2004048933-A2.
XX 10-JUN-2004.
XX 21-NOV-2003; 2003WO-US037481.
XX 21-NOV-2002; 2002US-0427982P.
PR 03-APR-2003; 2003US-0459782P.
PR
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XX (AMHP ) WYETH.  
PA (TWIN/) TWINE N C.  
PA (BURC/) BURCZYNSKI M E.  
PA (TREP/) TREPICCHIO W L.  
PA (DORN/) DORNER A.  
PA (STOV/) STOVER J A.  
PA (SLOW/) SLONI D K.  
XX  
XX Twine NC, Burczynski ME, Trepicchio WL, Dorner A, Stover JA;  
PI Sloni DK;  
XX WPI; 2004-460799/43.  
XX  
XX Diagnosing non-blood disease such as solid tumor, involves comparing  
PT differential expression profile of specific genes in peripheral blood  
PT sample of subject with reference expression profile of specific genes.  
XX  
XX Disclosure; SEQ ID NO 1327; 350pp; English.  
XX  
XX The invention relate to a method of diagnosing (M1) non-blood disease  
CC such as solid tumor by providing peripheral blood sample of human having  
CC non-blood disease, and comparing an expression profile of specific genes  
CC in the peripheral blood sample to reference expression profile of the  
CC genes, where each of the genes is differentially expressed in peripheral  
CC blood mononuclear cells (PBMCs) of patients having the disease as  
CC compared to PBMCs of normal humans. The method is useful for diagnosing  
CC non-blood disease such as solid tumor. The solid tumor is chosen from  
CC renal cell carcinoma (RCC), prostate cancer and head/neck cancer. The  
CC peripheral blood sample comprises enriched PBMCs. The peripheral blood  
CC sample is a whole blood sample (claimed). (M1) is useful for identifying  
CC genes that are differentially expressed in peripheral blood samples  
CC isolated at different stages of progression, development or treatment of  
CC RCC and/or other solid tumors. This sequence corresponds to a probe to  
CC detect a gene that is differentially expressed and detected by the method  
CC of the invention.  
XX  
XX Sequence 25 BP; 5 A; 9 C; 4 G; 7 T; 0 U; 0 Other;  
SQ  
Query Match 1.5%; Score 25; DB 1; Length 25;  
Best Local Similarity 100.0%; Pred. No. 19;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1562 CTAACACTCGACTCTGCTGCTCATG 1586  
Db 1 CTAACACTCGACTCTGCTGCTCATG 25  
RESULT 20  
ABN99658/C  
ID ABN99658 standard; DNA; 23 BP.  
XX  
XX ABN99658;  
XX  
XX 16-AUG-2002 (first entry)  
XX  
XX Human clusterin PCR primer 2.  
XX  
XX Human; antisense inhibition; antisense oligonucleotide; clusterin;  
KW hypercholesterolaemia; cardiovascular disorder; ss; PCR; primer;  
KW hyperproliferative disorder; hyperlipidemic disorder.  
XX  
XX Homo sapiens.  
XX  
XX WO200222635-A1.  
XX  
XX 21-MAR-2002.  
XX  
XX 10-SEP-2001; 2001WO-US028235.  
XX  
XX 11-SEP-2000; 2000US-00659791.  
XX  
XX (ISIS-) ISIS PHARM INC.

XX Monia BP, Freier SM;  
XX WPI; 2002-404805/43.  
XX  
XX Novel antisense compound targeted to nucleic acid molecule encoding  
PT clusterin, useful for treating animal having disease associated with  
PT clusterin such as hyperlipidemic disorder, cardiovascular disorder.  
XX  
XX Example 13; Page 80; 125pp; English.  
XX  
XX The invention comprises antisense oligonucleotides that are capable of  
CC inhibiting expression of the human clusterin gene. The antisense  
CC oligonucleotides of the invention are useful for inhibiting the  
CC expression of clusterin in cells. The antisense oligonucleotides are also  
CC useful for treating an animal with a disease or condition associated with  
CC clusterin (e.g. hypercholesterolaemia; cardiovascular disorders;  
CC hyperproliferative disorders; and hyperlipidemic disorders). The present  
CC DNA sequence represents a PCR primer used to amplify the human clusterin  
CC gene  
XX  
XX Sequence 23 BP; 5 A; 6 C; 5 G; 7 T; 0 U; 0 Other;  
SQ  
Query Match 1.4%; Score 23; DB 1; Length 23;  
Best Local Similarity 100.0%; Pred. No. 28;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 789 CTTGAGATGATACACGAGGCTCA 811  
Db 23 CTTGAGATGATACACGAGGCTCA 1  
RESULT 21  
ACF36411/C  
ID ACF36411 standard; DNA; 23 BP.  
XX  
XX ACF36411;  
XX  
XX 18-DEC-2003 (first entry)  
XX  
XX Human TRPM-2 cDNA amplifying RT-PCR antisense primer.  
XX  
XX TRPM-2; testosterone-repressed prostate message-2; cytostatic; RT-PCR;  
KW androgen; prostate cancer; anti-apoptotic protein; antisense; primer; ss.  
XX  
XX Homo sapiens.  
XX  
XX WO2003072591-A1.  
XX  
XX 04-SEP-2003.  
XX  
XX 20-FEB-2003; 2003WO-US005305.  
XX  
XX 22-FEB-2002; 2002US-00080794.  
XX  
XX (UYBR-) UNIV BRITISH COLUMBIA.  
XX  
XX Gleave M, Rennie PS, Miyake H, Nelson C, Monia BP;  
XX WPI; 2003-689981/65.  
XX  
XX New modified antisense oligonucleotide, useful particularly for treating  
PT prostatic cancer, inhibits the testosterone-repressed prostate message-2.  
XX  
XX Example 13; Page 20; 44pp; English.  
XX  
XX The invention relates to a compound consisting of an oligonucleotide with  
CC a phosphorothioate backbone throughout, in which: (a) sugars on  
CC nucleotide residues 1-4 and 18-21 are 2'-O-methoxyethyl modified, and the  
CC remaining nucleotides 5-17 are 2'-deoxy; and (b) the cytosines at  
CC positions 1, 4 and 19 are 5-methylated. Oligonucleotide shown in sequence  
CC ACF36398 (I) is used: (a) to delay progression of androgen-sensitive  
CC prostatic cancer cells to the androgen-independent state, in vivo or in

CC vitro; (b) to treat prostatic cancer (after initially withdrawing  
CC androgens to induce apoptosis); and (c) to increase sensitivity of cancer  
CC cells (prostatic, renal, non-small cell lung, urothelial transitional,  
CC ovarian and some breast cancer cells) that express abnormal levels of  
CC TRPM-2 to chemotherapy or radiation. The modifications present in (I)  
CC increase stability in vivo and activity (both in vivo or in vitro) and  
CC result in a synergistic increase in effect when (I) is used with  
CC chemotherapeutic agents or other antisense oligonucleotides directed  
CC against other antiapoptotic genes. The present sequence represents a RT-  
CC PCR primer for amplifying the anti-apoptotic protein TRPM-2 (testosterone  
CC -repressed prostate message-2) cDNA  
XX  
XX SQ Sequence 23 BP; 7 A; 8 C; 4 G; 4 T; 0 U; 0 Other;

Query Match 1.4%; Score 23; DB 1; Length 23;  
Best Local Similarity 100.0%; Pred. No. 28;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 957 AAGTCCGGGAGATCTTGTCTGT 979

Db 23 AAGTCCGGGAGATCTTGTCTGT 1

#### RESULT 22

ACF36410  
ID ACF36410 standard; DNA; 23 BP.

XX ACF36410;

XX 18-DEC-2003 (first entry)

XX Human TRPM-2 cDNA amplifying RT-PCR sense primer.

XX TRPM-2; testosterone-repressed prostate message-2; cytosolic; RT-PCR;  
KW androgen; prostate cancer; anti-apoptotic protein; antisense; primer; ss.  
XX Homo sapiens.

XX WO2003072591-A1.

XX 04-SEP-2003.

XX 20-FEB-2003; 2003WO-US005305.

XX 22-FEB-2002; 2002US-00080794.

XX (UYBR-) UNIV BRITISH COLUMBIA.

XX Gleave M, Rennie PS, Miyake H, Nelson C, Monia BP;

XX WPI; 2003-689981/65.

XX New modified antisense oligonucleotide, useful particularly for treating  
PT prostatic cancer, inhibits the testosterone-repressed prostate message-2.

XX Example 13; Page 20; 44pp; English.

XX The invention relates to a compound consisting of an oligonucleotide with  
CC a phosphorothioate backbone throughout, in which: (a) sugars on  
CC nucleotide residues 1-4 and 18-21 are 2'-O-methoxyethyl modified, and the  
CC remaining nucleotides 5-17 are 2'-deoxy; and (b) the cytosines at  
CC positions 1, 4 and 19 are 5-methylated. Oligonucleotide shown in sequence  
CC ACF36398 (I) is used: (a) to delay progression of androgen-sensitive  
CC prostatic cancer cells to the androgen-independent state, in vivo or in  
CC vitro; (b) to treat prostatic cancer (after initially withdrawing  
CC androgens to induce apoptosis); and (c) to increase sensitivity of cancer  
CC cells (prostatic, renal, non-small cell lung, urothelial transitional,  
CC ovarian and some breast cancer cells) that express abnormal levels of  
CC TRPM-2 to chemotherapy or radiation. The modifications present in (I)  
CC increase stability in vivo and activity (both in vivo or in vitro) and  
CC result in a synergistic increase in effect when (I) is used with  
CC chemotherapeutic agents or other antisense oligonucleotides directed  
CC against other antiapoptotic genes. The present sequence represents a RT-

CC PCR primer for amplifying the anti-apoptotic protein TRPM-2 (testosterone  
CC -repressed prostate message-2) cDNA

XX SQ Sequence 23 BP; 11 A; 3 C; 4 G; 5 T; 0 U; 0 Other;

Query Match 1.4%; Score 23; DB 1; Length 23;

Best Local Similarity 100.0%; Pred. No. 28;

Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 177 AAGGAAATTCAAAATGCTGTCAA 199

Db 1 AAGGAAATTCAAAATGCTGTCAA 23

#### RESULT 23

ADM83082/c

ID ADM83082 standard; DNA; 23 BP.

XX ADM83082;

XX 03-JUN-2004 (first entry)

XX Human TRPM-2 amplifying antisense RT-PCR primer.

XX Testosterone-repressed prostate message-2; TRPM-2; chemo-sensitivity;  
KW radiation-sensitivity; prostate cancer; bladder cancer; ovarian cancer;  
KW lung cancer; renal cell carcinoma; RCC; antisense gene therapy; human;  
KW reverse transcription; RT-PCR; primer; ss.

XX Homo sapiens.

XX US2003158130-A1.

XX 21-AUG-2003.

XX 28-SEP-2001; 2001US-00967726.

XX 25-FEB-2000; 2000WO-US004875.

XX 28-SEP-2000; 2000US-0236301P.

XX 10-AUG-2001; 2001US-00913325.

XX (GLEA/) GLEAVE M.

XX (RENN/) RENNIE P S.

XX (MIYA/) MIYAKE H.

XX (NELS/) NELSON C.

XX (ZELL/) ZELLWEGER T.

XX Gleave M, Rennie PS, Miyake H, Nelson C, Zellweiger T;

XX WPI; 2003-778017/73.

XX Enhancing the chemo-sensitivity or radiation-sensitivity of cancer cells  
PT that expresses testosterone-repressed prostate message-2 (TRPM-2)

PT comprises administering a composition that inhibits expression of TRPM-2.

XX Disclosure; SEQ ID NO 17; 14pp; English.

XX The present invention provides a method for treating cancer in which  
CC cancer cells express testosterone-repressed prostate message-2 (TRPM-2).  
CC The invention is useful for enhancing the chemo-sensitivity or radiation-  
CC sensitivity of cancer cells for treating cancer such as prostate cancer,  
CC bladder cancer, ovarian cancer, lung cancer and renal cell carcinoma  
CC (RCC). The invention is also useful in antisense gene therapy. The  
CC present sequence is human testosterone-repressed prostate message-2 (TRPM  
CC -2) amplifying RT-PCR primer. The primer is used in the exemplification  
CC of the invention.

XX SQ Sequence 23 BP; 7 A; 8 C; 4 G; 4 T; 0 U; 0 Other;

Query Match

Best Local Similarity 1.4%; Score 23; DB 1; Length 23;

Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
QY 957 AAGTGGCGGAGATCTTGTGTGT 979
DB 23 AAGTGGCGGAGATCTTGTGTGT 1

RESULT 24
ADM83081
ID ADM83081 standard; DNA; 23 BP.
XX
AC ADM83081;
XX
XX 03-JUN-2004 (first entry)
XX
XX Human TRPM-2 amplifying sense RT-PCR primer.
XX
XX Testosterone-repressed prostate message-2; TRPM-2; chemo-sensitivity;
XX radiation-sensitivity; prostate cancer; bladder cancer; ovarian cancer;
XX lung cancer; renal cell carcinoma; RCC; antisense gene therapy; human;
XX reverse transcription; RT-PCR; primer; ss.
XX
OS Homo sapiens.
XX
XX US2003158130-A1.
XX
XX 21-AUG-2003.
XX
XX 28-SEP-2001; 2001US-00967726.
XX
XX 25-FEB-2000; 2000WO-US004875.
XX
XX 28-SEP-2000; 2000US-0236301P.
XX
XX 10-AUG-2001; 2001US-00913325.
XX
XX (GLEA/) GLEAVE M.
XX (RENN/) RENNIE P S.
XX (MIYA/) MIYAKE H.
XX (NELS/) NELSON C.
XX (ZELL/) ZELLWEGER T.
XX
XX Gleave M, Rennie PS, Miyake H, Nelson C, Zellweger T;
XX WPI; 2003-778017/73.
XX
XX Enhancing the chemo-sensitivity or radiation-sensitivity of cancer cells
XX that expresses testosterone-repressed prostate message-2 (TRPM-2)
XX comprises administering a composition that inhibits expression of TRPM-2.
XX
XX Disclosure; SEQ ID NO 16; 14pp; English.
XX
XX The present invention provides a method for treating cancer in which
XX cancer cells express testosterone-repressed prostate message-2 (TRPM-2).
XX The invention is useful for enhancing the chemo-sensitivity or radiation-
XX sensitivity of cancer cells for treating cancer such as prostate cancer,
XX bladder cancer, ovarian cancer, lung cancer and renal cell carcinoma
XX (RCC). The invention is also useful in antisense gene therapy. The
XX present sequence is human testosterone-repressed prostate message-2 (TRPM
XX -2) amplifying RT-PCR primer. The primer is used in the exemplification
XX of the invention.
XX
XX Sequence 23 BP; 11 A; 3 C; 4 G; 5 T; 0 U; 0 Other;
XX
XX Query Match 1.4%; Score 23; DB 1; Length 23;
XX Best Local Similarity 100.0%; Pred. No. 28;
XX Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 177 AAGGAATTCAAATGCTGTCAA 199
DB 1 AAGGAATTCAAATGCTGTCAA 23

RESULT 25
ADM70521
ID ADM70521 standard; cDNA; 23 BP.
XX
```

```
AC ADL70521;
XX
XX 20-MAY-2004 (first entry)
XX
XX Human clusterin target for RNAi.
XX
XX RNA interference; RNAi; short interfering RNA; siRNA; human; clusterin;
XX cytostatic; neuroprotective; nootropic; gene silencing; DNA-RNA hybrid;
XX ss.
XX
XX Homo sapiens.
XX
XX Synthetic.
XX
XX WO2004018676-A2.
XX
XX 04-MAR-2004.
XX
XX 21-AUG-2003; 2003WO-CA001277.
XX
XX 21-AUG-2002; 2002US-0405193P.
XX 03-SEP-2002; 2002US-0408152P.
XX 20-MAY-2003; 2003US-0472387P.
XX
XX (UYER-) UNIV BRITISH COLUMBIA.
XX
XX Jansen B, Gleave ME, Signaevsky M, Beraldi E, Trougakos IP;
XX Gonos ES;
XX
XX WPI; 2004-226852/21.
XX
XX New RNA molecule less than 49 bases and having a sequence effective to
XX mediate degradation or block translation of mRNA that is the
XX transcriptional product of a target gene, useful for treating Alzheimer's
XX disease or cancer.
XX
XX Example 6; SEQ ID NO 66; 63pp; English.
XX
XX The present sequence is a human clusterin cDNA target for a double-
XX stranded short interfering RNA (siRNA) of the invention to demonstrate
XX ADL70523. It was used in an example from the invention to demonstrate
XX clusterin gene silencing in PC-3 prostate cancer cells. Clusterin, also
XX known as testosterone-repressed prostate message-2 (TRPM-2) or sulfated
XX glycoprotein-2 (Sgp-2), is expressed in increased amounts by prostate
XX tumour cells following androgen withdrawal, and has also been shown to be
XX critical for neuritic toxicity in mouse models of Alzheimer's disease.
XX siRNAs of the invention can be used alone or in combination with other
XX chemotherapy or apoptosis inducing treatments for the treatment of
XX prostate cancer, sarcomas such as osteosarcoma, renal cell carcinoma,
XX breast cancer, bladder cancer, lung cancer, colon cancer, ovarian cancer,
XX anaplastic large cell lymphoma and melanoma, and also for the treatment
XX of Alzheimer's disease.
XX
XX Sequence 23 BP; 5 A; 5 C; 7 G; 6 T; 0 U; 0 Other;
XX
XX Query Match 1.4%; Score 23; DB 1; Length 23;
XX Best Local Similarity 100.0%; Pred. No. 28;
XX Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 46 GCATGATGAAGACTCTGCTGCTG 68
DB 1 GCATGATGAAGACTCTGCTGCTG 23

RESULT 26
ADL70512
ID ADL70512 standard; cDNA; 23 BP.
XX
XX ADL70512;
XX
XX 20-MAY-2004 (first entry)
XX
XX Human clusterin target for RNAi.
XX
```

```
KW RNA interference; RNAi; short interfering RNA; siRNA; human; clusterin;
KW cytosstatic; neuroprotective; nootropic; gene silencing; DNA-RNA hybrid;
KW ss.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO2004018676-A2.
XX
XX 04-MAR-2004.
XX
XX 21-AUG-2003; 2003WO-CA001277.
XX
XX 21-AUG-2002; 2002US-0405193P.
PR 03-SEP-2002; 2002US-0408152P.
PR 20-MAY-2003; 2003US-0472387P.
XX
XX (UYBR-) UNIV BRITISH COLUMBIA.
XX
XX Jansen B, Gleave ME, Signaevsky M, Beraldi E, Trougakos IP;
PI Gonos ES;
XX
XX WPI; 2004-226852/21.
XX
XX New RNA molecule less than 49 bases and having a sequence effective to
PT mediate degradation or block translation of mRNA that is the
PT transcriptional product of a target gene, useful for treating Alzheimer's
PT disease or cancer.
XX
XX Example 6; SEQ ID NO 57; 63pp; English.
XX
XX The present sequence is a human clusterin cDNA target for a double-
CC stranded short interfering RNA (siRNA) of the invention ADL70513-
CC ADL70514. It was used in an example from the invention to demonstrate
CC clusterin gene silencing in PC-3 prostate cancer cells. Clusterin, also
CC known as testosterone-repressed prostate message-2 (TRPM-2) or sulfated
CC glycoprotein-2 (SGP-2), is expressed in increased amounts by prostate
CC tumour cells following androgen withdrawal, and has also been shown to be
CC critical for neuritic toxicity in mouse models of Alzheimer's disease.
CC siRNAs of the invention can be used alone or in combination with other
CC chemotherapies or apoptosis inducing treatments for the treatment of
CC prostate cancer, sarcomas such as osteosarcoma, renal cell carcinoma,
CC breast cancer, bladder cancer, lung cancer, colon cancer, ovarian cancer,
CC anaplastic large cell lymphoma and melanoma, and also for the treatment
CC of Alzheimer's disease.
XX
XX Sequence 23 BP; 5 A; 9 C; 3 G; 6 T; 0 U; 0 Other;
SQ
Query Match 1.4%; Score 23; DB 1; Length 23;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 480 AACACAGAGCTCGCCCTTCTACTT 502
DB 1 AACACAGAGCTCGCCCTTCTACTT 23
RESULT 27
ADL70515
ID ADL70515 standard; cDNA; 23 BP.
XX
XX ADL70515;
XX
XX 20-MAY-2004 (first entry)
XX
XX Human clusterin target for RNAi.
XX
XX RNA interference; RNAi; short interfering RNA; siRNA; human; clusterin;
KW cytosstatic; neuroprotective; nootropic; gene silencing; DNA-RNA hybrid;
KW ss.
XX
XX Homo sapiens.
XX Synthetic.
OS
```

```
XX WO2004018676-A2.
XX
XX 04-MAR-2004.
XX
XX 21-AUG-2003; 2003WO-CA001277.
XX
XX 21-AUG-2002; 2002US-0405193P.
PR 03-SEP-2002; 2002US-0408152P.
PR 20-MAY-2003; 2003US-0472387P.
XX
XX (UYBR-) UNIV BRITISH COLUMBIA.
XX
XX Jansen B, Gleave ME, Signaevsky M, Beraldi E, Trougakos IP;
PI Gonos ES;
XX
XX WPI; 2004-226852/21.
XX
XX New RNA molecule less than 49 bases and having a sequence effective to
PT mediate degradation or block translation of mRNA that is the
PT transcriptional product of a target gene, useful for treating Alzheimer's
PT disease or cancer.
XX
XX Example 6; SEQ ID NO 60; 63pp; English.
XX
XX The present sequence is a human clusterin cDNA target for a double-
CC stranded short interfering RNA (siRNA) of the invention ADL70516-
CC ADL70517. It was used in an example from the invention to demonstrate
CC clusterin gene silencing in PC-3 prostate cancer cells. Clusterin, also
CC known as testosterone-repressed prostate message-2 (TRPM-2) or sulfated
CC glycoprotein-2 (SGP-2), is expressed in increased amounts by prostate
CC tumour cells following androgen withdrawal, and has also been shown to be
CC critical for neuritic toxicity in mouse models of Alzheimer's disease.
CC siRNAs of the invention can be used alone or in combination with other
CC chemotherapies or apoptosis inducing treatments for the treatment of
CC prostate cancer, sarcomas such as osteosarcoma, renal cell carcinoma,
CC breast cancer, bladder cancer, lung cancer, colon cancer, ovarian cancer,
CC anaplastic large cell lymphoma and melanoma, and also for the treatment
CC of Alzheimer's disease.
XX
XX Sequence 23 BP; 4 A; 9 C; 5 G; 5 T; 0 U; 0 Other;
SQ
Query Match 1.4%; Score 23; DB 1; Length 23;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 711 AAGTCCCGCATCGTCCGACGCTT 733
DB 1 AAGTCCCGCATCGTCCGACGCTT 23
RESULT 28
ADL70518
ID ADL70518 standard; cDNA; 23 BP.
XX
XX ADL70518;
XX
XX 20-MAY-2004 (first entry)
XX
XX Human clusterin target for RNAi.
XX
XX RNA interference; RNAi; short interfering RNA; siRNA; human; clusterin;
KW cytosstatic; neuroprotective; nootropic; gene silencing; DNA-RNA hybrid;
KW ss.
XX
XX Homo sapiens.
XX Synthetic.
XX
XX WO2004018676-A2.
XX
XX 04-MAR-2004.
XX
XX 21-AUG-2003; 2003WO-CA001277.
XX
XX
```

XX 21-AUG-2002; 2002US-0405193P.  
PR 03-SEP-2002; 2002US-0408152P.  
PR 20-MAY-2003; 2003US-0472387P.  
XX (UYBR-) UNIV BRITISH COLUMBIA.  
XX Jansen B, Gleave ME, Signaevsky M, Beraldi E, Trougakos IP;  
PI Gonos ES;  
XX WPI; 2004-226852/21.  
XX New RNA molecule less than 49 bases and having a sequence effective to  
PT mediate degradation or block translation of mRNA that is the  
PT transcriptional product of a target gene, useful for treating Alzheimer's  
PT disease or cancer.  
XX Example 6; SEQ ID NO 63; 63pp; English.  
XX The present sequence is a human clusterin cDNA target for a double-  
CC stranded short interfering RNA (siRNA) of the invention ADL70519-  
CC ADL70520. It was used in an example from the invention to demonstrate  
CC clusterin gene silencing in PC-3 prostate cancer cells. Clusterin, also  
CC known as testosterone-repressed prostate message-2 (TRPM-2) or sulfated  
CC glycoprotein-2 (SGP-2), is expressed in increased amounts by prostate  
CC tumour cells following androgen withdrawal, and has also been shown to be  
CC critical for neuritic toxicity in mouse models of Alzheimer's disease.  
CC siRNAs of the invention can be used alone or in combination with other  
CC chemotherapies or apoptosis inducing treatments for the treatment of  
CC prostate cancer, sarcomas such as osteosarcoma, renal cell carcinoma,  
CC breast cancer, bladder cancer, lung cancer, colon cancer, ovarian cancer,  
CC anaplastic large cell lymphoma and melanoma, and also for the treatment  
CC of Alzheimer's disease.  
XX Sequence 23 BP; 10 A; 4 C; 1 G; 8 T; 0 U; 0 Other;  
SQ Query Match 1.4%; Score 23; DB 1; Length 23;  
Best Local Similarity 100.0%; Pred. No. 28;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1613 AACTAATTCATTAATAACTGCTT 1635  
DB 1 AACTAATTCATTAATAACTGCTT 23  
RESULT 29  
AAT39500  
ID AAT39500 standard; DNA; 21 BP.  
AC AAT39500;  
XX 21-MAY-1997 (first entry)  
XX Chromosome 8p clusterin gene (CL1) specific primer (nt 2504-2524).  
XX Chromosome 8p; polymerase chain reaction; PCR; primer; CL1;  
KW clusterin gene; human; steroidogenesis; acute regulatory protein;  
KW regional mapping; confirmation; hStAR; ss.  
XX Synthetic.  
OS WO9629338-A1.  
XX WO9629338-A1.  
XX 26-SEP-1996.  
XX 22-MAR-1996; 96WO-US003896.  
XX 23-MAR-1995; 95US-00410540.  
XX (REGC ) UNIV CALIFORNIA.  
PA (UYPE-) UNIV PENNSYLVANIA.  
XX Miller WL, Lin D, Strauss JF;

XX WPI; 1996-443130/44.  
XX Isolated human steroidogenesis acute regulatory protein gene - used for  
PT detection of mutation(s) of this gene that cause congenital lipid  
PT adrenal hyperplasia.  
XX Example 7; Page 51; 89pp; English.  
XX The present sequence is a human chromosome 8p clusterin gene (CL1)  
CC specific PCR primer, which was used in the confirmation of the regional  
CC mapping of the human steroidogenesis acute regulatory protein (hStAR)  
XX Sequence 21 BP; 8 A; 5 C; 6 G; 2 T; 0 U; 0 Other;  
SQ Query Match 1.3%; Score 21; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 39;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1354 AGAAGCGCTGCAGGAATACC 1374  
DB 1 AGAAGCGCTGCAGGAATACC 21  
RESULT 30  
AAA52783  
ID AAA52783 standard; DNA; 21 BP.  
XX AAA52783;  
AC AAA52783;  
XX 03-JAN-2001 (first entry)  
XX Porcine clusterin PCR primer #1.  
XX Pig; clusterin; cell migration; wound healing; angiogenesis; cancer;  
KW vascular trauma; vascular disease; atherosclerosis; restenosis;  
KW complement cytotoxicity inhibitor; SP-40; 40; apoJ;  
KW testosterone repressed prostate message-2; sulfated glycoprotein-2;  
KW PCR primer; ss.  
XX Sus scrofa.  
XX WO200034469-A1.  
XX 15-JUN-2000.  
XX 10-DEC-1999; 99WO-US029262.  
XX 11-DEC-1998; 98US-0111856P.  
XX (UYNY ) UNIV NEW YORK STATE RES FOUND.  
XX Millis AJT;  
XX WPI; 2000-431300/37.  
XX Clusterin and gp38K-related peptide capable of altering cell migration  
PT useful for treating atherosclerosis, cancer and stenosis following  
PT vascular trauma or disease.  
XX Disclosure; Page 12; 43pp; English.  
XX The present sequence is a PCR primer for the porcine clusterin gene.  
CC Clusterin (also known as complement cytotoxicity inhibitor, sulfated  
CC glycoprotein-2, testosterone repressed prostate message-2, SP-40, 40 and  
CC ApoJ) is essential for the migration of vascular smooth muscle cells  
CC (VSMC). The gene and protein can, therefore, be used to promote wound  
CC healing, angiogenesis and vasculogenesis, in the treatment of stenosis  
CC following vascular trauma or disease and to treat atherosclerosis, and  
CC antisense sequences can be used to treat cancer, as angiogenesis is vital  
CC for tumour survival  
XX Sequence 21 BP; 12 A; 2 C; 7 G; 0 T; 0 U; 0 Other;

DB	XX	Human testosterone-repressed prostate message-2 antisense oligo #7.
KW	XX	Human; testosterone-repressed prostate message-2; TRPM-2; clusterin;
KW	XX	sulfated glycoprotein-2; SGP-2; cancer; antisense oligonucleotide; ss.
OS	XX	Homo sapiens.
PN	XX	WO200049937-A2.
PN	XX	31-AUG-2000.
PD	XX	25-FEB-2000; 2000WO-US004875.
PF	XX	26-FEB-1999; 99US-0121726P.
PR	XX	(UYBR-) UNIV BRITISH COLUMBIA.
PR	XX	Gleave M, Rennie PS, Miyake H, Nelson C;
PA	XX	WPI; 2000-533132/48.
PI	XX	Treating prostatic tumors and renal cancers by antisense inhibition of
PI	XX	the testosterone-repressed prostate messenger-2 gene.
PS	XX	Example 5; Page 37; 38pp; English.
PS	XX	The present sequence is an antisense oligonucleotide directed at the
CC	XX	human testosterone-repressed prostate message-2 (TRPM-2, also known as
CC	XX	clusterin, sulfated glycoprotein-2 or SGP-2). The sequence was shown to
CC	XX	promote the regression of tumours, and oligonucleotides directed at human
CC	XX	TRPM-2 can be used in the treatment of tumour cells expressing the TRPM-2
CC	XX	gene. These include prostate cancer, renal cell cancer and some breast
CC	XX	cancer cells. In addition to this, they also increase the
CC	XX	chemosensitivity of the cells, meaning that conventional chemotherapy is
CC	XX	more effective
SQ	XX	Sequence 21 BP; 3 A; 5 C; 9 G; 4 T; 0 U; 0 Other;
Query Match 1.3%; Score 21; DB 1; Length 21;		
Best Local Similarity 100.0%; Pred. No. 39;		
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
OY	916	ACAACCTCCACGGGCTGCCTGC 936
Db	21	ACAACCTCCACGGGCTGCCTGC 1
RESULT 33		
AAA94230/c		
ID	AAA94230	standard; DNA; 21 BP.
AC	AAA94230;	
XX	12-JAN-2001	(first entry)
XX	Human testosterone-repressed prostate message-2 antisense oligo #6.	
XX	Human; testosterone-repressed prostate message-2; TRPM-2; clusterin;	
KW	sulfated glycoprotein-2; SGP-2; cancer; antisense oligonucleotide; ss.	
OS	Homo sapiens.	
PN	WO200049937-A2.	
PN	31-AUG-2000.	
PD	25-FEB-2000; 2000WO-US004875.	
PF	26-FEB-1999; 99US-0121726P.	
PR	(UYBR-) UNIV BRITISH COLUMBIA.	
PR	Gleave M, Rennie PS, Miyake H, Nelson C;	
PA	WPI; 2000-533132/48.	
PI	Treating prostatic tumors and renal cancers by antisense inhibition of	
PI	the testosterone-repressed prostate messenger-2 gene.	
PS	Claim 4; Page 36; 38pp; English.	
PS	The present sequence is an antisense oligonucleotide directed at the	
CC	human testosterone-repressed prostate message-2 (TRPM-2, also known as	
CC	clusterin, sulfated glycoprotein-2 or SGP-2). The sequence was shown to	
CC	promote the regression of tumours, and oligonucleotides directed at human	
CC	TRPM-2 can be used in the treatment of tumour cells expressing the TRPM-2	
CC	gene. These include prostate cancer, renal cell cancer and some breast	
CC	cancer cells. In addition to this, they also increase the	
CC	chemosensitivity of the cells, meaning that conventional chemotherapy is	
CC	more effective	
SQ	Sequence 21 BP; 3 A; 5 C; 6 G; 7 T; 0 U; 0 Other;	
Query Match 1.3%; Score 21; DB 1; Length 21;		
Best Local Similarity 100.0%; Pred. No. 39;		
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
OY	114	GACCAGACGGTCTCAGACAAT 134
Db	21	GACCAGACGGTCTCAGACAAT 1
RESULT 32		
AAA94231/c		
ID	AAA94231	standard; DNA; 21 BP.
AC	AAA94231;	
XX	12-JAN-2001	(first entry)
XX	Gleave M, Rennie PS, Miyake H, Nelson C;	

XX WPI; 2000-533132/48.  
XX  
XX Treating prostatic tumors and renal cancers by antisense inhibition of  
PT the testosterone-repressed prostate messenger-2 gene.  
XX  
XX  
XX  
XX Example 5; Page 37; 38pp; English.  
XX  
CC The present sequence is an antisense oligonucleotide directed at the  
CC human testosterone-repressed prostate message-2 (TRPM-2, also known as  
CC clusterin, sulfated glycoprotein-2 or SGP-2). The sequence was shown to  
CC promote the regression of tumours, and oligonucleotides directed at human  
CC TRPM-2 can be used in the treatment of tumour cells expressing the TRPM-2  
CC gene. These include prostate cancer, renal cell cancer and some breast  
CC cancer cells. In addition to this, they also increase the  
CC chemosensitivity of the cells, meaning that conventional chemotherapy is  
CC more effective  
XX  
XX Sequence 21 BP; 5 A; 5 C; 8 G; 3 T; 0 U; 0 Other;  
SQ  
Query Match 1.3%; Score 21; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 39;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
XX  
QY 716 CCGCATCGTCCGAGCTTGAT 736  
Db 21 CCGCATCGTCCGAGCTTGAT 1  
XXXXXXXXXXXXXXXXXXXX  
XXXXXXXXXXXXXXXXXXXX  
RESULT 34  
AA94232/c  
ID AAA94232 standard; DNA; 21 BP.  
XX  
AC AAA94232;  
XX  
XX 12-JAN-2001 (first entry)  
DT  
DE Human testosterone-repressed prostate message-2 antisense oligo #8.  
XX  
XX Human; testosterone-repressed prostate message-2; TRPM-2; clusterin;  
KW sulfated glycoprotein-2; SGP-2; cancer; antisense oligonucleotide; ss.  
XX  
XX Homo sapiens.  
OS  
XX WO200049937-A2.  
PN  
XX 31-AUG-2000.  
PD  
XX 25-FEB-2000; 2000WO-US004875.  
PF  
XX 26-FEB-1999; 99US-0121726P.  
PR  
XX (UYBR-) UNIV BRITISH COLUMBIA.  
PA  
XX Gleave M, Rennie PS, Miyake H, Nelson C;  
PI WPI; 2000-533132/48.  
XX  
XX Treating prostatic tumors and renal cancers by antisense inhibition of  
PT the testosterone-repressed prostate messenger-2 gene.  
XX  
XX Example 5; Page 37; 38pp; English.  
XX  
CC The present sequence is an antisense oligonucleotide directed at the  
CC human testosterone-repressed prostate message-2 (TRPM-2, also known as  
CC clusterin, sulfated glycoprotein-2 or SGP-2). The sequence was shown to  
CC promote the regression of tumours, and oligonucleotides directed at human  
CC TRPM-2 can be used in the treatment of tumour cells expressing the TRPM-2  
CC gene. These include prostate cancer, renal cell cancer and some breast  
CC cancer cells. In addition to this, they also increase the  
CC chemosensitivity of the cells, meaning that conventional chemotherapy is  
CC more effective  
XX  
XX Sequence 21 BP; 5 A; 5 C; 8 G; 3 T; 0 U; 0 Other;  
SQ  
Query Match 1.3%; Score 21; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 39;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
XX  
QY 716 CCGCATCGTCCGAGCTTGAT 736  
Db 21 CCGCATCGTCCGAGCTTGAT 1  
XXXXXXXXXXXXXXXXXXXX  
XXXXXXXXXXXXXXXXXXXX  
RESULT 34  
AA94232/c  
ID AAA94232 standard; DNA; 21 BP.  
XX  
AC AAA94232;  
XX  
XX 12-JAN-2001 (first entry)  
DT  
DE Human testosterone-repressed prostate message-2 antisense oligo #8.  
XX  
XX Human; testosterone-repressed prostate message-2; TRPM-2; clusterin;  
KW sulfated glycoprotein-2; SGP-2; cancer; antisense oligonucleotide; ss.  
XX  
XX Homo sapiens.  
OS  
XX WO200049937-A2.  
PN  
XX 31-AUG-2000.  
PD  
XX 25-FEB-2000; 2000WO-US004875.  
PF  
XX 26-FEB-1999; 99US-0121726P.  
PR  
XX (UYBR-) UNIV BRITISH COLUMBIA.  
PA  
XX Gleave M, Rennie PS, Miyake H, Nelson C;  
PI WPI; 2000-533132/48.  
XX  
XX Treating prostatic tumors and renal cancers by antisense inhibition of  
PT the testosterone-repressed prostate messenger-2 gene.  
XX  
XX Example 5; Page 37; 38pp; English.  
XX  
CC The present sequence is an antisense oligonucleotide directed at the  
CC human testosterone-repressed prostate message-2 (TRPM-2, also known as  
CC clusterin, sulfated glycoprotein-2 or SGP-2). The sequence was shown to  
CC promote the regression of tumours, and oligonucleotides directed at human  
CC TRPM-2 can be used in the treatment of tumour cells expressing the TRPM-2  
CC gene. These include prostate cancer, renal cell cancer and some breast  
CC cancer cells. In addition to this, they also increase the  
CC chemosensitivity of the cells, meaning that conventional chemotherapy is  
CC more effective  
XX  
XX Sequence 21 BP; 5 A; 5 C; 8 G; 3 T; 0 U; 0 Other;  
SQ  
Query Match 1.3%; Score 21; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 39;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
XX  
QY 716 CCGCATCGTCCGAGCTTGAT 736  
Db 21 CCGCATCGTCCGAGCTTGAT 1  
XXXXXXXXXXXXXXXXXXXX  
XXXXXXXXXXXXXXXXXXXX  
RESULT 34  
AA94232/c  
ID AAA94232 standard; DNA; 21 BP.  
XX  
AC AAA94232;  
XX  
XX 12-JAN-2001 (first entry)  
DT  
DE Human testosterone-repressed prostate message-2 antisense oligo #9.  
XX  
XX Human; testosterone-repressed prostate message-2; TRPM-2; clusterin;  
KW sulfated glycoprotein-2; SGP-2; cancer; antisense oligonucleotide; ss.  
XX  
XX Homo sapiens.  
OS  
XX WO200049937-A2.  
PN  
XX 31-AUG-2000.  
PD  
XX 25-FEB-2000; 2000WO-US004875.  
PF  
XX 26-FEB-1999; 99US-0121726P.  
PR  
XX (UYBR-) UNIV BRITISH COLUMBIA.  
PA  
XX Gleave M, Rennie PS, Miyake H, Nelson C;  
PI WPI; 2000-533132/48.  
XX  
XX Treating prostatic tumors and renal cancers by antisense inhibition of  
PT the testosterone-repressed prostate messenger-2 gene.  
XX  
XX Example 5; Page 38; 38pp; English.  
XX  
CC The present sequence is an antisense oligonucleotide directed at the  
CC human testosterone-repressed prostate message-2 (TRPM-2, also known as  
CC clusterin, sulfated glycoprotein-2 or SGP-2). The sequence was shown to  
CC promote the regression of tumours, and oligonucleotides directed at human  
CC TRPM-2 can be used in the treatment of tumour cells expressing the TRPM-2  
CC gene. These include prostate cancer, renal cell cancer and some breast  
CC cancer cells. In addition to this, they also increase the  
CC chemosensitivity of the cells, meaning that conventional chemotherapy is  
CC more effective  
XX  
XX Sequence 21 BP; 4 A; 3 C; 6 G; 8 T; 0 U; 0 Other;  
SQ  
Query Match 1.3%; Score 21; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 39;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
XX  
QY 1316 CTCCTGCTGGAGCAGCTGAA 1135  
Db 21 CTCCTGCTGGAGCAGCTGAA 1  
XXXXXXXXXXXXXXXXXXXX  
XXXXXXXXXXXXXXXXXXXX  
RESULT 36  
AAA94229/c  
ID AAA94229 standard; DNA; 21 BP.  
XX  
AC AAA94229;  
XX  
XX 12-JAN-2001 (first entry)  
DT

SQ Sequence 21 BP; 5 A; 6 C; 6 G; 4 T; 0 U; 0 Other;  
Query Match 1.3%; Score 21; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 39;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
XX  
QY 1115 CTCCTGCTGGAGCAGCTGAA 1135  
Db 21 CTCCTGCTGGAGCAGCTGAA 1  
XXXXXXXXXXXXXXXXXXXX  
XXXXXXXXXXXXXXXXXXXX  
RESULT 35  
AAA94233/c  
ID AAA94233 standard; DNA; 21 BP.  
XX  
AC AAA94233;  
XX  
XX 12-JAN-2001 (first entry)  
DT  
DE Human testosterone-repressed prostate message-2 antisense oligo #9.  
XX  
XX Human; testosterone-repressed prostate message-2; TRPM-2; clusterin;  
KW sulfated glycoprotein-2; SGP-2; cancer; antisense oligonucleotide; ss.  
XX  
XX Homo sapiens.  
OS  
XX WO200049937-A2.  
PN  
XX 31-AUG-2000.  
PD  
XX 25-FEB-2000; 2000WO-US004875.  
PF  
XX 26-FEB-1999; 99US-0121726P.  
PR  
XX (UYBR-) UNIV BRITISH COLUMBIA.  
PA  
XX Gleave M, Rennie PS, Miyake H, Nelson C;  
PI WPI; 2000-533132/48.  
XX  
XX Treating prostatic tumors and renal cancers by antisense inhibition of  
PT the testosterone-repressed prostate messenger-2 gene.  
XX  
XX Example 5; Page 38; 38pp; English.  
XX  
CC The present sequence is an antisense oligonucleotide directed at the  
CC human testosterone-repressed prostate message-2 (TRPM-2, also known as  
CC clusterin, sulfated glycoprotein-2 or SGP-2). The sequence was shown to  
CC promote the regression of tumours, and oligonucleotides directed at human  
CC TRPM-2 can be used in the treatment of tumour cells expressing the TRPM-2  
CC gene. These include prostate cancer, renal cell cancer and some breast  
CC cancer cells. In addition to this, they also increase the  
CC chemosensitivity of the cells, meaning that conventional chemotherapy is  
CC more effective  
XX  
XX Sequence 21 BP; 4 A; 3 C; 6 G; 8 T; 0 U; 0 Other;  
SQ  
Query Match 1.3%; Score 21; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 39;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
XX  
QY 1316 CTCCTGCTGGAGCAGCTGAA 1135  
Db 21 CTCCTGCTGGAGCAGCTGAA 1  
XXXXXXXXXXXXXXXXXXXX  
XXXXXXXXXXXXXXXXXXXX  
RESULT 36  
AAA94229/c  
ID AAA94229 standard; DNA; 21 BP.  
XX  
AC AAA94229;  
XX  
XX 12-JAN-2001 (first entry)  
DT

```
XX DE Human testosterone-repressed prostate message-2 antisense oligo #5.
XX KW Human; testosterone-repressed prostate message-2; TRPM-2; clusterin;
XX KW sulfated glycoprotein-2; SGP-2; cancer; antisense oligonucleotide; ss.
XX OS Homo sapiens.
XX PN WO200049937-A2.
XX PD 31-AUG-2000.
XX PF 25-FEB-2000; 2000WO-US004875.
XX PR 26-FEB-1999; 99US-0121726P.
XX PA (UYBR-) UNIV BRITISH COLUMBIA.
XX PI Gleave M, Rennie PS, Miyake H, Nelson C;
XX DR WPI; 2000-533132/48.
XX PT Treating prostatic tumors and renal cancers by antisense inhibition of
XX PT the testosterone-repressed prostate messenger-2 gene.
XX PS Example 5; Page 37; 38pp; English.
XX CC The present sequence is an antisense oligonucleotide directed at the
XX CC human testosterone-repressed prostate message-2 (TRPM-2, also known as
XX CC clusterin, sulfated glycoprotein-2 or SGP-2). The sequence was shown to
XX CC promote the regression of tumours, and oligonucleotides directed at human
XX CC TRPM-2 can be used in the treatment of tumour cells expressing the TRPM-2
XX CC gene. These include prostate cancer, renal cell cancer and some breast
XX CC cancer cells. In addition to this, they also increase the
XX CC chemosensitivity of the cells, meaning that conventional chemotherapy is
XX CC more effective
XX CC Sequence 21 BP; 5 A; 4 C; 9 G; 3 T; 0 U; 0 Other;
XX SQ
XX Query Match 1.3%; Score 21; DB 1; Length 21;
XX Best Local Similarity 100.0%; Pred.No. 39;
XX Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 515 TGACCGCATCGACTCCCTGCT 535
Db 21 TGACCGCATCGACTCCCTGCT 1
RESULT 37
AAA94226/c
ID AAA94226 standard; DNA; 21 BP.
AC AAA94226;
XX DT 12-JAN-2001 (first entry)
XX DE Human testosterone-repressed prostate message-2 antisense oligo #2.
XX KW Human; testosterone-repressed prostate message-2; TRPM-2; clusterin;
XX KW sulfated glycoprotein-2; SGP-2; cancer; antisense oligonucleotide; ss.
XX OS Homo sapiens.
XX PN WO200049937-A2.
XX PD 31-AUG-2000.
XX PF 25-FEB-2000; 2000WO-US004875.
XX PR 26-FEB-1999; 99US-0121726P.
XX PA (UYBR-) UNIV BRITISH COLUMBIA.
XX PI Gleave M, Rennie PS, Miyake H, Nelson C;
XX DR WPI; 2000-533132/48.
XX PT Treating prostatic tumors and renal cancers by antisense inhibition of
XX PT the testosterone-repressed prostate messenger-2 gene.
XX PS Example 5; Page 37; 38pp; English.
XX CC The present sequence is an antisense oligonucleotide directed at the
XX CC human testosterone-repressed prostate message-2 (TRPM-2, also known as
XX CC clusterin, sulfated glycoprotein-2 or SGP-2). The sequence was shown to
XX CC promote the regression of tumours, and oligonucleotides directed at human
XX CC TRPM-2 can be used in the treatment of tumour cells expressing the TRPM-2
XX CC gene. These include prostate cancer, renal cell cancer and some breast
XX CC cancer cells. In addition to this, they also increase the
XX CC chemosensitivity of the cells, meaning that conventional chemotherapy is
XX CC more effective
XX CC Sequence 21 BP; 5 A; 4 C; 9 G; 3 T; 0 U; 0 Other;
XX SQ
XX Query Match 1.3%; Score 21; DB 1; Length 21;
XX Best Local Similarity 100.0%; Pred.No. 39;
XX Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 515 TGACCGCATCGACTCCCTGCT 535
Db 21 TGACCGCATCGACTCCCTGCT 1
RESULT 37
AAA94226/c
ID AAA94226 standard; DNA; 21 BP.
AC AAA94226;
XX DT 12-JAN-2001 (first entry)
XX DE Human testosterone-repressed prostate message-2 antisense oligo #2.
XX KW Human; testosterone-repressed prostate message-2; TRPM-2; clusterin;
XX KW sulfated glycoprotein-2; SGP-2; cancer; antisense oligonucleotide; ss.
XX OS Homo sapiens.
XX PN WO200049937-A2.
XX PD 31-AUG-2000.
XX PF 25-FEB-2000; 2000WO-US004875.
XX PR 26-FEB-1999; 99US-0121726P.
XX PA (UYBR-) UNIV BRITISH COLUMBIA.
XX PI Gleave M, Rennie PS, Miyake H, Nelson C;
XX DR WPI; 2000-533132/48.
XX PT Treating prostatic tumors and renal cancers by antisense inhibition of
XX PT the testosterone-repressed prostate messenger-2 gene.
XX PS Example 5; Page 37; 38pp; English.
XX CC The present sequence is an antisense oligonucleotide directed at the
XX CC human testosterone-repressed prostate message-2 (TRPM-2, also known as
XX CC clusterin, sulfated glycoprotein-2 or SGP-2). The sequence was shown to
XX CC promote the regression of tumours, and oligonucleotides directed at human
XX CC TRPM-2 can be used in the treatment of tumour cells expressing the TRPM-2
XX CC gene. These include prostate cancer, renal cell cancer and some breast
XX CC cancer cells. In addition to this, they also increase the
XX CC chemosensitivity of the cells, meaning that conventional chemotherapy is
XX CC more effective
```

```
PI Gleave M, Rennie PS, Miyake H, Nelson C;
XX DR WPI; 2000-533132/48.
XX PT Treating prostatic tumors and renal cancers by antisense inhibition of
XX PT the testosterone-repressed prostate messenger-2 gene.
XX PS Claim 3; Page 36; 38pp; English.
XX CC The present sequence is an antisense oligonucleotide directed at the
XX CC human testosterone-repressed prostate message-2 (TRPM-2, also known as
XX CC clusterin, sulfated glycoprotein-2 or SGP-2). The sequence was shown to
XX CC promote the regression of tumours, and oligonucleotides directed at human
XX CC TRPM-2 can be used in the treatment of tumour cells expressing the TRPM-2
XX CC gene. These include prostate cancer, renal cell cancer and some breast
XX CC cancer cells. In addition to this, they also increase the
XX CC chemosensitivity of the cells, meaning that conventional chemotherapy is
XX CC more effective
XX CC Sequence 21 BP; 6 A; 6 C; 4 G; 5 T; 0 U; 0 Other;
XX SQ
XX Query Match 1.3%; Score 21; DB 1; Length 21;
XX Best Local Similarity 100.0%; Pred.No. 39;
XX Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 48 ATGATGAAGACTCTGCTGCTG 68
Db 21 ATGATGAAGACTCTGCTGCTG 1
RESULT 38
AAA94234/c
ID AAA94234 standard; DNA; 21 BP.
AC AAA94234;
XX DT 12-JAN-2001 (first entry)
XX DE Human testosterone-repressed prostate message-2 antisense oligo #10.
XX KW Human; testosterone-repressed prostate message-2; TRPM-2; clusterin;
XX KW sulfated glycoprotein-2; SGP-2; cancer; antisense oligonucleotide; ss.
XX OS Homo sapiens.
XX PN WO200049937-A2.
XX PD 31-AUG-2000.
XX PF 25-FEB-2000; 2000WO-US004875.
XX PR 26-FEB-1999; 99US-0121726P.
XX PA (UYBR-) UNIV BRITISH COLUMBIA.
XX PI Gleave M, Rennie PS, Miyake H, Nelson C;
XX DR WPI; 2000-533132/48.
XX PT Treating prostatic tumors and renal cancers by antisense inhibition of
XX PT the testosterone-repressed prostate messenger-2 gene.
XX PS Example 5; Page 38; 38pp; English.
XX CC The present sequence is an antisense oligonucleotide directed at the
XX CC human testosterone-repressed prostate message-2 (TRPM-2, also known as
XX CC clusterin, sulfated glycoprotein-2 or SGP-2). The sequence was shown to
XX CC promote the regression of tumours, and oligonucleotides directed at human
XX CC TRPM-2 can be used in the treatment of tumour cells expressing the TRPM-2
XX CC gene. These include prostate cancer, renal cell cancer and some breast
XX CC cancer cells. In addition to this, they also increase the
XX CC chemosensitivity of the cells, meaning that conventional chemotherapy is
XX CC more effective
```



```
XX SQ Sequence 21 BP; 1 A; 4 C; 12 G; 4 T; 0 U; 0 Other;
Query Match 1.3%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 39;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1516 AGGCCCCCACTCGGCCAGC 1536
Db 21 AGGCCCCCACTCGGCCAGC 1

RESULT 39
AAA94228/c
ID AAA94228 standard; DNA; 21 BP.
XX
AC AAA94228;
XX
DT 12-JAN-2001 (first entry)
XX Human testosterone-repressed prostate message-2 antisense oligo #4.
DE
DE Human; testosterone-repressed prostate message-2; TRPM-2; clusterin;
KW sulfated glycoprotein-2; SGP-2; cancer; antisense oligonucleotide; ss.
XX
OS Homo sapiens.
XX
PN WO200049937-A2.
XX
PD 31-AUG-2000.
XX
PF 25-FEB-2000; 2000WO-US004875.
XX
PR 26-FEB-1999; 99US-0121726P.
XX
XX (UYBR-) UNIV BRITISH COLUMBIA.
XX
PI Gleave M, Rennie PS, Miyake H, Nelson C;
XX WPI; 2000-533132/48.
XX
XX Treating prostatic tumors and renal cancers by antisense inhibition of
PT the testosterone-repressed prostate messenger-2 gene.
XX
PS Example 5; Page 36; 38pp; English.
XX
CC The present sequence is an antisense oligonucleotide directed at the
CC human testosterone-repressed prostate message-2 (TRPM-2, also known as
CC clusterin, sulfated glycoprotein-2 or SGP-2). The sequence was shown to
CC promote the regression of tumors, and oligonucleotides directed at human
CC TRPM-2 can be used in the treatment of tumour cells expressing the TRPM-2
CC gene. These include prostate cancer, renal cell cancer and some breast
CC cancer cells. In addition to this, they also increase the
CC chemosensitivity of the cells, meaning that conventional chemotherapy is
CC more effective
XX
SQ Sequence 21 BP; 2 A; 6 C; 3 G; 10 T; 0 U; 0 Other;

Query Match 1.3%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 39;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 316 AATCAGAGACAAAGCTGAAGG 336
Db 21 AATCAGAGACAAAGCTGAAGG 1

RESULT 40
AAA94225/c
ID AAA94225 standard; DNA; 21 BP.
XX
AC AAA94225;
XX
```

```
DT 12-JAN-2001 (first entry)
XX Human testosterone-repressed prostate message-2 antisense oligo #1.
DE
XX Human; testosterone-repressed prostate message-2; TRPM-2; clusterin;
KW sulfated glycoprotein-2; SGP-2; cancer; antisense oligonucleotide; ss.
XX
OS Homo sapiens.
XX
PN WO200049937-A2.
XX
PD 31-AUG-2000.
XX
PF 25-FEB-2000; 2000WO-US004875.
XX
PR 26-FEB-1999; 99US-0121726P.
XX
XX (UYBR-) UNIV BRITISH COLUMBIA.
XX
PI Gleave M, Rennie PS, Miyake H, Nelson C;
XX WPI; 2000-533132/48.
XX
XX Treating prostatic tumors and renal cancers by antisense inhibition of
PT the testosterone-repressed prostate messenger-2 gene.
XX
PS Example 5; Page 36; 38pp; English.
XX
CC The present sequence is an antisense oligonucleotide directed at the
CC human testosterone-repressed prostate message-2 (TRPM-2, also known as
CC clusterin, sulfated glycoprotein-2 or SGP-2). The sequence was shown to
CC promote the regression of tumors, and oligonucleotides directed at human
CC TRPM-2 can be used in the treatment of tumour cells expressing the TRPM-2
CC gene. These include prostate cancer, renal cell cancer and some breast
CC cancer cells. In addition to this, they also increase the
CC chemosensitivity of the cells, meaning that conventional chemotherapy is
CC more effective
XX
SQ Sequence 21 BP; 2 A; 6 C; 7 G; 6 T; 0 U; 0 Other;

Query Match 1.3%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 39;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 CCGAGGCGTGCAAGACTCCA 36
Db 21 CCGAGGCGTGCAAGACTCCA 1

RESULT 41
AAF97658
ID AAF97658 standard; DNA; 21 BP.
XX
AC AAF97658;
XX
DT 18-NOV-2004 (revised)
DT 06-JUN-2001 (first entry)
XX
XX Human gene single nucleotide polymorphism #2419.
DE
XX Human; variant thrombospondin 1; variant thrombospondin 4; SNP;
KW polymorphism; vascular disease; coronary artery disease; forensics;
KW myocardial infarction; atherosclerosis; stroke; venous thromboembolism;
KW pulmonary embolism; paternity test; ds.
XX
XX Homo sapiens.
XX Unidentified.
XX
FH Key Location/Qualifiers
FT variation 11
FT /*tag= a
FT /standard_name= "Single nucleotide polymorphism"
XX
```

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PN WO200118250-A2.
XX 15-MAR-2001.
XX
XX 07-SEP-2000; 2000WO-US024503.
XX
XX 10-SEP-1999; 99US-0153357P.
XX 26-JUL-2000; 2000US-0220947P.
XX 16-AUG-2000; 2000US-0225724P.
XX
XX (WHED ) WHITEHEAD INST BIOMEDICAL RES.
XX (MILL-) MILLENNIUM PHARM INC.
XX
XX Lander ES, Gargill M, Ireland JS, Bolk S, Daley GQ, Mccarthy JJ;
XX WPI; 2001-226749/23.
XX
XX Nucleic acids comprising single nucleotide polymorphisms, useful in
XX applications such as forensics, paternity testing, medicine, genetic
XX analysis and phenotype correlations to diseases such as diabetes and
XX atherosclerosis.
XX
XX Example; Page 212; 242pp; English.
XX
XX The present invention provides a method of diagnosing a vascular disease
XX in an individual, involving determining the sequence at various
XX polymorphic sites within the human thrombospondin 1 and thrombospondin 4
XX genes. The sequences at a number of polymorphic sites are also provided
XX in the specification. In particular, the method can be used in the
XX diagnosis of atherosclerosis, myocardial infarction, coronary heart
XX disease, stroke, peripheral vascular diseases, venous thromboembolism and
XX pulmonary embolism. Single nucleotide polymorphisms (SNPs) are also
XX useful in forensics, paternity testing, genetic analysis and phenotype
XX correlations to diseases. The present sequence is an example of one of
XX the human gene SNPs shown in the specification
XX
XX Revised record issued on 18-NOV-2004 : The variantion feature was
XX incorrectly given a captial V
XX
XX Sequence 21 BP; 7 A; 7 C; 6 G; 1 T; 0 U; 0 Other;
XX
XX Query Match 1.3%; Score 21; DB 1; Length 21;
XX Best Local Similarity 100.0%; Pred. No. 39;
XX Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1170 CTCACCGAAGGCGAAGACCAG 1190
Db |||||
1 CTCACCGAAGGCGAAGACCAG 21

RESULT 42
AAF97656
ID AAF97656 standard; DNA; 21 BP.
XX
XX AAF97656;
XX
XX 18-NOV-2004 (revised)
XX 06-JUN-2001 (first entry)
XX
XX Human gene single nucleotide polymorphism #2417.
XX
XX Human; variant thrombospondin 1; variant thrombospondin 4; SNP;
XX polymorphism; vascular disease; coronary artery disease; forensics;
XX myocardial infarction; atherosclerosis; stroke; venous thromboembolism;
XX pulmonary embolism; paternity test; ds.
XX
XX Homo sapiens.
XX Unidentified.
XX
XX Key Location/Qualifiers
XX Variation 11
XX /*tag= a
XX /standard_name= "Single nucleotide polymorphism"
XX FT

```

```

XX WO200118250-A2.
XX 15-MAR-2001.
XX
XX 07-SEP-2000; 2000WO-US024503.
XX
XX 10-SEP-1999; 99US-0153357P.
XX 26-JUL-2000; 2000US-0220947P.
XX 16-AUG-2000; 2000US-0225724P.
XX
XX (WHED ) WHITEHEAD INST BIOMEDICAL RES.
XX (MILL-) MILLENNIUM PHARM INC.
XX
XX Lander ES, Gargill M, Ireland JS, Bolk S, Daley GQ, Mccarthy JJ;
XX WPI; 2001-226749/23.
XX
XX Nucleic acids comprising single nucleotide polymorphisms, useful in
XX applications such as forensics, paternity testing, medicine, genetic
XX analysis and phenotype correlations to diseases such as diabetes and
XX atherosclerosis.
XX
XX Example; Page 212; 242pp; English.
XX
XX The present invention provides a method of diagnosing a vascular disease
XX in an individual, involving determining the sequence at various
XX polymorphic sites within the human thrombospondin 1 and thrombospondin 4
XX genes. The sequences at a number of polymorphic sites are also provided
XX in the specification. In particular, the method can be used in the
XX diagnosis of atherosclerosis, myocardial infarction, coronary heart
XX disease, stroke, peripheral vascular diseases, venous thromboembolism and
XX pulmonary embolism. Single nucleotide polymorphisms (SNPs) are also
XX useful in forensics, paternity testing, genetic analysis and phenotype
XX correlations to diseases. The present sequence is an example of one of
XX the human gene SNPs shown in the specification
XX
XX Revised record issued on 18-NOV-2004 : The variantion feature was
XX incorrectly given a captial V
XX
XX Sequence 21 BP; 8 A; 3 C; 7 G; 3 T; 0 U; 0 Other;
XX
XX Query Match 1.3%; Score 21; DB 1; Length 21;
XX Best Local Similarity 100.0%; Pred. No. 39;
XX Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1050 GAGAGGTTGACCGAATAATAC 1070
Db |||||
1 GAGAGGTTGACCGAATAATAC 21

RESULT 43
AAF97657
ID AAF97657 standard; DNA; 21 BP.
XX
XX AAF97657;
XX
XX 18-NOV-2004 (revised)
XX 06-JUN-2001 (first entry)
XX
XX Human gene single nucleotide polymorphism #2418.
XX
XX Human; variant thrombospondin 1; variant thrombospondin 4; SNP;
XX polymorphism; vascular disease; coronary artery disease; forensics;
XX myocardial infarction; atherosclerosis; stroke; venous thromboembolism;
XX pulmonary embolism; paternity test; ds.
XX
XX Homo sapiens.
XX Unidentified.
XX
XX Key Location/Qualifiers
XX Variation 11
XX /*tag= a
XX FT

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```
FT /standard_name= "Single nucleotide polymorphism"
XX WO200118250-A2.
XX 15-MAR-2001.
XX 07-SEP-2000; 2000WO-US024503.
XX 10-SEP-1999; 99US-0153357P.
XX 26-JUL-2000; 2000US-0220947P.
XX 16-AUG-2000; 2000US-0225724P.
XX (WHED ) WHITEHEAD INST BIOMEDICAL RES.
XX (MILL-) MILLENNIUM PHARM INC.
XX Lander ES, Gargill M, Ireland JS, Bolk S, Daley GQ, McCarthy JJ;
XX WPI; 2001-226749/23.
XX Nucleic acids comprising single nucleotide polymorphisms, useful in
XX applications such as forensics, paternity testing, medicine, genetic
XX analysis and phenotype correlations to diseases such as diabetes and
XX atherosclerosis.
XX Example; Page 212; 242pp; English.
XX The present invention provides a method of diagnosing a vascular disease
XX in an individual, involving determining the sequence at various
XX polymorphic sites within the human thrombospondin 1 and thrombospondin 4
XX genes. The sequences at a number of polymorphic sites are also provided
XX in the specification. In particular, the method can be used in the
XX diagnosis of atherosclerosis, myocardial infarction, coronary heart
XX disease, stroke, peripheral vascular diseases, venous thromboembolism and
XX pulmonary embolism. Single nucleotide polymorphisms (SNPs) are also
XX useful in forensics, paternity testing, genetic analysis and phenotype
XX correlations to diseases. The present sequence is an example of one of
XX the human gene SNPs shown in the specification
XX Revised record issued on 18-NOV-2004 : The variantion feature was
XX incorrectly given a captial V
XX Sequence 21 BP; 3 A; 9 C; 6 G; 3 T; 0 U; 0 Other;
XX Query Match 1.3%; Score 21; DB 1; Length 21;
XX Best Local Similarity 100.0%; Pred. No. 39;
XX Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 999 CCTCCAGGCTAAGCTGCGG 1019
DB 1 CCTCCAGGCTAAGCTGCGG 21
RESULT 44
AAF97659
ID AAF97659 standard; DNA; 21 BP.
XX AAF97659;
XX 18-NOV-2004 (revised)
DT 06-JUN-2001 (first entry)
XX Human gene single nucleotide polymorphism #2420.
XX Human; variant thrombospondin 1; variant thrombospondin 4; SNP;
XX polymorphism; vascular disease; coronary artery disease; forensics;
XX myocardial infarction; atherosclerosis; stroke; venous thromboembolism;
XX pulmonary embolism; paternity test; ds.
XX Homo sapiens.
XX OS Unidentified.
XX FT Variation 11
XX Location/Qualifiers
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FT /*tag= a
XX /standard_name= "Single nucleotide polymorphism"
XX WO200118250-A2.
XX 15-MAR-2001.
XX 07-SEP-2000; 2000WO-US024503.
XX 10-SEP-1999; 99US-0153357P.
XX 26-JUL-2000; 2000US-0220947P.
XX 16-AUG-2000; 2000US-0225724P.
XX (WHED ) WHITEHEAD INST BIOMEDICAL RES.
XX (MILL-) MILLENNIUM PHARM INC.
XX Lander ES, Gargill M, Ireland JS, Bolk S, Daley GQ, McCarthy JJ;
XX WPI; 2001-226749/23.
XX Nucleic acids comprising single nucleotide polymorphisms, useful in
XX applications such as forensics, paternity testing, medicine, genetic
XX analysis and phenotype correlations to diseases such as diabetes and
XX atherosclerosis.
XX Example; Page 213; 242pp; English.
XX The present invention provides a method of diagnosing a vascular disease
XX in an individual, involving determining the sequence at various
XX polymorphic sites within the human thrombospondin 1 and thrombospondin 4
XX genes. The sequences at a number of polymorphic sites are also provided
XX in the specification. In particular, the method can be used in the
XX diagnosis of atherosclerosis, myocardial infarction, coronary heart
XX disease, stroke, peripheral vascular diseases, venous thromboembolism and
XX pulmonary embolism. Single nucleotide polymorphisms (SNPs) are also
XX useful in forensics, paternity testing, genetic analysis and phenotype
XX correlations to diseases. The present sequence is an example of one of
XX the human gene SNPs shown in the specification
XX Revised record issued on 18-NOV-2004 : The variantion feature was
XX incorrectly given a captial V
XX Sequence 21 BP; 3 A; 9 C; 3 G; 6 T; 0 U; 0 Other;
XX Query Match 1.3%; Score 21; DB 1; Length 21;
XX Best Local Similarity 100.0%; Pred. No. 39;
XX Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1105 TCAACACCTCTCTCTGCTGG 1125
DB 1 TCAACACCTCTCTCTGCTGG 21
RESULT 45
ABN99659
ID ABN99659 standard; DNA; 21 BP.
XX AC ABN99659;
XX 16-AUG-2002 (first entry)
DT Human clusterin PCR probe.
XX Human; antisense inhibition; antisense oligonucleotide; clusterin;
XX hypercholesterolaemia; cardiovascular disorder; ss; PCR; probe;
XX hyperproliferative disorder; hyperlipidemic disorder.
XX Homo sapiens.
XX OS WO200222635-A1.
XX 21-MAR-2002.
XX
```

PF 10-SEP-2001; 2001WO-US028235.  
 PR 11-SEP-2000; 2000US-00659791.  
 XX (ISIS-) ISIS PHARM INC.  
 XX Monia BP, Freier SM;  
 XX WPI; 2002-404805/43.  
 XX Novel antisense compound targeted to nucleic acid molecule encoding  
 PT clusterin, useful for treating animal having disease associated with  
 PT clusterin such as hyperlipidemic disorder, cardiovascular disorder.  
 XX  
 XX Example 13; Page 80; 125pp; English.  
 XX The invention comprises antisense oligonucleotides that are capable of  
 CC inhibiting expression of the human clusterin gene. The antisense  
 CC oligonucleotides of the invention are useful for inhibiting the  
 CC expression of clusterin in cells. The antisense oligonucleotides are also  
 CC useful for treating an animal with a disease or condition associated with  
 CC clusterin (e.g. hypercholesterolaemia; cardiovascular disorders;  
 CC hyperproliferative disorders; and hyperlipidemic disorders). The present  
 CC DNA sequence represents a PCR probe specific for the human clusterin  
 CC gene. NOTE: The present sequence is labelled with a fluorescent reporter  
 CC dye (FAM) and a quencher dye (TAMRA)  
 XX  
 XX Sequence 21 BP; 3 A; 10 C; 3 G; 5 T; 0 U; 0 Other;  
 SQ  
 Query Match 1.3%; Score 21; DB 1; Length 21;  
 Best Local Similarity 100.0%; Pred. No. 39;  
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 766 TCACGCCCATGTTCCAGCCCT 786  
 Db 1 TCACGCCCATGTTCCAGCCCT 21  
 RESULT 46  
 \*ACF36397/C  
 ID ACF36397 standard; DNA; 21 BP.  
 AC ACF36397;  
 XX  
 DT 18-DEC-2003 (first entry)  
 XX  
 DE TRPM-2 antisense oligonucleotide.  
 XX  
 KW TRPM-2; testosterone-repressed prostate message-2; cytostatic; androgen;  
 KW prostate cancer; anti-apoptotic protein; antisense; ss.  
 XX  
 OS Synthetic.  
 OS Homo sapiens.  
 XX  
 FN WO2003072591-A1.  
 XX  
 PD 04-SEP-2003.  
 XX  
 PF 20-FEB-2003; 2003WO-US005305.  
 XX  
 PR 22-FEB-2002; 2002US-00080794.  
 XX  
 XX (UYBR-) UNIV BRITISH COLUMBIA.  
 XX  
 XX Gleave M, Rennie PS, Miyake H, Nelson C, Monia BP;  
 XX WPI; 2003-689981/65.  
 XX  
 XX New modified antisense oligonucleotide, useful particularly for treating  
 PT prostatic cancer, inhibits the testosterone-repressed prostate message-2.  
 XX  
 XX Example 5; Page 40; 44pp; English.

CC The invention relates to a compound consisting of an oligonucleotide with  
 CC a phosphorothioate backbone throughout, in which: (a) sugars on  
 CC nucleotide residues 1-4 and 18-21 are 2'-O-methoxyethyl modified, and the  
 CC remaining nucleotides 5-17 are 2'-deoxy; and (b) the cytosines at  
 CC positions 1, 4 and 19 are 5-methylated. Oligonucleotide shown in sequence  
 CC ACF36398 (I) is used: (a) to delay progression of androgen-sensitive  
 CC prostatic cancer cells to the androgen-independent state, in vivo or in  
 CC vitro; (b) to treat prostatic cancer (after initially withdrawing  
 CC androgens to induce apoptosis); and (c) to increase sensitivity of cancer  
 CC cells (prostatic, renal, non-small cell lung, urothelial transitional,  
 CC ovarian and some breast cancer cells) that express abnormal levels of  
 CC TRPM-2 to chemotherapy or radiation. The modifications present in (I)  
 CC increase stability in vivo and activity (both in vivo or in vitro) and  
 CC result in a synergistic increase in effect when (I) is used with  
 CC chemotherapeutic agents or other antisense oligonucleotides directed  
 CC against other antiapoptotic genes. The present sequence represents an  
 CC anti-apoptotic protein TRPM-2 (testosterone-repressed prostate message-2)  
 CC antisense oligonucleotide  
 XX  
 XX Sequence 21 BP; 2 A; 6 C; 7 G; 6 T; 0 U; 0 Other;  
 SQ  
 Query Match 1.3%; Score 21; DB 1; Length 21;  
 Best Local Similarity 100.0%; Pred. No. 39;  
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 16 CCGAGGGCGTGCAAGACTCCA 36  
 Db 21 CCGAGGGCGTGCAAGACTCCA 1  
 RESULT 47  
 ACF36405/C  
 ID ACF36405 standard; DNA; 21 BP.  
 XX  
 AC ACF36405;  
 XX  
 DT 18-DEC-2003 (first entry)  
 XX  
 DE TRPM-2 antisense oligonucleotide #11.  
 XX  
 KW TRPM-2; testosterone-repressed prostate message-2; cytostatic; androgen;  
 KW prostate cancer; anti-apoptotic protein; antisense; ss.  
 XX  
 OS Synthetic.  
 OS Homo sapiens.  
 XX  
 FN WO2003072591-A1.  
 XX  
 PD 04-SEP-2003.  
 XX  
 PF 20-FEB-2003; 2003WO-US005305.  
 XX  
 PR 22-FEB-2002; 2002US-00080794.  
 XX  
 XX (UYBR-) UNIV BRITISH COLUMBIA.  
 XX  
 XX Gleave M, Rennie PS, Miyake H, Nelson C, Monia BP;  
 XX WPI; 2003-689981/65.  
 XX  
 XX New modified antisense oligonucleotide, useful particularly for treating  
 PT prostatic cancer, inhibits the testosterone-repressed prostate message-2.  
 XX  
 XX Example 5; Page 42; 44pp; English.  
 XX  
 XX The invention relates to a compound consisting of an oligonucleotide with  
 CC a phosphorothioate backbone throughout, in which: (a) sugars on  
 CC nucleotide residues 1-4 and 18-21 are 2'-O-methoxyethyl modified, and the  
 CC remaining nucleotides 5-17 are 2'-deoxy; and (b) the cytosines at  
 CC positions 1, 4 and 19 are 5-methylated. Oligonucleotide shown in sequence  
 CC ACF36398 (I) is used: (a) to delay progression of androgen-sensitive  
 CC prostatic cancer cells to the androgen-independent state, in vivo or in  
 CC vitro; (b) to treat prostatic cancer (after initially withdrawing

CC androgens to induce apoptosis); and (c) to increase sensitivity of cancer  
 CC cells (prostatic, renal, non-small cell lung, urothelial transitional,  
 CC ovarian and some breast cancer cells) that express abnormal levels of  
 CC TRPM-2 to chemotherapy or radiation. The modifications present in (I)  
 CC increase stability in vivo and activity (both in vivo or in vitro) and  
 CC result in a synergistic increase in effect when (I) is used with  
 CC chemotherapeutic agents or other antisense oligonucleotides directed  
 CC against other antiapoptotic genes. Sequences ACF36399-406 represent  
 CC antisense oligonucleotides targeted against human anti-apoptotic protein  
 CC TRPM-2 (testosterone-repressed prostate message-2) gene  
 XX  
 SQ Sequence 21 BP; 4 A; 3 C; 6 G; 8 T; 0 U; 0 Other;  
 Query Match 1.3%; Score 21; DB 1; Length 21;  
 Best Local Similarity 100.0%; Pred. No. 39;  
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1316 CTCAGGAGAACCCCTAAATT 1336  
 |||||  
 Db 21 CTCAGGAGAACCCCTAAATT 1  
 RESULT 48  
 ACF36406/C  
 ID ACF36406 standard; DNA; 21 BP.  
 XX  
 AC ACF36406;  
 XX  
 DT 18-DEC-2003 (first entry)  
 XX  
 DE TRPM-2 antisense oligonucleotide #12.  
 XX  
 KW TRPM-2; testosterone-repressed prostate message-2; cytostatic; androgen;  
 KW prostate cancer; anti-apoptotic protein; antisense; ss.  
 XX  
 XX Synthetic.  
 OS Homo sapiens.  
 XX  
 PN WO2003072591-A1.  
 XX  
 PD 04-SEP-2003.  
 XX  
 PF 20-FEB-2003; 2003WO-US005305.  
 XX  
 PR 22-FEB-2002; 2002US-00080794.  
 XX  
 PA (UYBR-) UNIV BRITISH COLUMBIA.  
 XX  
 PI Gleave M, Rennie PS, Miyake H, Nelson C, Monia BP;  
 XX WPI; 2003-689981/65.  
 XX  
 PT New modified antisense oligonucleotide, useful particularly for treating  
 PT prostatic cancer, inhibits the testosterone-repressed prostate message-2.  
 XX  
 PS Example 5; Page 42; 44pp; English.  
 XX  
 CC The invention relates to a compound consisting of an oligonucleotide with  
 CC a phosphorothioate backbone throughout, in which: (a) sugars on  
 CC nucleotide residues 1-4 and 18-21 are 2'-O-methoxyethyl modified, and the  
 CC remaining nucleotides 5-17 are 2'-deoxy; and (b) the cytosines at  
 CC positions 1, 4 and 19 are 5-methylated. Oligonucleotide shown in sequence  
 CC ACF36398 (I) is used: (a) to delay progression of androgen-sensitive  
 CC prostatic cancer cells to the androgen-independent state, in vivo or in  
 CC vitro; (b) to treat prostatic cancer (after initially withdrawing  
 CC androgens to induce apoptosis); and (c) to increase sensitivity of cancer  
 CC cells (prostatic, renal, non-small cell lung, urothelial transitional,  
 CC ovarian and some breast cancer cells) that express abnormal levels of  
 CC TRPM-2 to chemotherapy or radiation. The modifications present in (I)  
 CC increase stability in vivo and activity (both in vivo or in vitro) and  
 CC result in a synergistic increase in effect when (I) is used with  
 CC chemotherapeutic agents or other antisense oligonucleotides directed  
 CC against other antiapoptotic genes. Sequences ACF36399-406 represent  
 CC antisense oligonucleotides targeted against human anti-apoptotic protein  
 CC TRPM-2 (testosterone-repressed prostate message-2) gene  
 XX

CC antisense oligonucleotides targeted against human anti-apoptotic protein  
 CC TRPM-2 (testosterone-repressed prostate message-2) gene  
 XX  
 SQ Sequence 21 BP; 1 A; 4 C; 12 G; 4 T; 0 U; 0 Other;  
 Query Match 1.3%; Score 21; DB 1; Length 21;  
 Best Local Similarity 100.0%; Pred. No. 39;  
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1516 AGGCCCCCAACTCCGCCAGC 1536  
 |||||  
 Db 21 AGGCCCCCAACTCCGCCAGC 1  
 RESULT 49  
 ACF36399/C  
 ID ACF36399 standard; DNA; 21 BP.  
 XX  
 AC ACF36399;  
 XX  
 DT 18-DEC-2003 (first entry)  
 XX  
 DE TRPM-2 antisense oligonucleotide #5.  
 XX  
 KW TRPM-2; testosterone-repressed prostate message-2; cytostatic; androgen;  
 KW prostate cancer; anti-apoptotic protein; antisense; ss.  
 XX  
 XX Synthetic.  
 OS Homo sapiens.  
 XX  
 PN WO2003072591-A1.  
 XX  
 PD 04-SEP-2003.  
 XX  
 PF 20-FEB-2003; 2003WO-US005305.  
 XX  
 PR 22-FEB-2002; 2002US-00080794.  
 XX  
 PA (UYBR-) UNIV BRITISH COLUMBIA.  
 XX  
 PI Gleave M, Rennie PS, Miyake H, Nelson C, Monia BP;  
 XX WPI; 2003-689981/65.  
 XX  
 PT New modified antisense oligonucleotide, useful particularly for treating  
 PT prostatic cancer, inhibits the testosterone-repressed prostate message-2.  
 XX  
 PS Example 5; Page 40; 44pp; English.  
 XX  
 CC The invention relates to a compound consisting of an oligonucleotide with  
 CC a phosphorothioate backbone throughout, in which: (a) sugars on  
 CC nucleotide residues 1-4 and 18-21 are 2'-O-methoxyethyl modified, and the  
 CC remaining nucleotides 5-17 are 2'-deoxy; and (b) the cytosines at  
 CC positions 1, 4 and 19 are 5-methylated. Oligonucleotide shown in sequence  
 CC ACF36398 (I) is used: (a) to delay progression of androgen-sensitive  
 CC prostatic cancer cells to the androgen-independent state, in vivo or in  
 CC vitro; (b) to treat prostatic cancer (after initially withdrawing  
 CC androgens to induce apoptosis); and (c) to increase sensitivity of cancer  
 CC cells (prostatic, renal, non-small cell lung, urothelial transitional,  
 CC ovarian and some breast cancer cells) that express abnormal levels of  
 CC TRPM-2 to chemotherapy or radiation. The modifications present in (I)  
 CC increase stability in vivo and activity (both in vivo or in vitro) and  
 CC result in a synergistic increase in effect when (I) is used with  
 CC chemotherapeutic agents or other antisense oligonucleotides directed  
 CC against other antiapoptotic genes. Sequences ACF36399-406 represent  
 CC antisense oligonucleotides targeted against human anti-apoptotic protein  
 CC TRPM-2 (testosterone-repressed prostate message-2) gene  
 XX  
 SQ Sequence 21 BP; 3 A; 5 C; 6 G; 7 T; 0 U; 0 Other;  
 Query Match 1.3%; Score 21; DB 1; Length 21;  
 Best Local Similarity 100.0%; Pred. No. 39;  
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
QY      114 GACCAGCGGTCTCAGACAAT 134
DB      21 GACCAGCGGTCTCAGACAAT 1

RESULT 50
ACF36402/c
ID ACF36402 standard; DNA; 21 BP.
XX
AC ACF36402;
XX
DT 18-DEC-2003 (first entry)
XX
DE TRPM-2 antisense oligonucleotide #8.
XX
TRPM-2; testosterone-repressed prostate message-2; cytostatic; androgen;
KW prostate cancer; anti-apoptotic protein; antisense; ss.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN WO2003072591-A1.
XX
PD 04-SEP-2003.
XX
PF 20-FEB-2003; 2003WO-US005305.
XX
PR 22-FEB-2002; 2002US-00080794.
XX
PA (UYBR-) UNIV BRITISH COLUMBIA.
XX
PI Gleave M, Rennie PS, Miyake H, Nelson C, Monia BP;
XX
DR WPI; 2003-689981/65.
XX
PT New modified antisense oligonucleotide, useful particularly for treating
PT prostatic cancer, inhibits the testosterone-repressed prostate message-2.
XX
PS Example 5; Page 41; 44pp; English.
XX
CC The invention relates to a compound consisting of an oligonucleotide with
CC a phosphorothioate backbone throughout, in which: (a) sugars on
CC nucleotide residues 1-4 and 18-21 are 2'-O-methoxyethyl modified, and the
CC remaining nucleotides 5-17 are 2'-deoxy; and (b) the cytosines at
CC positions 1, 4 and 19 are 5-methylated. Oligonucleotide shown in sequence
CC ACF36398 (I) is used: (a) to delay progression of androgen-sensitive
CC prostatic cancer cells to the androgen-independent state, in vivo or in
CC vitro; (b) to treat prostatic cancer (after initially withdrawing
CC androgens to induce apoptosis); and (c) to increase sensitivity of cancer
CC cells (prostatic, renal, non-small cell lung, urothelial transitional,
CC ovarian and some breast cancer cells) that express abnormal levels of
CC TRPM-2 to chemotherapy or radiation. The modifications present in (I)
CC increase stability in vivo and activity (both in vivo or in vitro) and
CC result in a synergistic increase in effect when (I) is used with
CC chemotherapeutic agents or other antisense oligonucleotides directed
CC against other antiapoptotic genes. Sequences ACF36399-406 represent
CC antisense oligonucleotides targeted against human anti-apoptotic protein
CC TRPM-2 (testosterone-repressed prostate message-2) gene
XX
SQ Sequence 21 BP; 5 A; 5 C; 8 G; 3 T; 0 U; 0 Other;

Query Match      1.3%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 39;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      716 CCGCATCGTCCGACGCTTGAT 736
DB      21 CCGCATCGTCCGACGCTTGAT 1

RESULT 51
ACF36401/c
ID ACF36401 standard; DNA; 21 BP.
XX
AC ACF36401;
XX
DT 18-DEC-2003 (first entry)
XX
DE TRPM-2 antisense oligonucleotide #7.
XX
TRPM-2; testosterone-repressed prostate message-2; cytostatic; androgen;
KW prostate cancer; anti-apoptotic protein; antisense; ss.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN WO2003072591-A1.
XX
PD 04-SEP-2003.
XX
PF 20-FEB-2003; 2003WO-US005305.
XX
PR 22-FEB-2002; 2002US-00080794.
XX
PA (UYBR-) UNIV BRITISH COLUMBIA.
XX
PI Gleave M, Rennie PS, Miyake H, Nelson C, Monia BP;
XX
DR WPI; 2003-689981/65.
XX
PT New modified antisense oligonucleotide, useful particularly for treating
PT prostatic cancer, inhibits the testosterone-repressed prostate message-2.
XX
PS Example 5; Page 41; 44pp; English.
XX
CC The invention relates to a compound consisting of an oligonucleotide with
CC a phosphorothioate backbone throughout, in which: (a) sugars on
CC nucleotide residues 1-4 and 18-21 are 2'-O-methoxyethyl modified, and the
CC remaining nucleotides 5-17 are 2'-deoxy; and (b) the cytosines at
CC positions 1, 4 and 19 are 5-methylated. Oligonucleotide shown in sequence
CC ACF36398 (I) is used: (a) to delay progression of androgen-sensitive
CC prostatic cancer cells to the androgen-independent state, in vivo or in
CC vitro; (b) to treat prostatic cancer (after initially withdrawing
CC androgens to induce apoptosis); and (c) to increase sensitivity of cancer
CC cells (prostatic, renal, non-small cell lung, urothelial transitional,
CC ovarian and some breast cancer cells) that express abnormal levels of
CC TRPM-2 to chemotherapy or radiation. The modifications present in (I)
CC increase stability in vivo and activity (both in vivo or in vitro) and
CC result in a synergistic increase in effect when (I) is used with
CC chemotherapeutic agents or other antisense oligonucleotides directed
CC against other antiapoptotic genes. Sequences ACF36399-406 represent
CC antisense oligonucleotides targeted against human anti-apoptotic protein
CC TRPM-2 (testosterone-repressed prostate message-2) gene
XX
SQ Sequence 21 BP; 5 A; 4 C; 9 G; 3 T; 0 U; 0 Other;

Query Match      1.3%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 39;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      515 TGACCGCATCGACTCCCTGCT 535
DB      21 TGACCGCATCGACTCCCTGCT 1

RESULT 52
ACF36398/c
ID ACF36398 standard; DNA; 21 BP.
XX
AC ACF36398;
XX
DT 18-DEC-2003 (first entry)
XX
DE TRPM-2 antisense oligonucleotide.
```

KW TRPM-2; testosterone-repressed prostate message-2; cytostatic; androgen;  
 KW prostate cancer; anti-apoptotic protein; antisense; ss.  
 XX Synthetic.  
 OS Homo sapiens.  
 XX WO2003072591-A1.  
 PN  
 XX  
 PD 04-SEP-2003.  
 XX  
 XX 20-FEB-2003; 2003WO-US005305.  
 PF  
 XX 22-FEB-2002; 2002US-00080794.  
 PR  
 XX (UYBR-) UNIV BRITISH COLUMBIA.  
 PA  
 XX Gleave M, Rennie PS, Miyake H, Nelson C, Monia BP;  
 PI WPI; 2003-689981/65.  
 XX  
 DR New modified antisense oligonucleotide, useful particularly for treating  
 XX prostatic cancer, inhibits the testosterone-repressed prostate message-2.  
 PT  
 XX Claim 1; Page 25; 44pp; English.  
 PS  
 XX The invention relates to a compound consisting of an oligonucleotide with  
 CC a phosphorothioate backbone throughout, in which: (a) sugars on  
 CC nucleotide residues 1-4 and 18-21 are 2'-O-methoxyethyl modified, and the  
 CC remaining nucleotides 5-17 are 2'-deoxy; and (b) the cytosines at  
 CC positions 1, 4 and 19 are 5-methylated. Oligonucleotide shown in sequence  
 CC ACF36398 (I) is used: (a) to delay progression of androgen-sensitive  
 CC prostatic cancer cells to the androgen-independent state, in vivo or in  
 CC vitro; (b) to treat prostatic cancer (after initially withdrawing  
 CC androgens to induce apoptosis); and (c) to increase sensitivity of cancer  
 CC cells (prostatic, renal, non-small cell lung, urothelial transitional,  
 CC ovarian and some breast cancer cells) that express abnormal levels of  
 CC TRPM-2 to chemotherapy or radiation. The modifications present in (I)  
 CC increase stability in vivo and activity (both in vivo or in vitro) and  
 CC result in a synergistic increase in effect when (I) is used with  
 CC chemotherapeutic agents or other antisense oligonucleotides directed  
 CC against other antiapoptotic genes. The present sequence represents a  
 CC specific example of an anti-apoptotic protein TRPM-2 (testosterone-  
 CC repressed prostate message-2) antisense oligonucleotide  
 XX  
 SQ Sequence 21 BP; 6 A; 6 C; 4 G; 5 T; 0 U; 0 Other;  
 Query Match 1.3%; Score 21; DB 1; Length 21;  
 Best Local Similarity 100.0%; Pred. No. 39;  
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 48 ATGATGAAGACTCTGCTGCTG 68  
 DB 21 ATGATGAAGACTCTGCTGCTG 1  
 RESULT 53  
 ACF36403/c  
 ID ACF36403 standard; DNA; 21 BP.  
 XX  
 XX ACF36403;  
 AC  
 XX 18-DEC-2003 (first entry)  
 DT  
 XX TRPM-2 antisense oligonucleotide #9.  
 DE  
 XX TRPM-2; testosterone-repressed prostate message-2; cytostatic; androgen;  
 KW prostate cancer; anti-apoptotic protein; antisense; ss.  
 XX Synthetic.  
 OS Homo sapiens.  
 XX WO2003072591-A1.  
 PN

PD 04-SEP-2003.  
 XX  
 XX 20-FEB-2003; 2003WO-US005305.  
 PF  
 XX 22-FEB-2002; 2002US-00080794.  
 PR  
 XX (UYBR-) UNIV BRITISH COLUMBIA.  
 PA  
 XX Gleave M, Rennie PS, Miyake H, Nelson C, Monia BP;  
 PI WPI; 2003-689981/65.  
 XX  
 DR New modified antisense oligonucleotide, useful particularly for treating  
 XX prostatic cancer, inhibits the testosterone-repressed prostate message-2.  
 PT  
 XX Example 5; Page 41; 44pp; English.  
 PS  
 XX The invention relates to a compound consisting of an oligonucleotide with  
 CC a phosphorothioate backbone throughout, in which: (a) sugars on  
 CC nucleotide residues 1-4 and 18-21 are 2'-O-methoxyethyl modified, and the  
 CC remaining nucleotides 5-17 are 2'-deoxy; and (b) the cytosines at  
 CC positions 1, 4 and 19 are 5-methylated. Oligonucleotide shown in sequence  
 CC ACF36398 (I) is used: (a) to delay progression of androgen-sensitive  
 CC prostatic cancer cells to the androgen-independent state, in vivo or in  
 CC vitro; (b) to treat prostatic cancer (after initially withdrawing  
 CC androgens to induce apoptosis); and (c) to increase sensitivity of cancer  
 CC cells (prostatic, renal, non-small cell lung, urothelial transitional,  
 CC ovarian and some breast cancer cells) that express abnormal levels of  
 CC TRPM-2 to chemotherapy or radiation. The modifications present in (I)  
 CC increase stability in vivo and activity (both in vivo or in vitro) and  
 CC result in a synergistic increase in effect when (I) is used with  
 CC chemotherapeutic agents or other antisense oligonucleotides directed  
 CC against other antiapoptotic genes. Sequences ACF36399-406 represent  
 CC antisense oligonucleotides targeted against human anti-apoptotic protein  
 CC TRPM-2 (testosterone-repressed prostate message-2) gene  
 XX  
 SQ Sequence 21 BP; 3 A; 5 C; 9 G; 4 T; 0 U; 0 Other;  
 Query Match 1.3%; Score 21; DB 1; Length 21;  
 Best Local Similarity 100.0%; Pred. No. 39;  
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 916 ACAACTCCACGGGCTGCTGTC 936  
 DB 21 ACAACTCCACGGGCTGCTGTC 1  
 RESULT 54  
 ACF36404/c  
 ID ACF36404 standard; DNA; 21 BP.  
 XX  
 XX ACF36404;  
 AC  
 XX 18-DEC-2003 (first entry)  
 DT  
 XX TRPM-2 antisense oligonucleotide #10.  
 DE  
 XX TRPM-2; testosterone-repressed prostate message-2; cytostatic; androgen;  
 KW prostate cancer; anti-apoptotic protein; antisense; ss.  
 XX Synthetic.  
 OS Homo sapiens.  
 XX WO2003072591-A1.  
 PN  
 XX 04-SEP-2003.  
 PD  
 XX 20-FEB-2003; 2003WO-US005305.  
 PF  
 XX 22-FEB-2002; 2002US-00080794.  
 PR  
 XX (UYBR-) UNIV BRITISH COLUMBIA.  
 PA

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PI Gleave M, Rennie PS, Miyake H, Nelson C, Monia BP;
XX WPI; 2003-689981/65.
DR
XX
XX New modified antisense oligonucleotide, useful particularly for treating
PT prostatic cancer, inhibits the testosterone-repressed prostate message-2.
XX
XX Example 5; Page 41; 44pp; English.
XX
XX The invention relates to a compound consisting of an oligonucleotide with
CC a phosphorothioate backbone throughout, in which: (a) sugars on
CC nucleotide residues 1-4 and 18-21 are 2'-O-methoxyethyl modified, and the
CC remaining nucleotides 5-17 are 2'-deoxy; and (b) the cytosines at
CC positions 1, 4 and 19 are 5-methylated. Oligonucleotide shown in sequence
CC ACF36398 (I) is used: (a) to delay progression of androgen-sensitive
CC prostatic cancer cells to the androgen-independent state, in vivo or in
CC vitro; (b) to treat prostatic cancer (after initially withdrawing
CC androgens to induce apoptosis); and (c) to increase sensitivity of cancer
CC cells (prostatic, renal, non-small cell lung, urothelial transitional,
CC ovarian and some breast cancer cells) that express abnormal levels of
CC TRPM-2 to chemotherapy or radiation. The modifications present in (I)
CC increase stability in vivo and activity (both in vivo or in vitro) and
CC result in a synergistic increase in effect when (I) is used with
CC chemotherapeutic agents or other antisense oligonucleotides directed
CC against other antiapoptotic genes. Sequences ACF36399-406 represent
CC antisense oligonucleotides targeted against human anti-apoptotic protein
CC TRPM-2 (testosterone-repressed prostate message-2) gene
XX
XX Sequence 21 BP; 5 A; 6 C; 6 G; 4 T; 0 U; 0 Other;
SQ
Query Match 1.3%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 39;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1115 CTCCTTGCTGGACGACTGAA 1135
DB 21 CTCCTTGCTGGACGACTGAA 1
RESULT 55
ACF36400/C
ID ACF36400 standard; DNA; 21 BP.
XX
XX ACF36400;
AC
XX
XX 18-DEC-2003 (first entry)
DT
XX
XX TRPM-2 antisense oligonucleotide #6.
DE
XX
XX TRPM-2; testosterone-repressed prostate message-2; cytostatic; androgen;
KW prostate cancer; anti-apoptotic protein; antisense; ss.
XX
XX Synthetic.
OS
XX Homo sapiens.
XX
XX WO2003072591-A1.
PN
XX
XX 04-SEP-2003.
PD
XX
XX 20-FEB-2003; 2003WO-US005305.
PF
XX
XX 22-FEB-2002; 2002US-00080794.
PR
XX
XX (UYBR-) UNIV BRITISH COLUMBIA.
PA
XX
XX Gleave M, Rennie PS, Miyake H, Nelson C, Monia BP;
PI
XX WPI; 2003-689981/65.
DR
XX
XX New modified antisense oligonucleotide, useful particularly for treating
PT prostatic cancer, inhibits the testosterone-repressed prostate message-2.
XX
XX Example 5; Page 40; 44pp; English.
PS

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```

XX The invention relates to a compound consisting of an oligonucleotide with
CC a phosphorothioate backbone throughout, in which: (a) sugars on
CC nucleotide residues 1-4 and 18-21 are 2'-O-methoxyethyl modified, and the
CC remaining nucleotides 5-17 are 2'-deoxy; and (b) the cytosines at
CC positions 1, 4 and 19 are 5-methylated. Oligonucleotide shown in sequence
CC ACF36398 (I) is used: (a) to delay progression of androgen-sensitive
CC prostatic cancer cells to the androgen-independent state, in vivo or in
CC vitro; (b) to treat prostatic cancer (after initially withdrawing
CC androgens to induce apoptosis); and (c) to increase sensitivity of cancer
CC cells (prostatic, renal, non-small cell lung, urothelial transitional,
CC ovarian and some breast cancer cells) that express abnormal levels of
CC TRPM-2 to chemotherapy or radiation. The modifications present in (I)
CC increase stability in vivo and activity (both in vivo or in vitro) and
CC result in a synergistic increase in effect when (I) is used with
CC chemotherapeutic agents or other antisense oligonucleotides directed
CC against other antiapoptotic genes. Sequences ACF36399-406 represent
CC antisense oligonucleotides targeted against human anti-apoptotic protein
CC TRPM-2 (testosterone-repressed prostate message-2) gene
XX
XX Sequence 21 BP; 2 A; 6 C; 3 G; 10 T; 0 U; 0 Other;
SQ
Query Match 1.3%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 39;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 316 AATCAGACACAAAGCTGAAGG 336
DB 21 AATCAGACACAAAGCTGAAGG 1
RESULT 56
ADF75347
ID ADF75347 standard; DNA; 21 BP.
XX
XX ADF75347;
AC
XX
XX 26-FEB-2004 (first entry)
DT
XX
XX Human RT-PCR primer to amplify an epigenetically silenced gene (SeqID27) .
DE
XX
XX human; primer; RT-PCR; PCR; ss; epigenetically silenced gene;
KW tumour suppressor; cancer; proliferative disorder; head and neck cancer;
KW oesophageal squamous cell carcinoma; ESCC; gene therapy;
KW methyltransferase inhibitor; 5Aza-dC; histone deacetylase inhibitor.
XX
XX Homo sapiens.
OS
XX
XX WO2003076594-A2.
PN
XX
XX 18-SEP-2003.
PD
XX
XX 07-MAR-2003; 2003WO-US007245.
PF
XX
XX 07-MAR-2002; 2002US-0362577P.
PR
XX
XX (UYJO ) UNIV JOHNS HOPKINS.
PA
XX
XX Sidransky D;
PI
XX
XX WPI; 2003-756817/71.
DR
XX
XX Identifying at least one epigenetically silenced gene associated with
PT cancer useful for treating cancer comprises contacting an array of genome
PT with nucleic acid molecule that reactivates expression of epigenetically
PT silenced gene.
XX
XX Example 1; SEQ ID NO 27; 97pp; English.
PS
XX
XX This invention relates to novel methods of screening to identify
CC epigenetically silenced genes. Specifically, it refers to the detection
CC of epigenetically silenced tumour suppressor genes in cancer cells, which
CC are transcriptionally inactive due to aberrant methylation at normally

```



CC unmethylated CpG islands. Accordingly, these genes provide diagnostic  
 CC markers for immortalised and transformed cells and hence can be used to  
 CC diagnose various proliferative disorders, particularly oesophageal cancer  
 CC and head and neck cancer. The present invention describes a genomic  
 CC screening method to identify silenced genes in a cell suspected of a  
 CC predisposition to, or exhibiting, unregulated growth. Accordingly,  
 CC oligonucleotides of the genes identified herein are useful for detecting  
 CC oesophageal squamous cell carcinoma (ESCC) or neck squamous cell  
 CC carcinoma. Furthermore, treatment can occur via gene therapy, using a  
 CC demethylation agent such as a methyltransferase inhibitor (5Aza-dC) or a  
 CC histone deacetylase inhibitor to restore expression of at least one  
 CC methylation silenced gene in cancer cells. This oligonucleotide sequence  
 CC is an RT-PCR primer used to amplify those genes that were up-regulated as  
 CC a result of treatment with a demethylation agent i.e. epigenetically  
 CC silenced genes of the invention.

SQ Sequence 21 BP; 6 A; 10 C; 3 G; 2 T; 0 U; 0 Other;

Query Match 1.3%; Score 21; DB 1; Length 21;  
 Best Local Similarity 100.0%; Pred. No. 39;  
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 994 ACAACCCCTCCAGGCTAAGC 1014  
 DB 1 ACAACCCCTCCAGGCTAAGC 21

RESULT 57

ADP75348/c  
 ID ADF75340 standard; DNA; 21 BP.

AC ADF75348;

DT 26-FEB-2004 (first entry)

XX Human RT-PCR primer to amplify an epigenetically silenced gene (SeqID28).  
 KW human; primer; RT-PCR; PCR; ss; epigenetically silenced gene;  
 KW tumour suppressor; cancer; proliferative disorder; head and neck cancer;  
 KW oesophageal squamous cell carcinoma; ESCC; gene therapy;  
 KW methyltransferase inhibitor; 5Aza-dC; histone deacetylase inhibitor.

OS Homo sapiens.

PN WO2003076594-A2.

PD 18-SEP-2003.

PF 07-MAR-2003; 2003WO-US007245.

PR 07-MAR-2002; 2002US-0362577P.

PA (UYJO ) UNIV JOHNS HOPKINS.

PI Sidransky D;

DR WPI; 2003-756817/71.

PT Identifying at least one epigenetically silenced gene associated with  
 PT cancer useful for treating cancer comprises contacting an array of genome  
 PT with nucleic acid molecule that reactives expression of epigenetically  
 PT silenced gene.

PS Example 1; SEQ ID NO 28; 97pp; English.

XX This invention relates to novel methods of screening to identify  
 CC epigenetically silenced genes. Specifically, it refers to the detection  
 CC of epigenetically silenced tumour suppressor genes in cancer cells, which  
 CC are transcriptionally inactive due to aberrant methylation at normally  
 CC unmethylated CpG islands. Accordingly, these genes provide diagnostic  
 CC markers for immortalised and transformed cells and hence can be used to  
 CC diagnose various proliferative disorders, particularly oesophageal cancer  
 CC and head and neck cancer. The present invention describes a genomic

CC screening method to identify silenced genes in a cell suspected of a  
 CC predisposition to, or exhibiting, unregulated growth. Accordingly,  
 CC oligonucleotides of the genes identified herein are useful for detecting  
 CC oesophageal squamous cell carcinoma (ESCC) or neck squamous cell  
 CC carcinoma. Furthermore, treatment can occur via gene therapy, using a  
 CC demethylation agent such as a methyltransferase inhibitor (5Aza-dC) or a  
 CC histone deacetylase inhibitor to restore expression of at least one  
 CC methylation silenced gene in cancer cells. This oligonucleotide sequence  
 CC is an RT-PCR primer used to amplify those genes that were up-regulated as  
 CC a result of treatment with a demethylation agent i.e. epigenetically  
 CC silenced genes of the invention.

SQ Sequence 21 BP; 5 A; 8 C; 3 G; 5 T; 0 U; 0 Other;

Query Match 1.3%; Score 21; DB 1; Length 21;  
 Best Local Similarity 100.0%; Pred. No. 39;  
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1334 ATTTATGGAGACCGTGGCGGA 1354  
 DB 21 ATTTATGGAGACCGTGGCGGA 1

RESULT 58

ADM83075/c

ID ADM83075 standard; DNA; 21 BP.

AC ADM83075;

XX 03-JUN-2004 (first entry)

DE Human TRPM-2 antisense oligonucleotide #10.

XX Testosterone-repressed prostate message-2; TRPM-2; chemo-sensitivity;  
 KW radiation-sensitivity; prostate cancer; bladder cancer; ovarian cancer;  
 KW lung cancer; renal cell carcinoma; RCC; antisense gene therapy; human;  
 KW antisense; ss.

OS Homo sapiens.

OS Synthetic.

XX Key Location/Qualifiers

FT modified\_base 1..21

FT /tag= a

FT /mod\_base= OTHER

FT /note= "Phosphorothioate backbone"

XX US2003158130-A1.

XX 21-AUG-2003.

XX 28-SEP-2001; 2001US-00967726.

XX 25-FEB-2000; 2000WO-US004875.

XX 28-SEP-2000; 2000US-0236301P.

XX 10-AUG-2001; 2001US-00913325.

XX (GLEA/) GLEAVE M.

XX (RENN/) RENNIE P S.

XX (MIYA/) MIYAKE H.

XX (NELS/) NELSON C.

XX (ZELL/) ZELLWEGER T.

XX Gleave M, Rennie PS, Miyake H, Nelson C, Zellweger T;

XX WPI; 2003-778017/73.

XX Enhancing the chemo-sensitivity or radiation-sensitivity of cancer cells  
 PT that expresses testosterone-repressed prostate message-2 (TRPM-2)  
 PT comprises administering a composition that inhibits expression of TRPM-2.  
 XX Disclosure; SEQ ID NO 10; 14pp; English.

XX

CC The present invention provides a method for treating cancer in which  
CC cancer cells express testosterone-repressed prostate message-2 (TRPM-2).  
CC The invention is useful for enhancing the chemo-sensitivity or radiation-  
CC sensitivity of cancer cells for treating cancer such as prostate cancer,  
CC bladder cancer, ovarian cancer, lung cancer and renal cell carcinoma  
CC (RCC). The invention is also useful in antisense gene therapy. The  
CC present sequence is human testosterone-repressed prostate message-2 (TRPM  
CC -2) antisense oligodeoxyribonucleotide (ODN).  
XX

Sequence 21 BP; 5 A; 6 C; 6 G; 4 T; 0 U; 0 Other;  
Query Match 1.3%; Score 21; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 39;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1115 CTCCTTGCTGGAGCAGCTGAA 1135

Db 21 CTCCTTGCTGGAGCAGCTGAA 1

RESULT 59

ADM83077/c

ID ADM83077 standard; DNA; 21 BP.

AC ADM83077;

XX 03-JUN-2004 (first entry)

DT Human TRPM-2 antisense oligonucleotide #12.

XX Testosterone-repressed prostate message-2; TRPM-2; chemo-sensitivity;

XX radiation-sensitivity; prostate cancer; bladder cancer; ovarian cancer;

XX lung cancer; renal cell carcinoma; RCC; antisense gene therapy; human;

XX antisense; ss.

OS Homo sapiens.

OS Synthetic.

XX Key Location/Qualifiers

FT modified\_base 1..21

FT /\*tag= a

FT /mod\_base= OTHER

FT /note= "Phosphorothioate backbone"

XX US2003158130-A1.

XX 21-AUG-2003.

XX 28-SEP-2001; 2001US-00967726.

XX 25-FEB-2000; 2000WO-US004875.

XX 28-SEP-2000; 2000US-0236301P.

XX 10-AUG-2001; 2001US-00913325.

XX (GLEA/) GLEAVE M.

XX (RENN/) RENNIE P S.

XX (MIYA/) MIYAKE H.

XX (NELS/) NELSON C.

XX (ZELL/) ZELLWEGER T.

XX Gleave M, Rennie PS, Miyake H, Nelson C, Zellweger T;

XX WPI; 2003-778017/73.

XX Enhancing the chemo-sensitivity or radiation-sensitivity of cancer cells

XX that expresses testosterone-repressed prostate message-2 (TRPM-2)

XX comprises administering a composition that inhibits expression of TRPM-2.

XX Claim 6; SEQ ID NO 12; 14pp; English.

XX The present invention provides a method for treating cancer in which

XX cancer cells express testosterone-repressed prostate message-2 (TRPM-2).

XX The invention is useful for enhancing the chemo-sensitivity or radiation-

CC sensitivity of cancer cells for treating cancer such as prostate cancer,  
CC bladder cancer, ovarian cancer, lung cancer and renal cell carcinoma  
CC (RCC). The invention is also useful in antisense gene therapy. The  
CC present sequence is human testosterone-repressed prostate message-2 (TRPM  
CC -2) antisense oligodeoxyribonucleotide (ODN).  
XX

Sequence 21 BP; 1 A; 4 C; 12 G; 4 T; 0 U; 0 Other;

Query Match

Best Local Similarity 1.3%; Score 21; DB 1; Length 21;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1516 AGGCCCCCAACTCCGCCGAGC 1536

Db 21 AGGCCCCCAACTCCGCCGAGC 1

RESULT 60

ADM83072/c

ID ADM83072 standard; DNA; 21 BP.

XX ADM83072;

XX 03-JUN-2004 (first entry)

DT Human TRPM-2 antisense oligonucleotide #7.

XX Testosterone-repressed prostate message-2; TRPM-2; chemo-sensitivity;

XX radiation-sensitivity; prostate cancer; bladder cancer; ovarian cancer;

XX lung cancer; renal cell carcinoma; RCC; antisense gene therapy; human;

XX antisense; ss.

XX Homo sapiens.

XX Synthetic.

XX Key Location/Qualifiers

FT modified\_base 1..21

FT /\*tag= a

FT /mod\_base= OTHER

FT /note= "Phosphorothioate backbone"

XX US2003158130-A1.

XX 21-AUG-2003.

XX 28-SEP-2001; 2001US-00967726.

XX 25-FEB-2000; 2000WO-US004875.

XX 28-SEP-2000; 2000US-0236301P.

XX 10-AUG-2001; 2001US-00913325.

XX (GLEA/) GLEAVE M.

XX (RENN/) RENNIE P S.

XX (MIYA/) MIYAKE H.

XX (NELS/) NELSON C.

XX (ZELL/) ZELLWEGER T.

XX Gleave M, Rennie PS, Miyake H, Nelson C, Zellweger T;

XX WPI; 2003-778017/73.

XX Enhancing the chemo-sensitivity or radiation-sensitivity of cancer cells

XX that expresses testosterone-repressed prostate message-2 (TRPM-2)

XX comprises administering a composition that inhibits expression of TRPM-2.

XX Disclosure; SEQ ID NO 7; 14pp; English.

XX The present invention provides a method for treating cancer in which

XX cancer cells express testosterone-repressed prostate message-2 (TRPM-2).

XX The invention is useful for enhancing the chemo-sensitivity or radiation-

XX sensitivity of cancer cells for treating cancer such as prostate cancer,

XX bladder cancer, ovarian cancer, lung cancer and renal cell carcinoma

XX (RCC). The invention is also useful in antisense gene therapy. The

CC present sequence is human testosterone-repressed prostate message-2 (TRPM-2)  
CC -2) antisense oligodeoxyribonucleotide (ODN).

XX Sequence 21 BP; 5 A; 4 C; 9 G; 3 T; 0 U; 0 Other;

Query Match 1.3%; Score 21; DB 1; Length 21;

Best Local Similarity 100.0%; Pred. No. 39;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 515 TGACCGATCGACTCCCTGCT 535

DB 21 TGACCGATCGACTCCCTGCT 1

RESULT 61

ADM83074/c

ID ADM83074 standard; DNA; 21 BP.

XX

AC ADM83074;

XX 03-JUN-2004 (first entry)

DE Human TRPM-2 antisense oligonucleotide #9.

XX Testosterone-repressed prostate message-2; TRPM-2; chemo-sensitivity;  
KW radiation-sensitivity; prostate cancer; bladder cancer; ovarian cancer;  
KW lung cancer; renal cell carcinoma; RCC; antisense gene therapy; human;  
KW antisense; ss.

XX Homo sapiens.

OS Synthetic.

XX

XX Key Location/Qualifiers

FT modified\_base 1..21

FT /tag= a

FT /mod\_base= OTHER

FT /note= "Phosphorothioate backbone"

XX US2003158130-A1.

XX 21-AUG-2003.

XX 28-SEP-2001; 2001US-00967726.

XX 25-FEB-2000; 2000WO-US004875.

XX 28-SEP-2000; 2000US-0236301P.

XX 10-AUG-2001; 2001US-00913325.

XX (GLEA/) GLEAVE M.

XX (RENN/) RENNIE P S.

XX (MIYA/) MIYAKE H.

XX (NELS/) NELSON C.

XX (ZELL/) ZELLWEGER T.

XX Gleave M, Rennie PS, Miyake H, Nelson C, Zellweger T;

XX WPI; 2003-778017/73.

XX Enhancing the chemo-sensitivity or radiation-sensitivity of cancer cells  
PT that expresses testosterone-repressed prostate message-2 (TRPM-2)  
PT comprises administering a composition that inhibits expression of TRPM-2.

XX Disclosure; SEQ ID NO 9; 14pp; English.

XX The present invention provides a method for treating cancer in which  
CC cancer cells express testosterone-repressed prostate message-2 (TRPM-2).  
CC The invention is useful for enhancing the chemo-sensitivity or radiation-  
CC sensitivity of cancer cells for treating cancer such as prostate cancer,  
CC bladder cancer, ovarian cancer, lung cancer and renal cell carcinoma  
CC (RCC). The invention is also useful in antisense gene therapy. The  
CC present sequence is human testosterone-repressed prostate message-2 (TRPM  
CC -2) antisense oligodeoxyribonucleotide (ODN).

SQ Sequence 21 BP; 3 A; 5 C; 9 G; 4 T; 0 U; 0 Other;

Query Match 1.3%; Score 21; DB 1; Length 21;

Best Local Similarity 100.0%; Pred. No. 39;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 916 ACAACTCCACGGGCTGCCTGC 936

DB 21 ACAACTCCACGGGCTGCCTGC 1

RESULT 62

ADM83076/c

ID ADM83076 standard; DNA; 21 BP.

XX

AC ADM83076;

XX 03-JUN-2004 (first entry)

DE Human TRPM-2 antisense oligonucleotide #11.

XX Testosterone-repressed prostate message-2; TRPM-2; chemo-sensitivity;  
KW radiation-sensitivity; prostate cancer; bladder cancer; ovarian cancer;  
KW lung cancer; renal cell carcinoma; RCC; antisense gene therapy; human;  
KW antisense; ss.

XX Homo sapiens.

OS Synthetic.

XX

XX Key Location/Qualifiers

FT modified\_base 1..21

FT /tag= a

FT /mod\_base= OTHER

FT /note= "Phosphorothioate backbone"

XX US2003158130-A1.

XX 21-AUG-2003.

XX 28-SEP-2001; 2001US-00967726.

XX 25-FEB-2000; 2000WO-US004875.

XX 28-SEP-2000; 2000US-0236301P.

XX 10-AUG-2001; 2001US-00913325.

XX (GLEA/) GLEAVE M.

XX (RENN/) RENNIE P S.

XX (MIYA/) MIYAKE H.

XX (NELS/) NELSON C.

XX (ZELL/) ZELLWEGER T.

XX Gleave M, Rennie PS, Miyake H, Nelson C, Zellweger T;

XX WPI; 2003-778017/73.

XX Enhancing the chemo-sensitivity or radiation-sensitivity of cancer cells  
PT that expresses testosterone-repressed prostate message-2 (TRPM-2)  
PT comprises administering a composition that inhibits expression of TRPM-2.

XX Disclosure; SEQ ID NO 11; 14pp; English.

XX The present invention provides a method for treating cancer in which  
CC cancer cells express testosterone-repressed prostate message-2 (TRPM-2).  
CC The invention is useful for enhancing the chemo-sensitivity or radiation-  
CC sensitivity of cancer cells for treating cancer such as prostate cancer,  
CC bladder cancer, ovarian cancer, lung cancer and renal cell carcinoma  
CC (RCC). The invention is also useful in antisense gene therapy. The  
CC present sequence is human testosterone-repressed prostate message-2 (TRPM  
CC -2) antisense oligodeoxyribonucleotide (ODN).

XX Sequence 21 BP; 4 A; 3 C; 6 G; 8 T; 0 U; 0 Other;

XX Query Match 1.3%; Score 21; DB 1; Length 21;

Best Local Similarity 100.0%; Pred. No. 39; Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1316 CTCGAGGAAGAACCTAAATT 1336  
Db 21 CTCGAGGAGACCTTAATT 1

RESULT 63  
ADM83068/c  
ID ADM83068 standard; DNA; 21 BP.  
XX AC ADM83068;  
XX DT 03-JUN-2004 (first entry)  
XX DE Human TRPM-2 antisense oligonucleotide #3.  
XX KW Testosterone-repressed prostate message-2; TRPM-2; chemo-sensitivity;  
XX KW radiation-sensitivity; prostate cancer; bladder cancer; ovarian cancer;  
XX KW lung cancer; renal cell carcinoma; RCC; antisense gene therapy; human;  
XX KW antisense; ss.  
XX OS Homo sapiens.  
XX OS Synthetic.  
FH Key Location/Qualifiers  
FT modified\_base 1..21 /\*tag= a  
FT FT /mod\_base= OTHER  
FT FT /note= "Phosphorothioate backbone"  
XX XX US2003158130-A1.  
XX PD 21-AUG-2003.  
XX PF 28-SEP-2001; 2001US-00967726.  
XX PR 25-FEB-2000; 2000WO-US004875.  
XX PR 28-SEP-2000; 2000US-0236301P.  
XX PR 10-AUG-2001; 2001US-00913325.  
XX PA (GLEA/) GLEAVE M.  
XX PA (RENN/) RENNIE P S.  
XX PA (MIYA/) MIYAKE H.  
XX PA (NELS/) NELSON C.  
XX PA (ZELL/) ZELWEGGER T.  
XX PI Gleave M, Rennie PS, Miyake H, Nelson C, Zellweger T;  
XX DR WPI; 2003-778017/73.  
XX PT Enhancing the chemo-sensitivity or radiation-sensitivity of cancer cells  
XX PT that expresses testosterone-repressed prostate message-2 (TRPM-2)  
XX PT comprises administering a composition that inhibits expression of TRPM-2.  
XX PS Disclosure; SEQ ID NO 3; 14pp; English.  
XX CC The present invention provides a method for treating cancer in which  
XX CC cancer cells express testosterone-repressed prostate message-2 (TRPM-2).  
XX CC The invention is useful for enhancing the chemo-sensitivity or radiation-  
XX CC sensitivity of cancer cells for treating cancer such as prostate cancer,  
XX CC bladder cancer, ovarian cancer, lung cancer and renal cell carcinoma  
XX CC (RCC). The invention is also useful in antisense gene therapy. The  
XX CC present sequence is human testosterone-repressed prostate message-2 (TRPM  
XX CC -2) antisense oligodeoxyribonucleotide (ODN).  
XX SQ Sequence 21 BP; 2 A; 6 C; 7 G; 6 T; 0 U; 0 Other;  
  
Query Match 1.3%; Score 21; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 39;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 48 ATGATGAAGACTTCTGCTG 68  
Db 21 ATGATGAAGACTTCTGCTG 1

RESULT 64  
ADM83069/c  
ID ADM83069 standard; DNA; 21 BP.  
XX AC ADM83069;  
XX DT 03-JUN-2004 (first entry)  
XX DE Human TRPM-2 antisense oligonucleotide #4.  
XX KW Testosterone-repressed prostate message-2; TRPM-2; chemo-sensitivity;  
XX KW radiation-sensitivity; prostate cancer; bladder cancer; ovarian cancer;  
XX KW lung cancer; renal cell carcinoma; RCC; antisense gene therapy; human;  
XX KW antisense; ss.  
XX OS Homo sapiens.  
XX OS Synthetic.  
FH Key Location/Qualifiers  
FT modified\_base 1..21 /\*tag= a  
FT FT /mod\_base= OTHER  
FT FT /note= "Phosphorothioate backbone"  
XX XX US2003158130-A1.  
XX PD 21-AUG-2003.  
XX PF 28-SEP-2001; 2001US-00967726.  
XX PR 25-FEB-2000; 2000WO-US004875.  
XX PR 28-SEP-2000; 2000US-0236301P.  
XX PR 10-AUG-2001; 2001US-00913325.  
XX PA (GLEA/) GLEAVE M.  
XX PA (RENN/) RENNIE P S.  
XX PA (MIYA/) MIYAKE H.  
XX PA (NELS/) NELSON C.  
XX PA (ZELL/) ZELWEGGER T.  
XX PI Gleave M, Rennie PS, Miyake H, Nelson C, Zellweger T;  
XX DR WPI; 2003-778017/73.  
XX PT Enhancing the chemo-sensitivity or radiation-sensitivity of cancer cells  
XX PT that expresses testosterone-repressed prostate message-2 (TRPM-2)  
XX PT comprises administering a composition that inhibits expression of TRPM-2.  
XX PS Claim 4; SEQ ID NO 4; 14pp; English.  
XX CC The present invention provides a method for treating cancer in which  
XX CC cancer cells express testosterone-repressed prostate message-2 (TRPM-2).  
XX CC The invention is useful for enhancing the chemo-sensitivity or radiation-  
XX CC sensitivity of cancer cells for treating cancer such as prostate cancer,  
XX CC bladder cancer, ovarian cancer, lung cancer and renal cell carcinoma  
XX CC (RCC). The invention is also useful in antisense gene therapy. The  
XX CC present sequence is human testosterone-repressed prostate message-2 (TRPM  
XX CC -2) antisense oligodeoxyribonucleotide (ODN).  
XX SQ Sequence 21 BP; 6 A; 6 C; 4 G; 5 T; 0 U; 0 Other;  
  
Query Match 1.3%; Score 21; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 39;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
RESULT 65
ADM83070/c
ID ADM83070 standard; DNA; 21 BP.
XX
XX
AC ADM83070;
XX
XX
DT 03-JUN-2004 (first entry)
XX
XX
DE Human TRPM-2 antisense oligonucleotide #5.
XX
XX
KW Testosterone-repressed prostate message-2; TRPM-2; chemo-sensitivity;
KW radiation-sensitivity; prostate cancer; bladder cancer; ovarian cancer;
KW lung cancer; renal cell carcinoma; RCC; antisense gene therapy; human;
KW antisense; ss.
XX
XX
OS Homo sapiens.
OS Synthetic.
XX
XX
FH Key Location/Qualifiers
FT modified_base 1..21
FT /*tag= a
FT /mod_base= OTHER
FT /note= "Phosphorothioate backbone"
XX
XX
US2003158130-A1.
XX
XX
PD 21-AUG-2003.
XX
XX
PF 28-SEP-2001; 2001US-00967726.
XX
XX
PR 25-FEB-2000; 2000WO-US004875.
PR 28-SEP-2000; 2000US-0236301P.
PR 10-AUG-2001; 2001US-00913325.
XX
XX
PA (GLEA/) GLEAVE M.
PA (RENN/) RENNIE P S.
PA (MIYA/) MIYAKE H.
PA (NELS/) NELSON C.
PA (ZELL/) ZELLWEGER T.
XX
XX
PI Gleave M, Rennie PS, Miyake H, Nelson C, Zellweger T;
XX
XX
WPI; 2003-778017/73.
XX
XX
PT Enhancing the chemo-sensitivity or radiation-sensitivity of cancer cells
PT that expresses testosterone-repressed prostate message-2 (TRPM-2).
PT comprises administering a composition that inhibits expression of TRPM-2.
XX
XX
PS Claim 5; SEQ ID NO 5; 14pp; English.
XX
XX
CC The present invention provides a method for treating cancer in which
CC cancer cells express testosterone-repressed prostate message-2 (TRPM-2).
CC The invention is useful for enhancing the chemo-sensitivity or radiation-
CC sensitivity of cancer cells for treating cancer such as prostate cancer,
CC bladder cancer, ovarian cancer, lung cancer and renal cell carcinoma
CC (RCC). The invention is also useful in antisense gene therapy. The
CC present sequence is human testosterone-repressed prostate message-2 (TRPM
CC -2) antisense oligodeoxyribonucleotide (ODN).
XX
XX
SQ Sequence 21 BP; 3 A; 5 C; 6 G; 7 T; 0 U; 0 Other;
XX
XX
Query Match 1.3%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 39;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 114 GACCAGACGGTCTCAGACAAAT 134
|||||
Db 21 GACCAGACGGTCTCAGACAAAT 1

RESULT 66
```

```
ADM83073/c
ID ADM83073 standard; DNA; 21 BP.
XX
XX
AC ADM83073;
XX
XX
DT 03-JUN-2004 (first entry)
XX
XX
DE Human TRPM-2 antisense oligonucleotide #8.
XX
XX
KW Testosterone-repressed prostate message-2; TRPM-2; chemo-sensitivity;
KW radiation-sensitivity; prostate cancer; bladder cancer; ovarian cancer;
KW lung cancer; renal cell carcinoma; RCC; antisense gene therapy; human;
KW antisense; ss.
XX
XX
OS Homo sapiens.
OS Synthetic.
XX
XX
FH Key Location/Qualifiers
FT modified_base 1..21
FT /*tag= a
FT /mod_base= OTHER
FT /note= "Phosphorothioate backbone"
XX
XX
US2003158130-A1.
XX
XX
PD 21-AUG-2003.
XX
XX
PF 28-SEP-2001; 2001US-00967726.
XX
XX
PR 25-FEB-2000; 2000WO-US004875.
PR 28-SEP-2000; 2000US-0236301P.
PR 10-AUG-2001; 2001US-00913325.
XX
XX
PA (GLEA/) GLEAVE M.
PA (RENN/) RENNIE P S.
PA (MIYA/) MIYAKE H.
PA (NELS/) NELSON C.
PA (ZELL/) ZELLWEGER T.
XX
XX
PI Gleave M, Rennie PS, Miyake H, Nelson C, Zellweger T;
XX
XX
WPI; 2003-778017/73.
XX
XX
PT Enhancing the chemo-sensitivity or radiation-sensitivity of cancer cells
PT that expresses testosterone-repressed prostate message-2 (TRPM-2)
PT comprises administering a composition that inhibits expression of TRPM-2.
XX
XX
PS Disclosure; SEQ ID NO 8; 14pp; English.
XX
XX
CC The present invention provides a method for treating cancer in which
CC cancer cells express testosterone-repressed prostate message-2 (TRPM-2).
CC The invention is useful for enhancing the chemo-sensitivity or radiation-
CC sensitivity of cancer cells for treating cancer such as prostate cancer,
CC bladder cancer, ovarian cancer, lung cancer and renal cell carcinoma
CC (RCC). The invention is also useful in antisense gene therapy. The
CC present sequence is human testosterone-repressed prostate message-2 (TRPM
CC -2) antisense oligodeoxyribonucleotide (ODN).
XX
XX
SQ Sequence 21 BP; 5 A; 5 C; 8 G; 3 T; 0 U; 0 Other;
XX
XX
Query Match 1.3%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 39;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 716 CCGCATCGTCGCGACGTTGAT 736
|||||
Db 21 CCGCATCGTCGCGACGTTGAT 1

RESULT 67
ADM83071/c
ID ADM83071 standard; DNA; 21 BP.
XX
```

```
AC ADM83071;
XX
XX
XX 03-JUN-2004 (first entry)
XX
XX Human TRPM-2 antisense oligonucleotide #6.
XX
XX Testosterone-repressed prostate message-2; TRPM-2; chemo-sensitivity;
KW radiation-sensitivity; prostate cancer; bladder cancer; ovarian cancer;
KW lung cancer; renal cell carcinoma; RCC; antisense gene therapy; human;
KW antisense; ss.
XX
XX Homo sapiens.
OS
XX Synthetic.
XX
XX Key Location/Qualifiers
FH modified_base 1..21
FT /*tag= a
FT /*mod_base= OTHER
FT /*note= "Phosphorothioate backbone"
XX
XX US2003158130-A1.
XX
XX 21-AUG-2003.
XX
XX 28-SEP-2001; 2001US-00967726.
XX
XX 25-FEB-2000; 2000WO-US004875.
PR 28-SEP-2000; 2000US-0236301P.
PR 10-AUG-2001; 2001US-00913325.
XX
XX (GLEA/) GLEAVE M.
PA (RENN/) RENNIE P S.
PA (MIYA/) MIYAKE H.
PA (NELS/) NELSON C.
PA (ZELL/) ZELLWEGER T.
XX
XX Gleave M, Rennie PS, Miyake H, Nelson C, Zellweger T;
XX
XX WPI; 2003-778017/73.
XX
XX Enhancing the chemo-sensitivity or radiation-sensitivity of cancer cells
PT that expresses testosterone-repressed prostate message-2 (TRPM-2)
PT comprises administering a composition that inhibits expression of TRPM-2.
XX
XX Disclosure; SEQ ID NO 6; 14pp; English.
XX
XX The present invention provides a method for treating cancer in which
CC cancer cells express testosterone-repressed prostate message-2 (TRPM-2).
CC The invention is useful for enhancing the chemo-sensitivity or radiation-
CC sensitivity of cancer cells for treating cancer such as prostate cancer,
CC bladder cancer, ovarian cancer, lung cancer and renal cell carcinoma
CC (RCC). The invention is also useful in antisense gene therapy. The
CC present sequence is human testosterone-repressed prostate message-2 (TRPM
CC -2) antisense oligodeoxyribonucleotide (ODN).
XX
XX Sequence 21 BP; 2 A; 6 C; 3 G; 10 T; 0 U; 0 Other;
SQ
Query Match 1.3%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 39;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 316 AATCAGACAAAGCTGAAGG 336
Db 21 AATCAGACAAAGCTGAAGG 1
RESULT 68
ADL70456
ID ADL70456 standard; RNA; 21 BP.
XX
XX AC ADL70456;
XX
XX 20-MAY-2004 (first entry)
DT
XX
XX RNAi for human clusterin.
DE
XX
XX RNA interference; RNAi; short interfering RNA; siRNA; human; clusterin;
KW cytosolic; neuroprotective; nontropic; gene silencing; DNA-RNA hybrid;
KW ss.
XX
XX Homo sapiens.
OS
XX Synthetic.
XX
XX Key Location/Qualifiers
FH modified_base 20..21
FT /*tag= a
FT /*mod_base= OTHER
FT /*note= "OTHER= GTdT"
XX
XX WO2004018676-A2.
XX
XX 04-MAR-2004.
XX
XX 21-AUG-2003; 2003WO-CA001277.
XX
XX 21-AUG-2002; 2002US-0405193P.
PR 03-SEP-2002; 2002US-0408152P.
PR 20-MAY-2003; 2003US-0472387P.
XX
XX (UYBR-) UNIV BRITISH COLUMBIA.
PA
XX Jansen B, Gleave ME, Signaevsky M, Beraldi E, Trougakos IP;
PI Gonos ES;
XX
XX WPI; 2004-226852/21.
XX
XX New RNA molecule less than 49 bases and having a sequence effective to
PT mediate degradation or block translation of mRNA that is the
PT transcriptional product of a target gene, useful for treating Alzheimer's
PT disease or cancer.
XX
XX Claim 4; SEQ ID NO 1; 63pp; English.
XX
XX The present sequence is the sense strand of a short interfering RNA
CC (siRNA) targeted to nucleotides 487-505 of human clusterin cDNA. The
CC antisense strand is also provided ADL70457. The siRNA can be used to
CC interfere with the expression of clusterin. Clusterin, also known as
CC testosterone-repressed prostate message-2 (TRPM-2) or sulfated
CC glycoprotein-2 (SGP-2), is expressed in increased amounts by prostate
CC tumour cells following androgen withdrawal, and has also been shown to be
CC critical for neuritic toxicity in mouse models of Alzheimer's disease.
CC siRNAs of the invention can be used alone or in combination with other
CC chemotherapy or apoptosis inducing treatments for the treatment of
CC prostate cancer, sarcomas such as osteosarcoma, renal cell carcinoma,
CC breast cancer, bladder cancer, lung cancer, colon cancer, ovarian cancer,
CC anaplastic large cell lymphoma and melanoma, and also for the treatment
CC of Alzheimer's disease.
XX
XX Sequence 21 BP; 3 A; 9 C; 3 G; 2 T; 4 U; 0 Other;
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QY 482 CCAGAGCTCGCCCTTCTACTT 502
Db 1 CCAGAGCUCCGCCUUCUACTT 21
RESULT 69
ADL70460
ID ADL70460 standard; RNA; 21 BP.
XX
XX AC ADL70460;
XX
XX 20-MAY-2004 (first entry)
DT
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```
XX RNAi for human clusterin.
DE
XX
XX RNA interference; RNAi; short interfering RNA; siRNA; human; clusterin;
KW cytosolic; neuroprotective; nontropic; gene silencing; DNA-RNA hybrid;
KW ss.
XX
XX Homo sapiens.
OS
XX Synthetic.
OS
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XX 03-SEP-2002; 2002US-0408152P.
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XX 20-MAY-2003; 2003US-0472387P.
PR
XX
XX (UYBR-) UNIV BRITISH COLUMBIA.
XX
XX Jansen B, Gleave ME, Signaevsky M, Beraldi E, Trougakos IP;
PI Gonos ES;
PI
XX
XX WPI; 2004-226852/21.
XX
XX New RNA molecule less than 49 bases and having a sequence effective to
PT mediate degradation or block translation of mRNA that is the
PT transcriptional product of a target gene, useful for treating Alzheimer's
PT disease or cancer.
XX
XX Claim 4; SEQ ID NO 5; 63pp; English.
XX
XX The present sequence is the sense strand of a short interfering RNA
CC (siRNA) targeted to nucleotides 1620-1638 of human clusterin cDNA. The
CC antisense strand is also provided ADL70461. The siRNA can be used to
CC interfere with the expression of clusterin. Clusterin, also known as
CC testosterone-repressed prostate message-2 (TRPM-2) or sulfated
CC glycoprotein-2 (SGP-2), is expressed in increased amounts by prostate
CC tumour cells following androgen withdrawal, and has also been shown to be
CC critical for neuritic toxicity in mouse models of Alzheimer's disease.
CC siRNAs of the invention can be used alone or in combination with other
CC chemotherapy or apoptosis inducing treatments for the treatment of
CC prostate cancer, sarcomas such as osteosarcoma, renal cell carcinoma,
CC breast cancer, bladder cancer, lung cancer, colon cancer, ovarian cancer,
CC anaplastic large cell lymphoma and melanoma, and also for the treatment
CC of Alzheimer's disease.
XX
XX Sequence 21 BP; 8 A; 4 C; 1 G; 2 T; 6 U; 0 Other;
SQ
Query Match 1.3%; Score 21; DB 1; Length 21;
Best Local Similarity 71.4%; Pred. No. 39;
Matches 19; Conservative 6; Mismatches 0; Indels 0; Gaps 0;
QY 1615 CTAATTCAATTAATAACTGTCTT 1635
DB 1 CUAUAUCAAUAUAAACUGUCTT 21
RESULT 70
ADL70513
ID ADL70513 standard; RNA; 21 BP.
XX
XX ADL70513;
AC
XX 20-MAY-2004 (first entry).
DT
```

```
XX RNAi for human clusterin.
DE
XX
XX RNA interference; RNAi; short interfering RNA; siRNA; human; clusterin;
KW cytosolic; neuroprotective; nontropic; gene silencing; DNA-RNA hybrid;
KW ss.
XX
XX Homo sapiens.
OS
XX Synthetic.
OS
XX
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XX 21-AUG-2003; 2003WO-CA001277.
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XX 21-AUG-2002; 2002US-0405193P.
PR
XX 03-SEP-2002; 2002US-0408152P.
PR
XX 20-MAY-2003; 2003US-0472387P.
PR
XX
XX (UYBR-) UNIV BRITISH COLUMBIA.
XX
XX Jansen B, Gleave ME, Signaevsky M, Beraldi E, Trougakos IP;
PI Gonos ES;
PI
XX
XX WPI; 2004-226852/21.
XX
XX New RNA molecule less than 49 bases and having a sequence effective to
PT mediate degradation or block translation of mRNA that is the
PT transcriptional product of a target gene, useful for treating Alzheimer's
PT disease or cancer.
XX
XX Claim 4; SEQ ID NO 58; 63pp; English.
XX
XX The present sequence is the sense strand of a short interfering RNA
CC (siRNA) targeted to a specific portion ADL70512 of human clusterin cDNA.
CC The antisense strand is also provided ADL70514. The siRNA can be used to
CC interfere with the expression of clusterin. Clusterin, also known as
CC testosterone-repressed prostate message-2 (TRPM-2) or sulfated
CC glycoprotein-2 (SGP-2), is expressed in increased amounts by prostate
CC tumour cells following androgen withdrawal, and has also been shown to be
CC critical for neuritic toxicity in mouse models of Alzheimer's disease.
CC siRNAs of the invention can be used alone or in combination with other
CC chemotherapy or apoptosis inducing treatments for the treatment of
CC prostate cancer, sarcomas such as osteosarcoma, renal cell carcinoma,
CC breast cancer, bladder cancer, lung cancer, colon cancer, ovarian cancer,
CC anaplastic large cell lymphoma and melanoma, and also for the treatment
CC of Alzheimer's disease. In an example from the invention, the present
CC siRNA was used to examine the effects of clusterin gene silencing in PC-3
CC prostate cancer cells. A reduction in clusterin transcript was observed.
XX
XX Sequence 21 BP; 3 A; 9 C; 3 G; 2 T; 4 U; 0 Other;
SQ
Query Match 1.3%; Score 21; DB 1; Length 21;
Best Local Similarity 81.0%; Pred. No. 39;
Matches 17; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
QY 482 CCAGAGCTCGCCCTTCTACTT 502
DB 1 CCAGAGCTCGCCCTTCTACTT 21
RESULT 71
ADL70458
ID ADL70458 standard; RNA; 21 BP.
XX
XX ADL70458;
AC
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10828394-1\_1-1643.rng.sl

Tue Sep 13 10:53:20 2005

```
XX 20-MAY-2004 (first entry)
DT XX
XX RNAi for human clusterin.
DE XX
XX RNA interference; RNAi; short interfering RNA; siRNA; human; clusterin;
KW cytosolic; neuroprotective; nontropic; gene silencing; DNA-RNA hybrid;
KW ss.
XX Homo sapiens.
OS Synthetic.
OS
XX Key Location/Qualifiers
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FN
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XX 03-SEP-2002; 2002US-0408152P.
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XX 20-MAY-2003; 2003US-0472387P.
PR
XX (UYBR-) UNIV BRITISH COLUMBIA.
PA
XX Jansen B, Gleave ME, Signaevsky M, Beraldi E, Trougakos IP;
PI Gonos ES;
PI
XX WPI; 2004-226852/21.
DR
XX New RNA molecule less than 49 bases and having a sequence effective to
XX mediate degradation or block translation of mRNA that is the
XX transcriptional product of a target gene, useful for treating Alzheimer's
XX disease or cancer.
XX
XX Claim 4; SEQ ID NO 3; 63pp; English.
XX
XX The present sequence is the sense strand of a short interfering RNA
XX (siRNA) targeted to nucleotides 1105-1123 of human clusterin cDNA. The
XX antisense strand is also provided ADL70459. The siRNA can be used to
XX interfere with the expression of clusterin. Clusterin, also known as
XX testosterone-repressed prostate message-2 (TRPM-2) or sulfated
XX glycoprotein-2 (SGP-2), is expressed in increased amounts by prostate
XX tumour cells following androgen withdrawal, and has also been shown to be
XX critical for neuritic toxicity in mouse models of Alzheimer's disease.
XX siRNAs of the invention can be used alone or in combination with other
XX chemotherapies or apoptosis inducing treatments for the treatment of
XX prostate cancer, sarcomas such as osteosarcoma, renal cell carcinoma,
XX breast cancer, bladder cancer, lung cancer, colon cancer, ovarian cancer,
XX anaplastic large cell lymphoma and melanoma, and also for the treatment
XX of Alzheimer's disease.
XX
XX Sequence 21 BP; 4 A; 9 C; 2 G; 2 T; 4 U; 0 Other;
SQ
Query Match 1.3%; Score 21; DB 1; Length 21;
Best Local Similarity 81.0%; Pred. No. 39;
Matches 17; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
QY 1100 GATGCTCAACACCTCTCTCTT 1120
DB 1 GAUGGCUACACCCUCCTT 21
RESULT 72
ADL70520/c
ID ADL70520 standard; RNA; 21 BP.
XX
AC ADL70520;
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XX 20-MAY-2004 (first entry)
DT XX
XX RNAi for human clusterin.
DE XX
XX RNA interference; RNAi; short interfering RNA; siRNA; human; clusterin;
KW cytosolic; neuroprotective; nontropic; gene silencing; DNA-RNA hybrid;
KW ss.
XX Homo sapiens.
OS Synthetic.
OS
XX Key Location/Qualifiers
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XX 04-MAR-2004.
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XX 21-AUG-2003; 2003WO-CA001277.
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XX 21-AUG-2002; 2002US-0405193P.
PR
XX 03-SEP-2002; 2002US-0408152P.
PR
XX 20-MAY-2003; 2003US-0472387P.
PR
XX (UYBR-) UNIV BRITISH COLUMBIA.
PA
XX Jansen B, Gleave ME, Signaevsky M, Beraldi E, Trougakos IP;
PI Gonos ES;
PI
XX WPI; 2004-226852/21.
DR
XX New RNA molecule less than 49 bases and having a sequence effective to
XX mediate degradation or block translation of mRNA that is the
XX transcriptional product of a target gene, useful for treating Alzheimer's
XX disease or cancer.
XX
XX Claim 4; SEQ ID NO 65; 63pp; English.
XX
XX The present sequence is the antisense strand of a short interfering RNA
XX (siRNA) targeted to a specific portion ADL70518 of human clusterin cDNA.
XX The sense strand is also provided ADL70519. The siRNA can be used to
XX interfere with the expression of clusterin. Clusterin, also known as
XX testosterone-repressed prostate message-2 (TRPM-2) or sulfated
XX glycoprotein-2 (SGP-2), is expressed in increased amounts by prostate
XX tumour cells following androgen withdrawal, and has also been shown to be
XX critical for neuritic toxicity in mouse models of Alzheimer's disease.
XX siRNAs of the invention can be used alone or in combination with other
XX chemotherapies or apoptosis inducing treatments for the treatment of
XX prostate cancer, sarcomas such as osteosarcoma, renal cell carcinoma,
XX breast cancer, bladder cancer, lung cancer, colon cancer, ovarian cancer,
XX anaplastic large cell lymphoma and melanoma, and also for the treatment
XX of Alzheimer's disease. In an example from the invention, the present
XX siRNA was used to examine the effects of clusterin gene silencing in PC-3
XX prostate cancer cells. A reduction in clusterin transcript was observed.
XX
XX Sequence 21 BP; 6 A; 1 C; 4 G; 2 T; 8 U; 0 Other;
SQ
Query Match 1.3%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 39;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1613 AACTAATTCATAAACTGTC 1633
DB 21 AACTAATTCATAAACTGTC 1
RESULT 73
ADL70461/c
ID ADL70461 standard; RNA; 21 BP.
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XX AC ADL70461;
XX DT 20-MAY-2004 (first entry)
XX DE RNAi for human clusterin.
XX KW RNA interference; RNAi; short interfering RNA; siRNA; human; clusterin;
XX KW cyostatic; neuroprotective; nootropic; gene silencing; DNA-RNA hybrid;
XX KW ss.
XX OS Homo sapiens.
XX OS Synthetic.
XX FH Key Location/Qualifiers
XX FT modified_base 20..21
XX FT /*tag= a
XX FT /mod_base= OTHER
XX FT /note= "OTHER= dtdt"
XX PN WO2004018676-A2.
XX PD 04-MAR-2004.
XX PF 21-AUG-2003; 2003WO-CA001277.
XX PR 21-AUG-2002; 2002US-0405193P.
XX PR 03-SEP-2002; 2002US-0408152P.
XX PR 20-MAY-2003; 2003US-0472387P.
XX PA (UYBR-) UNIV BRITISH COLUMBIA.
XX PI Jansen B, Gleave ME, Signaevsky M, Beraldi E, Trougakos IP;
XX PI Gonos ES;
XX XX WPI; 2004-226852/21.
XX XX New RNA molecule less than 49 bases and having a sequence effective to
XX PT mediate degradation or block translation of mRNA that is the
XX PT transcriptional product of a target gene, useful for treating Alzheimer's
XX PT disease or cancer.
XX PS Claim 4; SEQ ID NO 6; 63pp; English.
XX CC The present sequence is the antisense strand of a short interfering RNA
XX CC (siRNA) targeted to nucleotides 1620-1638 of human clusterin cDNA. The
XX CC sense strand is also provided ADL70460. The siRNA can be used to
XX CC interfere with the expression of clusterin. Clusterin, also known as
XX CC testosterone-repressed prostate message-2 (TRPM-2) or sulfated
XX CC glycoprotein-2 (SGP-2), is expressed in increased amounts by prostate
XX CC tumour cells following androgen withdrawal, and has also been shown to be
XX CC critical for neuritic toxicity in mouse models of Alzheimer's disease.
XX CC siRNAs of the invention can be used alone or in combination with other
XX CC chemotherapy or apoptosis inducing treatments for the treatment of
XX CC prostate cancer, sarcomas such as osteosarcoma, renal cell carcinoma,
XX CC breast cancer, bladder cancer, lung cancer, colon cancer, ovarian cancer,
XX CC anaplastic large cell lymphoma and melanoma, and also for the treatment
XX CC of Alzheimer's disease.
XX SQ Sequence 21 BP; 6 A; 1 C; 4 G; 2 T; 8 U; 0 Other;
Query Match 1.3%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 39;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1613 AACTAATTCATAAACTGTC 1633
| | | | | | | | | | | | | | | | | | | | |
Db 21 AACTAATTCATAAACTGTC 1
| | | | | | | | | | | | | | | | | | | | |
RESULT 74
ADL70519
ID ADL70519 standard; RNA; 21 BP.
```

```
XX AC ADL70519;
XX DT 20-MAY-2004 (first entry)
XX DE RNAi for human clusterin.
XX KW RNA interference; RNAi; short interfering RNA; siRNA; human; clusterin;
XX KW cyostatic; neuroprotective; nootropic; gene silencing; DNA-RNA hybrid;
XX KW ss.
XX OS Homo sapiens.
XX OS Synthetic.
XX FH Key Location/Qualifiers
XX FT modified_base 20..21
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XX PN WO2004018676-A2.
XX PD 04-MAR-2004.
XX PF 21-AUG-2003; 2003WO-CA001277.
XX PR 21-AUG-2002; 2002US-0405193P.
XX PR 03-SEP-2002; 2002US-0408152P.
XX PR 20-MAY-2003; 2003US-0472387P.
XX PA (UYBR-) UNIV BRITISH COLUMBIA.
XX PI Jansen B, Gleave ME, Signaevsky M, Beraldi E, Trougakos IP;
XX PI Gonos ES;
XX XX WPI; 2004-226852/21.
XX XX New RNA molecule less than 49 bases and having a sequence effective to
XX PT mediate degradation or block translation of mRNA that is the
XX PT transcriptional product of a target gene, useful for treating Alzheimer's
XX PT disease or cancer.
XX PS Claim 4; SEQ ID NO 64; 63pp; English.
XX CC The present sequence is the sense strand of a short interfering RNA
XX CC (siRNA) targeted to a specific portion ADL70518 of human clusterin cDNA.
XX CC The antisense strand is also provided ADL70520. The siRNA can be used to
XX CC interfere with the expression of clusterin. Clusterin, also known as
XX CC testosterone-repressed prostate message-2 (TRPM-2) or sulfated
XX CC glycoprotein-2 (SGP-2), is expressed in increased amounts by prostate
XX CC tumour cells following androgen withdrawal, and has also been shown to be
XX CC critical for neuritic toxicity in mouse models of Alzheimer's disease.
XX CC siRNAs of the invention can be used alone or in combination with other
XX CC chemotherapy or apoptosis inducing treatments for the treatment of
XX CC prostate cancer, sarcomas such as osteosarcoma, renal cell carcinoma,
XX CC breast cancer, bladder cancer, lung cancer, colon cancer, ovarian cancer,
XX CC anaplastic large cell lymphoma and melanoma, and also for the treatment
XX CC of Alzheimer's disease. In an example from the invention, the present
XX CC siRNA was used to examine the effects of clusterin gene silencing in PC-3
XX CC prostate cancer cells. A reduction in clusterin transcript was observed.
XX SQ Sequence 21 BP; 8 A; 4 C; 1 G; 2 T; 6 U; 0 Other;
Query Match 1.3%; Score 21; DB 1; Length 21;
Best Local Similarity 71.4%; Pred. No. 39;
Matches 15; Conservative 6; Mismatches 0; Indels 0; Gaps 0;
QY 1615 CTAATTCATAAACTGCTT 1635
| | | | | | | | | | | | | | | | | | | | |
Db 1 CUAUUCUAUAAACUGUCTT 21
| | | | | | | | | | | | | | | | | | | | |
RESULT 75
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```
ADL70517/C
ID ADL70517 standard; RNA; 21 BP.
XX
AC ADL70517;
XX
DT 20-MAY-2004 (first entry)
XX
DE RNAi for human clusterin.
XX
XX RNA interference; RNAi; short interfering RNA; siRNA; human; clusterin;
KW cytosstatic; neuroprotective; nontropic; gene silencing; DNA-RNA hybrid;
KW ss.
XX
OS Homo sapiens.
OS Synthetic.
XX
XX Key Location/Qualifiers
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PR 20-MAY-2003; 2003US-0472387P.
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XX (UYBR-) UNIV BRITISH COLUMBIA.
XX
XX Jansen B, Gleave ME, Signaevsky M, Beraldi E, Trougakos IP;
PI Gonos ES;
XX
XX WPI; 2004-226852/21.
XX
XX New RNA molecule less than 49 bases and having a sequence effective to
PT mediate degradation or block translation of mRNA that is the
PT transcriptional product of a target gene, useful for treating Alzheimer's
PT disease or cancer.
XX
XX Claim 4; SEQ ID NO 62; 63pp; English.
XX
XX The present sequence is the antisense strand of a short interfering RNA
CC (siRNA) targeted to a specific portion ADL70515 of human clusterin cDNA.
CC The sense strand is also provided ADL70516. The siRNA can be used to
CC interfere with the expression of clusterin. Clusterin, also known as
CC testosterone-repressed prostate message-2 (TRPM-2) or sulfated
CC glycoprotein-2 (SGP-2), is expressed in increased amounts by prostate
CC tumour cells following androgen withdrawal, and has also been shown to be
CC critical for neuritic toxicity in mouse models of Alzheimer's disease.
CC siRNAs of the invention can be used alone or in combination with other
CC chemotherapy or apoptosis inducing treatments for the treatment of
CC prostate cancer, sarcomas such as osteosarcoma, renal cell carcinoma,
CC breast cancer, bladder cancer, lung cancer, colon cancer, ovarian cancer,
CC anaplastic large cell lymphoma and melanoma, and also for the treatment
CC of Alzheimer's disease. In an example from the invention, the present
CC siRNA was used to examine the effects of clusterin gene silencing in PC-3
CC prostate cancer cells. A reduction in clusterin transcript was observed.
XX
XX Sequence 21 BP; 3 A; 5 C; 9 G; 2 T; 2 U; 0 Other;
SQ
Query Match 1.3%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 39;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 711 AAGTCCCGCATCGTCCGCAGC 731
DB 21 AAGTCCCGCATCGTCCGCAGC 1
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```
RESULT 76
ADL70516
ID ADL70516 standard; RNA; 21 BP.
XX
AC ADL70516;
XX
DT 20-MAY-2004 (first entry)
XX
XX RNAi for human clusterin.
XX
XX RNA interference; RNAi; short interfering RNA; siRNA; human; clusterin;
KW cytosstatic; neuroprotective; nontropic; gene silencing; DNA-RNA hybrid;
KW ss.
XX
OS Homo sapiens.
OS Synthetic.
XX
XX Key Location/Qualifiers
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PR 20-MAY-2003; 2003US-0472387P.
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XX (UYBR-) UNIV BRITISH COLUMBIA.
XX
XX Jansen B, Gleave ME, Signaevsky M, Beraldi E, Trougakos IP;
PI Gonos ES;
XX
XX WPI; 2004-226852/21.
XX
XX New RNA molecule less than 49 bases and having a sequence effective to
PT mediate degradation or block translation of mRNA that is the
PT transcriptional product of a target gene, useful for treating Alzheimer's
PT disease or cancer.
XX
XX Claim 4; SEQ ID NO 61; 63pp; English.
XX
XX The present sequence is the sense strand of a short interfering RNA
CC (siRNA) targeted to a specific portion ADL70515 of human clusterin cDNA.
CC The antisense strand is also provided ADL70517. The siRNA can be used to
CC interfere with the expression of clusterin. Clusterin, also known as
CC testosterone-repressed prostate message-2 (TRPM-2) or sulfated
CC glycoprotein-2 (SGP-2), is expressed in increased amounts by prostate
CC tumour cells following androgen withdrawal, and has also been shown to be
CC critical for neuritic toxicity in mouse models of Alzheimer's disease.
CC siRNAs of the invention can be used alone or in combination with other
CC chemotherapy or apoptosis inducing treatments for the treatment of
CC prostate cancer, sarcomas such as osteosarcoma, renal cell carcinoma,
CC breast cancer, bladder cancer, lung cancer, colon cancer, ovarian cancer,
CC anaplastic large cell lymphoma and melanoma, and also for the treatment
CC of Alzheimer's disease. In an example from the invention, the present
CC siRNA was used to examine the effects of clusterin gene silencing in PC-3
CC prostate cancer cells. A reduction in clusterin transcript was observed.
XX
XX Sequence 21 BP; 2 A; 9 C; 5 G; 2 T; 3 U; 0 Other;
SQ
Query Match 1.3%; Score 21; DB 1; Length 21;
Best Local Similarity 85.7%; Pred. No. 39;
Matches 18; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
OY 713 GTCCCGCATCGTCCGCAGCTT 733
|:|||||:|:|||||
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Db 1 GUCCCGCAUCGCGCAGCTT 21

RESULT 77  
ADL70457/c  
ID ADL70457 standard; RNA; 21 BP.  
XX  
AC ADL70457;  
XX  
DT 20-MAY-2004 (first entry)  
XX  
DE RNAi for human clusterin.  
XX  
KW RNA interference; RNAi; short interfering RNA; siRNA; human; clusterin;  
KW cytosolic; neuroprotective; nootropic; gene silencing; DNA-RNA hybrid;  
KW ss.  
XX  
OS Homo sapiens.  
OS Synthetic.  
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PR 20-MAY-2003; 2003US-0472387P.  
XX  
PA (UYBR-) UNIV BRITISH COLUMBIA.  
XX  
PI Jansen B, Gleave ME, Signaevsky M, Beraldi E, Trougakos IP;  
PI Gonos ES;  
XX  
WPI; 2004-226852/21.  
XX  
PT New RNA molecule less than 49 bases and having a sequence effective to  
PT mediate degradation or block translation of mRNA that is the  
PT transcriptional product of a target gene, useful for treating Alzheimer's  
PT disease or cancer.  
XX  
PS Claim 4; SEQ ID NO 2; 63pp; English.  
XX  
CC The present sequence is the antisense strand of a short interfering RNA  
CC (siRNA) targeted to nucleotides 487-505 of human clusterin cDNA. The  
CC sense strand is also provided ADL70456. The siRNA can be used to  
CC interfere with the expression of clusterin. Clusterin, also known as  
CC testosterone-repressed prostate message-2 (TRPM-2) or sulfated  
CC glycoprotein-2 (SGP-2), is expressed in increased amounts by prostate  
CC tumour cells following androgen withdrawal, and has also been shown to be  
CC critical for neuritic toxicity in mouse models of Alzheimer's disease.  
CC siRNAs of the invention can be used alone or in combination with other  
CC chemotherapy or apoptosis inducing treatments for the treatment of  
CC prostate cancer, sarcomas such as osteosarcoma, renal cell carcinoma,  
CC breast cancer, bladder cancer, lung cancer, colon cancer, ovarian cancer,  
CC anaplastic large cell lymphoma and melanoma, and also for the treatment  
CC of Alzheimer's disease.  
XX  
SQ Sequence 21 BP; 4 A; 3 C; 9 G; 2 T; 3 U; 0 Other;

Query Match 1.3%; Score 21; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 39;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 480 AACCGAGCTCGCCCTTCTAC 500  
|||||

Db 21 AACGAGCTCGCCCTTCTAC 1

RESULT 78  
ADL70459/c  
ID ADL70459 standard; RNA; 21 BP.  
XX  
AC ADL70459;  
XX  
DT 20-MAY-2004 (first entry)  
XX  
DE RNAi for human clusterin.  
XX  
KW RNA interference; RNAi; short interfering RNA; siRNA; human; clusterin;  
KW cytosolic; neuroprotective; nootropic; gene silencing; DNA-RNA hybrid;  
KW ss.  
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OS Homo sapiens.  
OS Synthetic.  
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FT /note= "OTHER= dtdt"  
XX  
PN WO2004018676-A2.  
XX  
PD 04-MAR-2004.  
XX  
PF 21-AUG-2003; 2003WO-CA001277.  
XX  
PR 21-AUG-2002; 2002US-0405193P.  
PR 03-SEP-2002; 2002US-0408152P.  
PR 20-MAY-2003; 2003US-0472387P.  
XX  
PA (UYBR-) UNIV BRITISH COLUMBIA.  
XX  
PI Jansen B, Gleave ME, Signaevsky M, Beraldi E, Trougakos IP;  
PI Gonos ES;  
XX  
WPI; 2004-226852/21.  
XX  
PT New RNA molecule less than 49 bases and having a sequence effective to  
PT mediate degradation or block translation of mRNA that is the  
PT transcriptional product of a target gene, useful for treating Alzheimer's  
PT disease or cancer.  
XX  
PS Claim 4; SEQ ID NO 4; 63pp; English.  
XX  
CC The present sequence is the antisense strand of a short interfering RNA  
CC (siRNA) targeted to nucleotides 1105-1123 of human clusterin cDNA. The  
CC sense strand is also provided ADL70458. The siRNA can be used to  
CC interfere with the expression of clusterin. Clusterin, also known as  
CC testosterone-repressed prostate message-2 (TRPM-2) or sulfated  
CC glycoprotein-2 (SGP-2), is expressed in increased amounts by prostate  
CC tumour cells following androgen withdrawal, and has also been shown to be  
CC critical for neuritic toxicity in mouse models of Alzheimer's disease.  
CC siRNAs of the invention can be used alone or in combination with other  
CC chemotherapy or apoptosis inducing treatments for the treatment of  
CC prostate cancer, sarcomas such as osteosarcoma, renal cell carcinoma,  
CC breast cancer, bladder cancer, lung cancer, colon cancer, ovarian cancer,  
CC anaplastic large cell lymphoma and melanoma, and also for the treatment  
CC of Alzheimer's disease.  
XX  
SQ Sequence 21 BP; 4 A; 2 C; 9 G; 2 T; 4 U; 0 Other;

Query Match 1.3%; Score 21; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 39;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1098 AAGATGCTCAACACCTCTCC 1118  
|||||

Db 21 AAGATGCTCAACACCTGCTCC 1

RESULT 79  
ADL70514/c  
ID ADL70514 standard; RNA; 21 BP.  
XX AC ADL70514;  
XX DT 20-MAY-2004 (first entry)  
XX DE RNAi for human clusterin.  
XX KW RNA interference; RNAi; short interfering RNA; siRNA; human; clusterin;  
XX KW cytosolic; neuroprotective; neurotropic; gene silencing; DNA-RNA hybrid;  
XX KW ss.  
XX OS Homo sapiens.  
XX OS Synthetic.

XX Key Location/Qualifiers  
FT modified\_base 20..21  
FT /\*tag= a  
FT /mod\_base= OTHER  
FT /note= "OTHER= dtdt"  
XX PN W02004018676-A2.  
XX XX  
XX PD 04-MAR-2004.  
XX PF 21-AUG-2003; 2003WO-CA001277.  
XX PR 21-AUG-2002; 2002US-0405193P.  
XX PR 03-SEP-2002; 2002US-0408152P.  
XX PR 20-MAY-2003; 2003US-0472387P.  
XX XX  
XX PA (UYBR-) UNIV BRITISH COLUMBIA.  
XX XX  
XX PI Jansen B, Gleave ME, Signaevsky M, Beraldi E, Trougakos IP;  
XX PI Gonos ES;  
XX WPI; 2004-226852/21.  
XX DR  
XX XX  
XX PT New RNA molecule less than 49 bases and having a sequence effective to  
XX PT mediate degradation or block translation of mRNA that is the  
XX PT transcriptional product of a target gene, useful for treating Alzheimer's  
XX PT disease or cancer.  
XX PS Claim 4; SEQ ID NO 59; 63pp; English.

XX The present sequence is the antisense strand of a short interfering RNA  
XX (siRNA) targeted to a specific portion ADL70512 of human clusterin cDNA.  
XX The sense strand is also provided ADL70513. The siRNA can be used to  
XX interfere with the expression of clusterin. Clusterin, also known as  
XX testosterone-repressed prostate message-2 (TRPM-2) or sulfated  
XX glycoprotein-2 (SGP-2), is expressed in increased amounts by prostate  
XX tumour cells following androgen withdrawal, and has also been shown to be  
XX critical for neuritic toxicity in mouse models of Alzheimer's disease.  
XX siRNAs of the invention can be used alone or in combination with other  
XX chemotherapeutic or apoptotic inducing treatments for the treatment of  
XX prostate cancer, sarcomas such as osteosarcoma, renal cell carcinoma,  
XX breast cancer, bladder cancer, lung cancer, colon cancer, ovarian cancer,  
XX anaplastic large cell lymphoma and melanoma, and also for the treatment  
XX of Alzheimer's disease. In an example from the invention, the present  
XX siRNA was used to examine the effects of clusterin gene silencing in PC-3  
XX prostate cancer cells. A reduction in clusterin transcript was observed.

SQ Sequence 21 BP; 4 A; 3 C; 9 G; 2 T; 3 U; 0 Other;  
Query Match 1.3%; Score 21; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 39;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 480 AACACAGCTCGCCCTTCTAC 500  
Db 21 AACACAGCTCGCCCTTCTAC 1

RESULT 80  
ADL70410/c  
ID ADL70410 standard; DNA; 21 BP.  
XX AC ADL70410;  
XX DT 20-MAY-2004 (first entry)  
XX DE Antisense oligonucleotide to human clusterin.  
XX KW Human; clusterin; antisense; melanoma; cytostatic; gene silencing; ss.  
XX XX Homo sapiens.  
XX OS Synthetic.

XX Key Location/Qualifiers  
FT modified\_base 1..21  
FT /\*tag= b  
FT /mod\_base= OTHER  
FT /note= "OTHER= optional phosphorothioate nucleotides"  
XX PN W02004018675-A1.  
XX XX  
XX PD 04-MAR-2004.  
XX PF 21-AUG-2003; 2003WO-CA001276.  
XX PR 21-AUG-2002; 2002US-0405193P.  
XX PR 03-SEP-2002; 2002US-0408152P.  
XX PR 02-DEC-2002; 2002US-0319748P.  
XX PR 20-MAY-2003; 2003US-0472387P.  
XX XX  
XX PA (UYBR-) UNIV BRITISH COLUMBIA.  
XX PA (GLEA/) GLEAVE M E.  
XX XX  
XX PI Jansen B;  
XX WPI; 2004-226851/21.  
XX DR  
XX PT Treating melanoma in a mammalian subject comprises administering to the  
XX PT subject a therapeutic agent effective to reduce the effective amount of  
XX PT clusterin in the melanoma cells.  
XX PS Claim 6; SEQ ID NO 8; 32pp; English.

XX The present sequence is that of an antisense oligonucleotide targeted to  
XX human clusterin ADL70403. The invention relates to the treatment of  
XX melanoma through reduction in the effective amount of clusterin. The  
XX therapeutic agent may be an antisense oligonucleotide ADL70404-ADL70421  
XX or short interfering RNA (siRNA) ADL70422-ADL70445 targeted to clusterin.  
XX The antisense oligonucleotides are complementary to a region of the  
XX clusterin mRNA spanning either the translation initiation site or the  
XX termination site. They may be modified to increase stability in vivo,  
XX e.g. they may be employed as phosphorothioate derivatives and may have 2'  
XX -O-(2-methoxyethyl) modifications in the 5' and 3' 'wings'. A method for  
XX regulating expression of bcl-xL in a subject or cell line comprises  
XX administering an agent effective to modulate the amount of clusterin  
XX expression. In clusterin-expressing cells, expression of bcl-xL is down-  
XX regulated when the effective amount of clusterin is reduced. Such  
XX inhibition is significant because bcl-xL is known to act as an inhibitor

```
CC of apoptosis.
XX SQ Sequence 21 BP; 5 A; 5 C; 8 G; 3 T; 0 U; 0 Other;
Query Match 1.3%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 39;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 716 CGCATCGTCCGCGAGTTGAT 736
DB 21 CGCATCGTCCGCGAGTTGAT 1

RESULT 81
ADL70440
ID ADL70440 standard; RNA; 21 BP.
XX AC ADL70440;
XX DT 20-MAY-2004 (first entry)
XX DE RNAi for human clusterin.
XX KW Human; clusterin; RNAi; melanoma; cytostatic; gene silencing;
XX KW short interfering RNA; siRNA; DNA-RNA hybrid; ss.
XX OS Homo sapiens.
XX OS Synthetic.
XX FH Key Location/Qualifiers
XX FT modified_base 20..21
XX FT /*tag= a
XX FT /mod_base= OTHER
XX FT /note= "OTHER= TT"
XX PN WO2004018675-A1.
XX PD 04-MAR-2004.
XX PF 21-AUG-2003; 2003WO-CA001276.
XX PR 21-AUG-2002; 2002US-0405193P.
XX PR 03-SEP-2002; 2002US-0408152P.
XX PR 02-DEC-2002; 2002US-0319748P.
XX PR 20-MAY-2003; 2003US-0472387P.
XX PA (UYBR-) UNIV BRITISH COLUMBIA.
XX PA (GLEA/) GLEAVE M E.
XX PI Jansen B;
XX DR WPI; 2004-226851/21.
XX PT Treating melanoma in a mammalian subject comprises administering to the
XX PT subject a therapeutic agent effective to reduce the effective amount of
XX PT clusterin in the melanoma cells.
XX PS Claim 20; SEQ ID NO 38; 32pp; English.
XX CC The present sequence is that of a short interfering RNA (siRNA) molecule
XX CC targeted to human clusterin ADL70403. The invention relates to the
XX CC treatment of melanoma through reduction in the effective amount of
XX CC clusterin. The therapeutic agent may be an antisense oligonucleotide
XX CC ADL70404-ADL70421 or short interfering RNA (siRNA) ADL70422-ADL70445
XX CC targeted to clusterin. The siRNAs molecules direct cleavage of clusterin
XX CC mRNA. A method for regulating expression of bcl-xL in a subject or cell
XX CC line comprises administering an agent effective to modulate the amount of
XX CC clusterin expression. In clusterin-expressing cells, expression of bcl-xL
XX CC is down-regulated when the effective amount of clusterin is reduced. Such
XX CC inhibition is significant because bcl-xL is known to act as an inhibitor
XX CC of apoptosis.
XX SQ Sequence 21 BP; 2 A; 9 C; 5 G; 2 T; 3 U; 0 Other;

Query Match 1.3%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 39;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 713 GTCCCGCATCGTCCGCGAGCTT 733
DB 1 GUCCCGCAUCGUCCGCGAGCTT 21

RESULT 82
ADL70422
ID ADL70422 standard; RNA; 21 BP.
XX AC ADL70422;
XX DT 20-MAY-2004 (first entry)
XX DE RNAi for human clusterin.
XX KW Human; clusterin; RNAi; melanoma; cytostatic; gene silencing;
XX KW short interfering RNA; siRNA; DNA-RNA hybrid; ss.
XX OS Homo sapiens.
XX OS Synthetic.
XX FH Key Location/Qualifiers
XX FT modified_base 20..21
XX FT /*tag= a
XX FT /mod_base= OTHER
XX FT /note= "OTHER= TT"
XX PN WO2004018675-A1.
XX PD 04-MAR-2004.
XX PF 21-AUG-2003; 2003WO-CA001276.
XX PR 21-AUG-2002; 2002US-0405193P.
XX PR 03-SEP-2002; 2002US-0408152P.
XX PR 02-DEC-2002; 2002US-0319748P.
XX PR 20-MAY-2003; 2003US-0472387P.
XX PA (UYBR-) UNIV BRITISH COLUMBIA.
XX PA (GLEA/) GLEAVE M E.
XX PI Jansen B;
XX DR WPI; 2004-226851/21.
XX PT Treating melanoma in a mammalian subject comprises administering to the
XX PT subject a therapeutic agent effective to reduce the effective amount of
XX PT clusterin in the melanoma cells.
XX PS Claim 10; SEQ ID NO 20; 32pp; English.
XX CC The present sequence is that of a short interfering RNA (siRNA) molecule
XX CC targeted to human clusterin ADL70403. The invention relates to the
XX CC treatment of melanoma through reduction in the effective amount of
XX CC clusterin. The therapeutic agent may be an antisense oligonucleotide
XX CC ADL70404-ADL70421 or short interfering RNA (siRNA) ADL70422-ADL70445
XX CC targeted to clusterin. The siRNAs molecules direct cleavage of clusterin
XX CC mRNA. A method for regulating expression of bcl-xL in a subject or cell
XX CC line comprises administering an agent effective to modulate the amount of
XX CC clusterin expression. In clusterin-expressing cells, expression of bcl-xL
XX CC is down-regulated when the effective amount of clusterin is reduced. Such
XX CC inhibition is significant because bcl-xL is known to act as an inhibitor
XX CC of apoptosis.
XX SQ Sequence 21 BP; 3 A; 9 C; 3 G; 2 T; 4 U; 0 Other;

Query Match 1.3%; Score 21; DB 1; Length 21;
Best Local Similarity 81.0%; Pred. No. 39;
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Matches 17; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 482 CCAGAGCTCGCCCTTCTACTT 502  
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Db 1 CCAGAGCUGCCCUUUAATT 21

RESULT 83  
ADL70413/c  
ID ADL70413 standard; DNA; 21 BP.  
XX AC ADL70413;  
XX 20-MAY-2004 (first entry)  
XX Antisense oligonucleotide to human clusterin.  
XX Human; clusterin; antisense; melanoma; cytostatic; gene silencing; ss.  
XX Homo sapiens.  
XX Synthetic.  
XX Key Location/Qualifiers  
FH modified\_base 1..21  
FT /\*tag= b  
FT /mod\_base= OTHER  
FT /note= "OTHER= optional phosphorothioate nucleotides"  
FT modified\_base 1..4  
FT /\*tag= a  
FT /mod\_base= OTHER  
FT /note= "OTHER= optional 2'-methoxyethyl modifications"  
FT modified\_base 18..21  
FT /\*tag= c  
FT /mod\_base= OTHER  
FT /note= "OTHER= optional 2'-methoxyethyl modifications"  
XX WO2004018675-A1.  
XX 04-MAR-2004.  
XX 21-AUG-2003; 2003WO-CA001276.  
XX 21-AUG-2002; 2002US-0405193P.  
XX 03-SEP-2002; 2002US-0408152P.  
XX 02-DEC-2002; 2002US-0319748P.  
XX 20-MAY-2003; 2003US-0472387P.  
XX (UYBR-) UNIV BRITISH COLUMBIA.  
XX (GLEA/) GLEAVE M E.  
XX Jansen B;  
XX WPI; 2004-226851/21.  
XX Treating melanoma in a mammalian subject comprises administering to the  
XX subject a therapeutic agent effective to reduce the effective amount of  
XX clusterin in the melanoma cells.  
XX Claim 6; SEQ ID NO 11; 32pp; English.  
XX The present sequence is that of an antisense oligonucleotide targeted to  
XX human clusterin ADL70403. The invention relates to the treatment of  
XX melanoma through reduction in the effective amount of clusterin. The  
XX therapeutic agent may be an antisense oligonucleotide ADL70404-ADL70421  
XX or short interfering RNA (siRNA) ADL70422-ADL70445 targeted to clusterin.  
XX The antisense oligonucleotides are complementary to a region of the  
XX clusterin mRNA spanning either the translation initiation site or the  
XX termination site. They may be modified to increase stability in vivo,  
XX e.g. they may be employed as phosphorothioate derivatives and may have 2'  
XX -O-(2-methoxyethyl) modifications in the 5' and 3' wings. A method for  
XX regulating expression of bcl-xL in a subject or cell line comprises  
XX administering an agent effective to modulate the amount of clusterin  
XX expression. In clusterin-expressing cells, expression of bcl-xL is down-

CC regulated when the effective amount of clusterin is reduced. Such  
CC inhibition is significant because bcl-xL is known to act as an inhibitor  
CC of apoptosis.  
XX Sequence 21 BP; 4 A; 3 C; 6 G; 8 T; 0 U; 0 Other;  
SQ Query Match 1.3%; Score 21; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred No. 39;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1316 CTCGAGGAGAACCTTAATT 1336  
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Db 21 CTCGAGGAGAACCTTAATT 1

RESULT 84  
ADL70408/c  
ID ADL70408 standard; DNA; 21 BP.  
XX AC ADL70408;  
XX 20-MAY-2004 (first entry)  
XX Antisense oligonucleotide to human clusterin.  
XX Human; clusterin; antisense; melanoma; cytostatic; gene silencing; ss.  
XX Homo sapiens.  
XX Synthetic.  
XX Key Location/Qualifiers  
FH modified\_base 1..21  
FT /\*tag= b  
FT /mod\_base= OTHER  
FT /note= "OTHER= optional phosphorothioate nucleotides"  
FT modified\_base 1..4  
FT /\*tag= a  
FT /mod\_base= OTHER  
FT /note= "OTHER= optional 2'-methoxyethyl modifications"  
FT modified\_base 18..21  
FT /\*tag= c  
FT /mod\_base= OTHER  
FT /note= "OTHER= optional 2'-methoxyethyl modifications"  
XX WO2004018675-A1.  
XX 04-MAR-2004.  
XX 21-AUG-2003; 2003WO-CA001276.  
XX 21-AUG-2002; 2002US-0405193P.  
XX 03-SEP-2002; 2002US-0408152P.  
XX 02-DEC-2002; 2002US-0319748P.  
XX 20-MAY-2003; 2003US-0472387P.  
XX (UYBR-) UNIV BRITISH COLUMBIA.  
XX (GLEA/) GLEAVE M E.  
XX Jansen B;  
XX WPI; 2004-226851/21.  
XX Treating melanoma in a mammalian subject comprises administering to the  
XX subject a therapeutic agent effective to reduce the effective amount of  
XX clusterin in the melanoma cells.  
XX Claim 6; SEQ ID NO 6; 32pp; English.  
XX The present sequence is that of an antisense oligonucleotide targeted to  
XX human clusterin ADL70403. The invention relates to the treatment of  
XX melanoma through reduction in the effective amount of clusterin. The  
XX therapeutic agent may be an antisense oligonucleotide ADL70404-ADL70421  
XX or short interfering RNA (siRNA) ADL70422-ADL70445 targeted to clusterin.

CC The antisense oligonucleotides are complementary to a region of the  
CC clusterin mRNA spanning either the translation initiation site or the  
CC termination site. They may be modified to increase stability in vivo,  
CC e.g. they may be employed as phosphorothioate derivatives and may have 2'  
CC -O-(2-methoxyethyl) modifications in the 5' and 3' 'wings'. A method for  
CC regulating expression of bcl-xL in a subject or cell line comprises  
CC administering an agent effective to modulate the amount of clusterin  
CC expression. In clusterin-expressing cells, expression of bcl-xL is down-  
CC regulated when the effective amount of clusterin is reduced. Such  
CC inhibition is significant because bcl-xL is known to act as an inhibitor  
CC of apoptosis.  
XX  
SQ Sequence 21 BP; 2 A; 6 C; 3 G; 10 T; 0 U; 0 Other;

Query Match 1.3%; Score 21; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 39;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 316 AATCAGAGACAAAGCTGAAGG 336  
DB 21 AATCAGAGACAAAGCTGAAGG 1

RESULT 85  
ADL70412/c  
ID ADL70412 standard; DNA; 21 BP.  
XX  
AC ADL70412;  
XX  
DT 20-MAY-2004 (first entry)  
XX  
DE Antisense oligonucleotide to human clusterin.  
XX  
KW Human; clusterin; antisense; melanoma; cytostatic; gene silencing; ss.  
XX  
OS Homo sapiens.  
OS Synthetic.  
XX  
FH Key Location/Qualifiers  
FT modified\_base 1..21  
FT /\*tag= b  
FT /mod\_base= OTHER  
FT /note= "OTHER= optional phosphorothioate nucleotides"  
FT modified\_base 1..4  
FT /\*tag= a  
FT /mod\_base= OTHER  
FT /note= "OTHER= optional 2'-O-methoxyethyl modifications"  
FT modified\_base 18..21  
FT /\*tag= c  
FT /mod\_base= OTHER  
FT /note= "OTHER= optional 2'-O-methoxyethyl modifications"  
XX  
PN WO2004018675-A1.

XX  
XX  
PD 04-MAR-2004.  
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XX 21-AUG-2003; 2003WO-CA001276.  
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XX 21-AUG-2002; 2002US-0405193P.  
PR 03-SEP-2002; 2002US-0408152P.  
PR 02-DEC-2002; 2002US-0319748P.  
PR 20-MAY-2003; 2003US-0472387P.  
XX  
XX (UYBR-) UNIV BRITISH COLUMBIA.  
PA (GLEA/) GLEAVE M E.  
XX  
XX Jansen B;  
XX  
XX WPI; 2004-236851/21.

XX Treating melanoma in a mammalian subject comprises administering to the  
PT subject a therapeutic agent effective to reduce the effective amount of  
PT clusterin in the melanoma cells.

XX Claim 6; SEQ ID NO 10; 32pp; English.  
XX  
XX The present sequence is that of an antisense oligonucleotide targeted to  
CC human clusterin ADL70403. The invention relates to the treatment of  
CC melanoma through reduction in the effective amount of clusterin. The  
CC therapeutic agent may be an antisense oligonucleotide ADL70404-ADL70421  
CC or short interfering RNA (siRNA) ADL70422-ADL70445 targeted to clusterin.  
CC The antisense oligonucleotides are complementary to a region of the  
CC clusterin mRNA spanning either the translation initiation site or the  
CC termination site. They may be modified to increase stability in vivo,  
CC e.g. they may be employed as phosphorothioate derivatives and may have 2'  
CC -O-(2-methoxyethyl) modifications in the 5' and 3' 'wings'. A method for  
CC regulating expression of bcl-xL in a subject or cell line comprises  
CC administering an agent effective to modulate the amount of clusterin  
CC expression. In clusterin-expressing cells, expression of bcl-xL is down-  
CC regulated when the effective amount of clusterin is reduced. Such  
CC inhibition is significant because bcl-xL is known to act as an inhibitor  
CC of apoptosis.  
XX  
SQ Sequence 21 BP; 5 A; 6 C; 4 G; 4 T; 0 U; 0 Other;

Query Match 1.3%; Score 21; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 39;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1115 CTCCTTGCTGGAGCAGCTGAA 1135  
DB 21 CTCCTTGCTGGAGCAGCTGAA 1

RESULT 86  
ADL70425/c  
ID ADL70425 standard; RNA; 21 BP.  
XX  
AC ADL70425;  
XX  
DT 20-MAY-2004 (first entry)  
XX  
DE RNAi for human clusterin.  
XX  
KW Human; clusterin; RNAi; melanoma; cytostatic; gene silencing;  
KW short interfering RNA; siRNA; DNA-RNA hybrid; ss.  
XX  
OS Homo sapiens.  
OS Synthetic.  
XX  
FH Key Location/Qualifiers  
FT modified\_base 20..21  
FT /\*tag= a  
FT /mod\_base= OTHER  
FT /note= "OTHER= TT"  
XX  
PN WO2004018675-A1.  
XX  
XX 04-MAR-2004.  
XX  
XX 21-AUG-2003; 2003WO-CA001276.  
XX  
XX 21-AUG-2002; 2002US-0405193P.  
PR 03-SEP-2002; 2002US-0408152P.  
PR 02-DEC-2002; 2002US-0319748P.  
PR 20-MAY-2003; 2003US-0472387P.  
XX  
XX (UYBR-) UNIV BRITISH COLUMBIA.  
PA (GLEA/) GLEAVE M E.  
XX  
XX Jansen B;  
XX  
XX WPI; 2004-226851/21.  
XX Treating melanoma in a mammalian subject comprises administering to the  
PT subject a therapeutic agent effective to reduce the effective amount of

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PT clusterin in the melanoma cells.
XX
PS Claim 10; SEQ ID NO 23; 32pp; English.
XX
XX The present sequence is that of a short interfering RNA (siRNA) molecule
CC targeted to human clusterin ADL70403. The invention relates to the
CC treatment of melanoma through reduction in the effective amount of
CC clusterin. The therapeutic agent may be an antisense oligonucleotide
CC ADL70404-ADL70421 or short interfering RNA (siRNA) ADL70422-ADL70445
CC targeted to clusterin. The siRNAs molecules direct cleavage of clusterin
CC mRNA. A method for regulating expression of bcl-xL in a subject or cell
CC line comprises administering an agent effective to modulate the amount of
CC clusterin expression. In clusterin-expressing cells, expression of bcl-xL
CC is down-regulated when the effective amount of clusterin is reduced. Such
CC inhibition is significant because bcl-xL is known to act as an inhibitor
CC of apoptosis.
XX
SQ Sequence 21 BP; 4 A; 2 C; 9 G; 2 T; 4 U; 0 Other;
Query Match 1.3%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 39;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1098 AGATGCTCAACACCTCTCC 1118
Db 21 AGATGCTCAACACCTCTCC 1
RESULT 87
ADL70442
ID ADL70442 standard; RNA; 21 BP.
AC ADL70442;
XX
XX 20-MAY-2004 (first entry)
XX
XX RNAi for human clusterin.
XX
XX Human; clusterin; RNAi; melanoma; cytostatic; gene silencing;
XX short interfering RNA; siRNA; DNA-RNA hybrid; ss.
XX
XX Homo sapiens.
XX Synthetic.
XX
XX Key Location/Qualifiers
FT modified_base 20..21
FT /*tag= a
FT /mod_base= OTHER
FT /note= "OTHER= TT"
XX
XX WO2004018675-A1.
XX
XX 04-MAR-2004.
XX
XX 21-AUG-2003; 2003WO-CA001276.
XX
XX 21-AUG-2002; 2002US-0405193P.
XX 03-SEP-2002; 2002US-0408152P.
XX 02-DEC-2002; 2002US-0319748P.
XX 20-MAY-2003; 2003US-0472387P.
XX
XX (UYBR-) UNIV BRITISH COLUMBIA.
XX (GLEA/) GLEAVE M E.
XX
XX Jansen B;
XX
XX WPI; 2004-226951/21.
XX
XX Treating melanoma in a mammalian subject comprises administering to the
XX subject a therapeutic agent effective to reduce the effective amount of
XX clusterin in the melanoma cells.
XX
XX Claim 20; SEQ ID NO 40; 32pp; English.
PS
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XX
XX The present sequence is that of a short interfering RNA (siRNA) molecule
CC targeted to human clusterin ADL70403. The invention relates to the
CC treatment of melanoma through reduction in the effective amount of
CC clusterin. The therapeutic agent may be an antisense oligonucleotide
CC ADL70404-ADL70421 or short interfering RNA (siRNA) ADL70422-ADL70445
CC targeted to clusterin. The siRNAs molecules direct cleavage of clusterin
CC mRNA. A method for regulating expression of bcl-xL in a subject or cell
CC line comprises administering an agent effective to modulate the amount of
CC clusterin expression. In clusterin-expressing cells, expression of bcl-xL
CC is down-regulated when the effective amount of clusterin is reduced. Such
CC inhibition is significant because bcl-xL is known to act as an inhibitor
CC of apoptosis.
XX
SQ Sequence 21 BP; 8 A; 4 C; 1 G; 2 T; 6 U; 0 Other;
Query Match 1.3%; Score 21; DB 1; Length 21;
Best Local Similarity 71.4%; Pred. No. 39;
Matches 15; Conservative 6; Mismatches 0; Indels 0; Gaps 0;
QY 1615 CTAATTCATATAAACTGCTT 1635
Db 1 CUAUUCAAUAAAACUGUCTT 21
RESULT 88
ADL70406/c
ID ADL70406 standard; DNA; 21 BP.
XX
XX ADL70406;
XX
XX 20-MAY-2004 (first entry)
XX
XX Antisense oligonucleotide to human clusterin.
XX
XX Human; clusterin; antisense; melanoma; cytostatic; gene silencing; ss.
XX
XX Homo sapiens.
XX Synthetic.
XX
XX Key Location/Qualifiers
FT modified_base 1..21
FT /*tag= b
FT /mod_base= OTHER
FT /note= "OTHER= phosphorothioate nucleotides"
XX
XX modified_base 1..4
XX /*tag= a
XX /mod_base= OTHER
XX /note= "OTHER= 2'O-methoxyethyl modifications"
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XX modified_base 18..21
XX /*tag= c
XX /mod_base= OTHER
XX /note= "OTHER= 2'O-methoxyethyl modifications"
XX
XX WO2004018675-A1.
XX
XX 04-MAR-2004.
XX
XX 21-AUG-2003; 2003WO-CA001276.
XX
XX 21-AUG-2002; 2002US-0405193P.
XX 03-SEP-2002; 2002US-0408152P.
XX 02-DEC-2002; 2002US-0319748P.
XX 20-MAY-2003; 2003US-0472387P.
XX
XX (UYBR-) UNIV BRITISH COLUMBIA.
XX (GLEA/) GLEAVE M E.
XX
XX Jansen B;
XX
XX WPI; 2004-226951/21.
XX
XX Treating melanoma in a mammalian subject comprises administering to the
XX
```



PT subject a therapeutic agent effective to reduce the effective amount of  
 XX clusterin in the melanoma cells.

PS Claim 7; SEQ ID NO 4; 32pp; English.

XX The present sequence is that of an antisense oligonucleotide targeted to  
 CC human clusterin ADL70403. The invention relates to the treatment of  
 CC melanoma through reduction in the effective amount of clusterin. The  
 CC therapeutic agent may be an antisense oligonucleotide ADL70404-ADL70421  
 CC or short interfering RNA (siRNA) ADL70422-ADL70445 targeted to clusterin.  
 CC The antisense oligonucleotides are complementary to a region of the  
 CC clusterin mRNA spanning either the translation initiation site or the  
 CC termination site. They may be modified to increase stability in vivo,  
 CC e.g. they may be employed as phosphorothioate derivatives and may have 2'  
 CC -O-(2-methoxyethyl) (MOE) modifications in the 5' and 3' 'wings'. The  
 CC present antisense oligonucleotide is particularly preferred. It is  
 CC targeted to the translation initiation codon and next 6 codons of the  
 CC human clusterin sequence. It has a phosphorothioate backbone throughout  
 CC and MOE wings, the remaining nucleotides being 2'-deoxynucleotides. In an  
 CC example from the invention, this antisense oligonucleotide provided a  
 CC dose-dependent down-regulation of clusterin in human melanoma cells,  
 CC leading to an increase in apoptotic cell death. In one melanoma cell line  
 CC (607B) this alone was sufficient to lead to complete cell death. In  
 CC another melanoma cell line, the surviving cells showed increased  
 CC sensitivity to subsequent treatment with cisplatin. A claimed method for  
 CC regulating expression of bcl-xL in a subject or cell line comprises  
 CC administering an agent effective to modulate the amount of clusterin  
 CC expression. In clusterin-expressing cells, expression of bcl-xL is down-  
 CC regulated when the effective amount of clusterin is reduced. Such  
 CC inhibition is significant because bcl-xL is known to act as an inhibitor  
 CC of apoptosis.

SQ Sequence 21 BP; 6 A; 6 C; 4 G; 5 T; 0 U; 0 Other;

Query Match 1.3%; Score 21; DB 1; Length 21;  
 Best Local Similarity 100.0%; Pred. No. 39;  
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 48 ATGATGAAGACTCTGCTGCTG 68  
 |||||  
 DB 21 ATGATGAAGACTCTGCTGCTG 1

RESULT 89

ADL70423/c  
 ID ADL70423 standard; RNA; 21 BP.

XX AC ADL70423;

XX 20-MAY-2004 (first entry)

XX RNAi for human clusterin.

XX Human; clusterin; RNAi; melanoma; cytostatic; gene silencing;  
 XX short interfering RNA; siRNA; DNA-RNA hybrid; ss.

XX Homo sapiens.

XX Synthetic.

XX Key Location/Qualifiers  
 FH modified\_base 20..21  
 FT /\*tag= a  
 FT /mod\_base= OTHER  
 FT /note= "OTHER= TT"

XX WO2004018675-A1.

XX 04-MAR-2004.

XX 21-AUG-2003; 2003WO-CA001276.

XX 21-AUG-2002; 2002US-0405193P.

XX 03-SEP-2002; 2002US-0408152P.

PR 02-DEC-2002; 2002US-0319748P.  
 XX 20-MAY-2003; 2003US-0472387P.  
 PA (UYBR-) UNIV BRITISH COLUMBIA.  
 PA (GLEA/) GLEAVE M E.

XX Jansen B;

XX WPI; 2004-226851/21.

XX Treating melanoma in a mammalian subject comprises administering to the  
 PT subject a therapeutic agent effective to reduce the effective amount of  
 PT clusterin in the melanoma cells.

XX Claim 10; SEQ ID NO 21; 32pp; English.

XX The present sequence is that of a short interfering RNA (siRNA) molecule  
 CC targeted to human clusterin ADL70403. The invention relates to the  
 CC treatment of melanoma through reduction in the effective amount of  
 CC clusterin. The therapeutic agent may be an antisense oligonucleotide  
 CC ADL70404-ADL70421 or short interfering RNA (siRNA) ADL70422-ADL70445  
 CC targeted to clusterin. The siRNAs molecules direct cleavage of clusterin  
 CC mRNA. A method for regulating expression of bcl-xL in a subject or cell  
 CC line comprises administering an agent effective to modulate the amount of  
 CC clusterin expression. In clusterin-expressing cells, expression of bcl-xL  
 CC is down-regulated when the effective amount of clusterin is reduced. Such  
 CC inhibition is significant because bcl-xL is known to act as an inhibitor  
 CC of apoptosis.

SQ Sequence 21 BP; 4 A; 3 C; 9 G; 2 T; 3 U; 0 Other;

Query Match 1.3%; Score 21; DB 1; Length 21;  
 Best Local Similarity 100.0%; Pred. No. 39;  
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 480 AACGAGAGCTCGCCCTTCTAC 500  
 |||||  
 DB 21 AACGAGAGCTCGCCCTTCTAC 1

RESULT 90

ADL70441/c

ID ADL70441 standard; RNA; 21 BP.

XX AC ADL70441;

XX 20-MAY-2004 (first entry)

XX RNAi for human clusterin.

XX Human; clusterin; RNAi; melanoma; cytostatic; gene silencing;  
 XX short interfering RNA; siRNA; DNA-RNA hybrid; ss.

XX Homo sapiens.

XX Synthetic.

XX Key Location/Qualifiers  
 FH modified\_base 20..21  
 FT /\*tag= a  
 FT /mod\_base= OTHER  
 FT /note= "OTHER= TT"

XX WO2004018675-A1.

XX 04-MAR-2004.

XX 21-AUG-2003; 2003WO-CA001276.

XX 21-AUG-2002; 2002US-0405193P.

XX 03-SEP-2002; 2002US-0408152P.

XX 02-DEC-2002; 2002US-0319748P.

XX 20-MAY-2003; 2003US-0472387P.

```
PA (UYBR-) UNIV BRITISH COLUMBIA.
PA (GLEA/) GLEAVE M E.
XX Jansen B;
XX WPI; 2004-226851/21.
XX
XX Treating melanoma in a mammalian subject comprises administering to the
XX subject a therapeutic agent effective to reduce the effective amount of
XX clusterin in the melanoma cells.
XX
XX Claim 20; SEQ ID NO 39; 32pp; English.
XX
XX The present sequence is that of a short interfering RNA (siRNA) molecule
XX targeted to human clusterin ADL70403. The invention relates to the
XX treatment of melanoma through reduction in the effective amount of
XX clusterin. The therapeutic agent may be an antisense oligonucleotide
XX ADL70404-ADL70421 or short interfering RNA (siRNA) ADL70422-ADL70445
XX targeted to clusterin. The siRNAs molecules direct cleavage of clusterin
XX mRNA. A method for regulating expression of bcl-xL in a subject or cell
XX line comprises administering an agent effective to modulate the amount of
XX clusterin expression. In clusterin-expressing cells, expression of bcl-xL
XX is down-regulated when the effective amount of clusterin is reduced. Such
XX inhibition is significant because bcl-xL is known to act as an inhibitor
XX of apoptosis.
XX
XX Sequence 21 BP; 3 A; 5 C; 9 G; 2 T; 2 U; 0 Other;
SQ
Query Match 1.3%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 39;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 711 AAGTCCCGCATCGTCGCAGC 731
Db 21 AAGTCCCGCATCGTCGCAGC 1
RESULT 91
ADL70443/c
ID ADL70443 standard; RNA; 21 BP.
XX
XX ADL70443;
XX
XX 20-MAY-2004 (first entry)
XX
XX RNAi for human clusterin.
XX
XX Human; clusterin; RNAi; melanoma; cytostatic; gene silencing;
XX short interfering RNA; siRNA; DNA-RNA hybrid; ss.
XX
XX Homo sapiens.
XX Synthetic.
XX
XX Key Location/Qualifiers
XX modified_base 20..21
XX /tag= a
XX /mod_base= OTHER
XX /note= "OTHER= IT"
XX
XX WO2004018675-A1.
XX
XX 04-MAR-2004.
XX
XX 21-AUG-2003; 2003WO-CA001276.
XX
XX 21-AUG-2002; 2002US-0405193P.
XX 03-SEP-2002; 2002US-0408152P.
XX 02-DEC-2002; 2002US-0319748P.
XX 20-MAY-2003; 2003US-0472387P.
XX
XX (UYBR-) UNIV BRITISH COLUMBIA.
XX (GLEA/) GLEAVE M E.
XX
PI Jansen B;
XX WPI; 2004-226851/21.
XX
XX Treating melanoma in a mammalian subject comprises administering to the
XX subject a therapeutic agent effective to reduce the effective amount of
XX clusterin in the melanoma cells.
XX
XX Claim 20; SEQ ID NO 41; 32pp; English.
XX
XX The present sequence is that of a short interfering RNA (siRNA) molecule
XX targeted to human clusterin ADL70403. The invention relates to the
XX treatment of melanoma through reduction in the effective amount of
XX clusterin. The therapeutic agent may be an antisense oligonucleotide
XX ADL70404-ADL70421 or short interfering RNA (siRNA) ADL70422-ADL70445
XX targeted to clusterin. The siRNAs molecules direct cleavage of clusterin
XX mRNA. A method for regulating expression of bcl-xL in a subject or cell
XX line comprises administering an agent effective to modulate the amount of
XX clusterin expression. In clusterin-expressing cells, expression of bcl-xL
XX is down-regulated when the effective amount of clusterin is reduced. Such
XX inhibition is significant because bcl-xL is known to act as an inhibitor
XX of apoptosis.
XX
XX Sequence 21 BP; 6 A; 1 C; 4 G; 2 T; 8 U; 0 Other;
SQ
Query Match 1.3%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 39;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1613 AACTAATTCATTAATAAAGCTGTC 1633
Db 21 AACTAATTCATTAATAAAGCTGTC 1
RESULT 92
ADL70411/c
ID ADL70411 standard; DNA; 21 BP.
XX
XX ADL70411;
XX
XX 20-MAY-2004 (first entry)
XX
XX Antisense oligonucleotide to human clusterin.
XX
XX Human; clusterin; antisense; melanoma; cytostatic; gene silencing; ss.
XX
XX Homo sapiens.
XX Synthetic.
XX
XX Key Location/Qualifiers
XX modified_base 1..21
XX /tag= b
XX /mod_base= OTHER
XX /note= "OTHER= optional phosphorothioate nucleotides"
XX
XX modified_base 1..4
XX /tag= a
XX /mod_base= OTHER
XX /note= "OTHER= optional 2'-O-methoxyethyl modifications"
XX
XX modified_base 18..21
XX /tag= c
XX /mod_base= OTHER
XX /note= "OTHER= optional 2'-O-methoxyethyl modifications"
XX
XX WO2004018675-A1.
XX
XX 04-MAR-2004.
XX
XX 21-AUG-2003; 2003WO-CA001276.
XX
XX 21-AUG-2002; 2002US-0405193P.
XX 03-SEP-2002; 2002US-0408152P.
XX 02-DEC-2002; 2002US-0319748P.
XX 20-MAY-2003; 2003US-0472387P.
XX
XX (UYBR-) UNIV BRITISH COLUMBIA.
XX (GLEA/) GLEAVE M E.
XX
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XX (UYBR-) UNIV BRITISH COLUMBIA.
PA (GLEA/) GLEAVE M E.
XX Jansen B;
PI WPI; 2004-226851/21.
XX
XX Treating melanoma in a mammalian subject comprises administering to the
PT subject a therapeutic agent effective to reduce the effective amount of
PT clusterin in the melanoma cells.
XX
XX Claim 6; SEQ ID NO 9; 32pp; English.
XX
XX The present sequence is that of an antisense oligonucleotide targeted to
CC human clusterin ADL70403. The invention relates to the treatment of
CC melanoma through reduction in the effective amount of clusterin. The
CC therapeutic agent may be an antisense oligonucleotide ADL70404-ADL70421
CC or short interfering RNA (siRNA) ADL70422-ADL70445 targeted to clusterin.
CC The antisense oligonucleotides are complementary to a region of the
CC clusterin mRNA spanning either the translation initiation site or the
CC termination site. They may be modified to increase stability in vivo,
CC e.g. they may be employed as phosphorothioate derivatives and may have 2'
CC -O-(2-methoxyethyl) modifications in the 5' and 3' 'wings'. A method for
CC regulating expression of bcl-xL in a subject or cell line comprises
CC administering an agent effective to modulate the amount of clusterin
CC expression. In clusterin-expressing cells, expression of bcl-xL is down-
CC regulated when the effective amount of clusterin is reduced. Such
CC inhibition is significant because bcl-xL is known to act as an inhibitor
CC of apoptosis.
XX
XX Sequence 21 BP; 3 A; 5 C; 9 G; 4 T; 0 U; 0 Other;
SQ
Query Match 1.3%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 39;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 916 ACAACTCCACGGCTGCCTGC 936
Db 21 ACAACTCCACGGCTGCCTGC 1
RESULT 93
ADL70439/c
ID ADL70439 standard; RNA; 21 BP.
XX
XX ADL70439;
AC
XX
XX 20-MAY-2004 (first entry)
DT
XX
XX RNAi for human clusterin.
DE
XX
XX Human; clusterin; RNAi; melanoma; cytostatic; gene silencing;
KW short interfering RNA; siRNA; DNA-RNA hybrid; ss.
XX
XX Homo sapiens.
OS
XX Synthetic.
OS
XX Key Location/Qualifiers
FH modified_base 20..21
FT /*tag= a
FT /mod_base= OTHER
FT /note= "OTHER= TT"
XX
XX WO2004018675-A1.
PN
XX
XX 04-MAR-2004.
PD
XX
XX 21-AUG-2003; 2003WO-CA001276.
PP
XX
XX 21-AUG-2002; 2002US-0405193P.
PR
XX 03-SEP-2002; 2002US-0408152P.
PR
XX 02-DEC-2002; 2002US-0319748P.
PR
XX 20-MAY-2003; 2003US-0472387P.
PR
XX (UYBR-) UNIV BRITISH COLUMBIA.
PA
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PR 20-MAY-2003; 2003US-0472387P.
XX
XX (UYBR-) UNIV BRITISH COLUMBIA.
PA (GLEA/) GLEAVE M E.
XX
XX Jansen B;
PI
XX
XX WPI; 2004-226851/21.
XX
XX Treating melanoma in a mammalian subject comprises administering to the
PT subject a therapeutic agent effective to reduce the effective amount of
PT clusterin in the melanoma cells.
XX
XX Claim 20; SEQ ID NO 37; 32pp; English.
XX
XX The present sequence is that of a short interfering RNA (siRNA) molecule
CC targeted to human clusterin ADL70403. The invention relates to the
CC treatment of melanoma through reduction in the effective amount of
CC clusterin. The therapeutic agent may be an antisense oligonucleotide
CC ADL70404-ADL70421 or short interfering RNA (siRNA) ADL70422-ADL70445
CC targeted to clusterin. The siRNAs molecules direct cleavage of clusterin
CC mRNA. A method for regulating expression of bcl-xL in a subject or cell
CC line comprises administering an agent effective to modulate the amount of
CC clusterin expression. In clusterin-expressing cells, expression of bcl-xL
CC is down-regulated when the effective amount of clusterin is reduced. Such
CC inhibition is significant because bcl-xL is known to act as an inhibitor
CC of apoptosis.
XX
XX Sequence 21 BP; 4 A; 3 C; 9 G; 2 T; 3 U; 0 Other;
SQ
Query Match 1.3%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 39;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 480 RACCAGAGCTCGCCCTTCTAC 500
Db 21 RACCAGAGCTCGCCCTTCTAC 1
RESULT 94
ADL70438
ID ADL70438 standard; RNA; 21 BP.
XX
XX ADL70438;
AC
XX
XX 20-MAY-2004 (first entry)
DT
XX
XX RNAi for human clusterin.
DE
XX
XX Human; clusterin; RNAi; melanoma; cytostatic; gene silencing;
KW short interfering RNA; siRNA; DNA-RNA hybrid; ss.
XX
XX Homo sapiens.
OS
XX Synthetic.
OS
XX Key Location/Qualifiers
FH modified_base 20..21
FT /*tag= a
FT /mod_base= OTHER
FT /note= "OTHER= TT"
XX
XX WO2004018675-A1.
PN
XX
XX 04-MAR-2004.
PD
XX
XX 21-AUG-2003; 2003WO-CA001276.
PP
XX
XX 21-AUG-2002; 2002US-0405193P.
PR
XX 03-SEP-2002; 2002US-0408152P.
PR
XX 02-DEC-2002; 2002US-0319748P.
PR
XX 20-MAY-2003; 2003US-0472387P.
PR
XX (UYBR-) UNIV BRITISH COLUMBIA.
PA
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PA (GLEA/) GLEAVE M E.
XX
XX PI
XX Jansen B;
XX WPI; 2004-226851/21.
XX
XX PT Treating melanoma in a mammalian subject comprises administering to the
XX PT subject a therapeutic agent effective to reduce the effective amount of
XX PT clusterin in the melanoma cells.
XX
XX PS Claim 20; SEQ ID NO 36; 32pp; English.
XX
XX CC The present sequence is that of a short interfering RNA (siRNA) molecule
XX CC targeted to human clusterin ADL70403. The invention relates to the
XX CC treatment of melanoma through reduction in the effective amount of
XX CC clusterin. The therapeutic agent may be an antisense oligonucleotide
XX CC ADL70404-ADL70421 or short interfering RNA (siRNA) ADL70422-ADL70445
XX CC targeted to clusterin. The siRNAs molecules direct cleavage of clusterin
XX CC mRNA. A method for regulating expression of bcl-xL in a subject or cell
XX CC line comprises administering an agent effective to modulate the amount of
XX CC clusterin expression. In clusterin-expressing cells, expression of bcl-xL
XX CC is down-regulated when the effective amount of clusterin is reduced. Such
XX CC inhibition is significant because bcl-xL is known to act as an inhibitor
XX CC of apoptosis.
XX
XX SQ Sequence 21 BP; 3 A; 9 C; 3 G; 2 T; 4 U; 0 Other;
XX
XX Query Match 1.3%; Score 21; DB 1; Length 21;
XX Best Local Similarity 81.0%; Pred. No. 39;
XX Matches 17; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
XX
QY 482 CCAGAGCTCGCCCTTCTACTT 502
DB |||||:||||:||||:||||:
1 CCAGAGCUCGCCUUCUACTT 21
XX
RESULT 95
ADL70414/c
ID ADL70414 standard; DNA; 21 BP.
XX
XX AC ADL70414;
XX
XX DT 20-MAY-2004 (first entry)
XX
XX DE Antisense oligonucleotide to human clusterin.
XX
XX KW Human; clusterin; antisense; melanoma; cytostatic; gene silencing; ss.
XX
XX OS Homo sapiens.
XX OS Synthetic.
XX
XX FH Key Location/Qualifiers
XX modified_base 1..21
XX /*tag= b
XX /mod_base= OTHER
XX /note= "OTHER= optional phosphorothioate nucleotides"
XX modified_base 1..4
XX /*tag= a
XX /mod_base= OTHER
XX /note= "OTHER= optional 2'-O-methoxyethyl modifications"
XX modified_base 18..21
XX /*tag= c
XX /mod_base= OTHER
XX /note= "OTHER= optional 2'-O-methoxyethyl modifications"
XX
XX PN WO2004018675-A1.
XX
XX PD 04-WAR-2004.
XX
XX PF 21-AUG-2003; 2003WO-CA001276.
XX
XX PR 21-AUG-2002; 2002US-0405193P.
XX PR 03-SEP-2002; 2002US-0408152P.
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PR 02-DEC-2002; 2002US-0319748P.
XX
XX PR 20-MAY-2003; 2003US-0472387P.
XX
XX PA (UYER-) UNIV BRITISH COLUMBIA.
XX PA (GLEA/) GLEAVE M E.
XX
XX XX Jansen B;
XX
XX DR WPI; 2004-226851/21.
XX
XX PT Treating melanoma in a mammalian subject comprises administering to the
XX PT subject a therapeutic agent effective to reduce the effective amount of
XX PT clusterin in the melanoma cells.
XX
XX PS Claim 6; SEQ ID NO 12; 32pp; English.
XX
XX CC The present sequence is that of an antisense oligonucleotide targeted to
XX CC human clusterin ADL70403. The invention relates to the treatment of
XX CC melanoma through reduction in the effective amount of clusterin. The
XX CC therapeutic agent may be an antisense oligonucleotide ADL70404-ADL70421
XX CC or short interfering RNA (siRNA) ADL70422-ADL70445 targeted to clusterin.
XX CC The antisense oligonucleotides are complementary to a region of the
XX CC clusterin mRNA spanning either the translation initiation site or the
XX CC termination site. They may be modified to increase stability in vivo,
XX CC e.g. they may be employed as phosphorothioate derivatives and may have 2'
XX CC -O-(2-methoxyethyl) modifications in the 5' and 3' 'wings'. A method for
XX CC regulating expression of bcl-xL in a subject or cell line comprises
XX CC administering an agent effective to modulate the amount of clusterin
XX CC expression. In clusterin-expressing cells, expression of bcl-xL is down-
XX CC regulated when the effective amount of clusterin is reduced. Such
XX CC inhibition is significant because bcl-xL is known to act as an inhibitor
XX CC of apoptosis.
XX
XX SQ Sequence 21 BP; 1 A; 4 C; 12 G; 4 T; 0 U; 0 Other;
XX
XX Query Match 1.3%; Score 21; DB 1; Length 21;
XX Best Local Similarity 100.0%; Pred. No. 39;
XX Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1516 AGGCCCCCAACTCGGCCAGC 1536
DB |||||:||||:||||:||||:
21 AGGCCCCCAACTCGGCCAGC 1
XX
RESULT 96
ADL70409/c
ID ADL70409 standard; DNA; 21 BP.
XX
XX AC ADL70409;
XX
XX DT 20-MAY-2004 (first entry)
XX
XX DE Antisense oligonucleotide to human clusterin.
XX
XX KW Human; clusterin; antisense; melanoma; cytostatic; gene silencing; ss.
XX
XX OS Homo sapiens.
XX OS Synthetic.
XX
XX FH Key Location/Qualifiers
XX modified_base 1..21
XX /*tag= b
XX /mod_base= OTHER
XX /note= "OTHER= optional phosphorothioate nucleotides"
XX modified_base 1..4
XX /*tag= a
XX /mod_base= OTHER
XX /note= "OTHER= optional 2'-O-methoxyethyl modifications"
XX modified_base 18..21
XX /*tag= c
XX /mod_base= OTHER
XX /note= "OTHER= optional 2'-O-methoxyethyl modifications"
XX
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FT modified_base 18..21      /*tag= c
FT /mod_base= OTHER
FT /note= "OTHER= optional 2'O-methoxyethyl modifications"
XX
XX WO2004018675-A1.
XX
XX 04-MAR-2004.
XX
XX 21-AUG-2003; 2003WO-CA001276.
XX
XX 21-AUG-2002; 2002US-0405193P.
XX 03-SEP-2002; 2002US-0408152P.
XX 02-DEC-2002; 2002US-0319748P.
XX 20-MAY-2003; 2003US-0472387P.
XX
XX (UYBR-) UNIV BRITISH COLUMBIA.
XX (GLEA/) GLEAVE M E.
XX
XX Jansen B;
XX
XX WPI; 2004-226851/21.
XX
XX Treating melanoma in a mammalian subject comprises administering to the
XX subject a therapeutic agent effective to reduce the effective amount of
XX clusterin in the melanoma cells.
XX
XX Claim 6; SEQ ID NO 3; 32pp; English.
XX
XX The present sequence is that of an antisense oligonucleotide targeted to
XX human clusterin ADL70403. The invention relates to the treatment of
XX melanoma through reduction in the effective amount of clusterin. The
XX therapeutic agent may be an antisense oligonucleotide ADL70404-ADL70421
XX or short interfering RNA (siRNA) ADL70422-ADL70445 targeted to clusterin.
XX The antisense oligonucleotides are complementary to a region of the
XX clusterin mRNA spanning either the translation initiation site or the
XX termination site. They may be modified to increase stability in vivo,
XX e.g. they may be employed as phosphorothioate derivatives and may have 2'
XX -O-(2-methoxyethyl) modifications in the 5' and 3' 'wings'. A method for
XX regulating expression of bcl-xL in a subject or cell line comprises
XX administering an agent effective to modulate the amount of clusterin
XX expression. In clusterin-expressing cells, expression of bcl-xL is down-
XX regulated when the effective amount of clusterin is reduced. Such
XX inhibition is significant because bcl-xL is known to act as an inhibitor
XX of apoptosis.
XX
XX Sequence 21 BP; 2 A; 6 C; 7 G; 6 T; 0 U; 0 Other;
XX
XX Query Match 1.3%; Score 21; DB 1; Length 21;
XX Best Local Similarity 100.0%; Pred. No. 39;
XX Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 CCGAGGCGTGCAGAGACTCCA 16
Db |||||
21 CCGAGGCGTGCAGAGACTCCA 1

RESULT 99
ADL70407/c
ID ADL70407 standard; DNA; 21 BP.
XX
XX ADL70407;
XX
XX 20-MAY-2004 (first entry)
XX
XX Antisense oligonucleotide to human clusterin.
XX
XX Human; clusterin; antisense; melanoma; cytostatic; gene silencing; ss.
XX
XX Homo sapiens.
XX
XX Synthetic.
XX
XX Key Location/Qualifiers

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FT modified_base 1..21      /*tag= b
FT /mod_base= OTHER
FT /note= "OTHER= optional phosphorothioate nucleotides"
XX
XX modified_base 1..4
XX /*tag= a
XX /mod_base= OTHER
XX /note= "OTHER= optional 2'O-methoxyethyl modifications"
XX
XX modified_base 18..21
XX /*tag= c
XX /mod_base= OTHER
XX /note= "OTHER= optional 2'O-methoxyethyl modifications"
XX
XX WO2004018675-A1.
XX
XX 04-MAR-2004.
XX
XX 21-AUG-2003; 2003WO-CA001276.
XX
XX 21-AUG-2002; 2002US-0405193P.
XX 03-SEP-2002; 2002US-0408152P.
XX 02-DEC-2002; 2002US-0319748P.
XX 20-MAY-2003; 2003US-0472387P.
XX
XX (UYBR-) UNIV BRITISH COLUMBIA.
XX (GLEA/) GLEAVE M E.
XX
XX Jansen B;
XX
XX WPI; 2004-226851/21.
XX
XX Treating melanoma in a mammalian subject comprises administering to the
XX subject a therapeutic agent effective to reduce the effective amount of
XX clusterin in the melanoma cells.
XX
XX Claim 6; SEQ ID NO 5; 32pp; English.
XX
XX The present sequence is that of an antisense oligonucleotide targeted to
XX human clusterin ADL70403. The invention relates to the treatment of
XX melanoma through reduction in the effective amount of clusterin. The
XX therapeutic agent may be an antisense oligonucleotide ADL70404-ADL70421
XX or short interfering RNA (siRNA) ADL70422-ADL70445 targeted to clusterin.
XX The antisense oligonucleotides are complementary to a region of the
XX clusterin mRNA spanning either the translation initiation site or the
XX termination site. They may be modified to increase stability in vivo,
XX e.g. they may be employed as phosphorothioate derivatives and may have 2'
XX -O-(2-methoxyethyl) modifications in the 5' and 3' 'wings'. A method for
XX regulating expression of bcl-xL in a subject or cell line comprises
XX administering an agent effective to modulate the amount of clusterin
XX expression. In clusterin-expressing cells, expression of bcl-xL is down-
XX regulated when the effective amount of clusterin is reduced. Such
XX inhibition is significant because bcl-xL is known to act as an inhibitor
XX of apoptosis.
XX
XX Sequence 21 BP; 3 A; 5 C; 6 G; 7 T; 0 U; 0 Other;
XX
XX Query Match 1.3%; Score 21; DB 1; Length 21;
XX Best Local Similarity 100.0%; Pred. No. 39;
XX Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 114 GACCAGACGGTCTCAGACAAT 134
Db |||||
21 GACCAGACGGTCTCAGACAAT 1

RESULT 100
ADL70424
ID ADL70424 standard; RNA; 21 BP.
XX
XX ADL70424;
XX
XX 20-MAY-2004 (first entry)
XX
XX

```

DE RNAi for human clusterin.  
XX Human; clusterin; RNAi; melanoma; cytostatic; gene silencing;  
KW short interfering RNA; siRNA; DNA-RNA hybrid; ss.  
XX  
OS Homo sapiens.  
OS Synthetic.  
XX  
FH Key Location/Qualifiers  
FT modified\_base 20..21  
FT /\*tag= a  
FT /mod\_base= OTHER  
FT /note= "OTHER= TT"  
XX  
XX WO2004018675-A1.  
XX  
XX 04-MAR-2004.  
XX  
XX 21-AUG-2003; 2003WO-CA001276.  
XX  
XX 21-AUG-2002; 2002US-0405193P.  
PR 03-SEP-2002; 2002US-0408152P.  
PR 02-DEC-2002; 2002US-0319748P.  
PR 20-MAY-2003; 2003US-0472387P.  
XX  
XX (UYBR-) UNIV BRITISH COLUMBIA.  
PA (GLEA/) GLEAVE M E.  
PA  
PI Jansen B;  
XX  
XX WPI; 2004-226851/21.  
DR  
XX Treating melanoma in a mammalian subject comprises administering to the  
PT subject a therapeutic agent effective to reduce the effective amount of  
PT clusterin in the melanoma cells.  
XX  
XX Claim 10; SEQ ID NO 22; 32pp; English.  
XX  
XX The present sequence is that of a short interfering RNA (siRNA) molecule  
CC targeted to human clusterin ADL70403. The invention relates to the  
CC treatment of melanoma through reduction in the effective amount of  
CC clusterin. The therapeutic agent may be an antisense oligonucleotide  
CC ADL70404-ADL70421 or short interfering RNA (siRNA) ADL70422-ADL70445  
CC targeted to clusterin. The siRNAs molecules direct cleavage of clusterin  
CC mRNA. A method for regulating expression of bcl-xL in a subject or cell  
CC line comprises administering an agent effective to modulate the amount of  
CC clusterin expression. In clusterin-expressing cells, expression of bcl-xL  
CC is down-regulated when the effective amount of clusterin is reduced. Such  
CC inhibition is significant because bcl-xL is known to act as an inhibitor  
CC of apoptosis.  
XX  
XX Sequence 21 BP; 4 A; 9 C; 2 G; 2 T; 4 U; 0 Other;  
SQ

Query Match 1.3%; Score 21; DB 1; Length 21;  
Best Local Similarity 81.0%; Pred. No. 39;  
Matches 17; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1100 GATGCTCAACACTCTCTCTT 1120  
Db 1 GAUGCUCACACCCUCCCTT 21  
||:|||||:|||||:|||||  
||:|||||:|||||:|||||

RESULT 101  
AAA66325  
ID AAA66325 standard; DNA; 24 BP.  
XX  
XX AAA66325;  
XX  
XX 09-OCT-2000 (first entry)  
DT  
XX  
XX Dog genomic marker oligonucleotide sequence SEQ ID NO:187.  
DE  
XX Dog; genome; genomic marker; radiation hybrid map; identification;  
KW

KW chromosome location; gene marker; polymorphic microsatellite marker;  
KW phenotype; behaviour; pedigree; ss.  
XX  
XX Canis familiaris.  
OS  
PN WO200029615-A2.  
XX  
XX 25-MAY-2000.  
XX  
XX 15-NOV-1999; 99WO-IB001907.  
PF  
XX  
XX 13-NOV-1998; 98US-0108193P.  
PR  
XX  
XX (CNRS ) CNRS CENT NAT RECH SCI.  
PA  
XX  
XX Galibert F, Andre C;  
PI  
XX  
XX WPI; 2000-387821/33.  
DR  
XX  
XX New radiation hybrid map of the dog, Canine familiaris, genome, useful  
PT for e.g. identifying genes implicated in phenotypic and behavioral traits  
PT or in genetic diseases and for studying dog pedigrees.  
XX  
XX Claim 1; Page 61; 87pp; English.  
XX  
XX The present invention describes a radiation hybrid map of the dog (Canine  
CC familiaris) genome comprising the genome location of a marker selected  
CC from AA66139 to AA66942. The radiation hybrid map is useful for  
CC identifying and localising dog genes, since it covers approximately 80 %  
CC of the dog genome and provides a dense map integrating different types  
CC (i.e. Type I and Type II) of markers. The map and the dog genome markers  
CC (or complementary sequences) are especially useful to identify genes  
CC responsible for phenotypic and behavioural traits in dogs, to identify  
CC morbid genes, to analyse diseases and identify implicated genes in such  
CC diseases and their alleles, and to study dog pedigrees. They may also be  
CC useful for isolating corresponding human gene sequences e.g. genes  
CC involved in genetic diseases  
XX  
XX Sequence 24 BP; 5 A; 8 C; 6 G; 5 T; 0 U; 0 Other;  
SQ

Query Match 1.3%; Score 20.8; DB 1; Length 24;  
Best Local Similarity 91.7%; Pred. No. 67;  
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1467 CCCCCAGAGAGAGCTGCACGTC 1490  
Db 1 CCCCTAGAGAGAGCTTCGATGTC 24  
|||||:|||||:|||||:|||||

RESULT 102  
ABN99680/C  
ID ABN99680 standard; DNA; 20 BP.  
XX  
XX ABN99680;  
XX  
XX 16-AUG-2002 (first entry)  
DT  
XX  
XX Human clusterin inhibiting antisense oligonucleotide 14.  
DE  
XX  
XX Human; antisense inhibition; antisense oligonucleotide; clusterin;  
KW hypercholesterolaemia; cardiovascular disorder; ss;  
KW hyperproliferative disorder; hyperlipidemic disorder;  
KW phosphorothioate backbone; 2'-O-methoxyethyl wing.  
XX  
XX Homo sapiens.  
OS  
XX  
XX WO200222635-A1.  
PN  
XX  
XX 21-MAR-2002.  
PD  
XX  
XX 10-SEP-2001; 2001WO-US028235.  
PF  
XX  
XX 11-SEP-2000; 2000US-00659791.  
PR

XX (ISIS-) ISIS PHARM INC.  
XX PA Monia BP, Freier SM;  
XX PI WPI; 2002-404805/43.  
XX DR  
XX Novel antisense compound targeted to nucleic acid molecule encoding  
PT clusterin, useful for treating animal having disease associated with  
PT clusterin such as hyperlipidemic disorder, cardiovascular disorder.  
XX  
XX Claim 3; Page 83; 125pp; English.  
XX  
XX The invention comprises antisense oligonucleotides that are capable of  
CC inhibiting expression of the human clusterin gene. The antisense  
CC oligonucleotides of the invention are useful for inhibiting the  
CC expression of clusterin in cells. The antisense oligonucleotides are also  
CC useful for treating an animal with a disease or condition associated with  
CC expression of clusterin in cells. The antisense oligonucleotides are also  
CC useful for treating an animal with a disease or condition associated with  
CC clusterin (e.g. hypercholesterolaemia; cardiovascular disorders;  
CC hyperproliferative disorders; and hyperlipidemic disorders). The present  
CC DNA sequence represents a clusterin antisense oligonucleotide of the  
CC invention. NOTE: The present DNA sequence has a phosphorothioate backbone  
CC and also contains 2'-O-methoxyethyl wings  
XX  
XX Sequence 20 BP; 2 A; 5 C; 6 G; 7 T; 0 U; 0 Other;  
SQ  
Query Match 1.2%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 45;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 324 ACAAGCTGAAGAGTCCC 343  
Db 20 ACAAGCTGAAGAGTCCC 1  
RESULT 103  
ID ABN99682/c  
XX ABN99682 standard; DNA; 20 BP.  
XX AC ABN99682;  
XX  
XX 16-AUG-2002 (first entry)  
XX  
XX Human clusterin inhibiting antisense oligonucleotide 16.  
XX  
XX Human; antisense inhibition; antisense oligonucleotide; clusterin;  
KW hypercholesterolaemia; cardiovascular disorder; ss;  
KW hyperproliferative disorder; hyperlipidemic disorder;  
KW phosphorothioate backbone; 2'-O-methoxyethyl wing.  
XX  
XX Homo sapiens.  
XX  
XX WO200222635-A1.  
XX  
XX 21-MAR-2002.  
XX  
XX 10-SEP-2001; 2001WO-US028235.  
XX  
XX 11-SEP-2000; 2000US-00659791.  
XX  
XX (ISIS-) ISIS PHARM INC.  
XX PA Monia BP, Freier SM;  
XX PI WPI; 2002-404805/43.  
XX  
XX Novel antisense compound targeted to nucleic acid molecule encoding  
PT clusterin, useful for treating animal having disease associated with  
PT clusterin such as hyperlipidemic disorder, cardiovascular disorder.  
XX  
XX Claim 3; Page 83; 125pp; English.  
XX  
XX The invention comprises antisense oligonucleotides that are capable of

CC inhibiting expression of the human clusterin gene. The antisense  
CC oligonucleotides of the invention are useful for inhibiting the  
CC expression of clusterin in cells. The antisense oligonucleotides are also  
CC useful for treating an animal with a disease or condition associated with  
CC clusterin (e.g. hypercholesterolaemia; cardiovascular disorders;  
CC hyperproliferative disorders; and hyperlipidemic disorders). The present  
CC DNA sequence represents a clusterin antisense oligonucleotide of the  
CC invention. NOTE: The present DNA sequence has a phosphorothioate backbone  
CC and also contains 2'-O-methoxyethyl wings  
XX  
XX Sequence 20 BP; 4 A; 8 C; 4 G; 4 T; 0 U; 0 Other;  
SQ  
Query Match 1.2%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 45;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 364 TGATGGCCCTCTGGAGAG 383  
Db 20 TGATGGCCCTCTGGAGAG 1  
RESULT 104  
ID ABN99684/c  
XX ABN99684 standard; DNA; 20 BP.  
XX AC ABN99684;  
XX  
XX 16-AUG-2002 (first entry)  
XX  
XX Human clusterin inhibiting antisense oligonucleotide 18.  
XX  
XX Human; antisense inhibition; antisense oligonucleotide; clusterin;  
KW hypercholesterolaemia; cardiovascular disorder; ss;  
KW hyperproliferative disorder; hyperlipidemic disorder;  
KW phosphorothioate backbone; 2'-O-methoxyethyl wing.  
XX  
XX Homo sapiens.  
XX  
XX WO200222635-A1.  
XX  
XX 21-MAR-2002.  
XX  
XX 10-SEP-2001; 2001WO-US028235.  
XX  
XX 11-SEP-2000; 2000US-00659791.  
XX  
XX (ISIS-) ISIS PHARM INC.  
XX PI Monia BP, Freier SM;  
XX XX WPI; 2002-404805/43.  
XX  
XX Novel antisense compound targeted to nucleic acid molecule encoding  
PT clusterin, useful for treating animal having disease associated with  
PT clusterin such as hyperlipidemic disorder, cardiovascular disorder.  
XX  
XX Claim 3; Page 83; 125pp; English.  
XX  
XX The invention comprises antisense oligonucleotides that are capable of  
CC inhibiting expression of the human clusterin gene. The antisense  
CC oligonucleotides of the invention are useful for inhibiting the  
CC expression of clusterin in cells. The antisense oligonucleotides are also  
CC useful for treating an animal with a disease or condition associated with  
CC clusterin (e.g. hypercholesterolaemia; cardiovascular disorders;  
CC hyperproliferative disorders; and hyperlipidemic disorders). The present  
CC DNA sequence represents a clusterin antisense oligonucleotide of the  
CC invention. NOTE: The present DNA sequence has a phosphorothioate backbone  
CC and also contains 2'-O-methoxyethyl wings  
XX  
XX Sequence 20 BP; 5 A; 4 C; 6 G; 5 T; 0 U; 0 Other;  
SQ  
Query Match 1.2%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 45;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;





PF 10-SEP-2001; 2001WO-US028235.  
XX  
PR 11-SEP-2000; 2000US-00659791.  
XX  
PA (ISIS-) ISIS PHARM INC.  
XX  
PI Monia BP, Freier SM;  
XX  
DR WPI; 2002-404805/43.  
XX  
PT Novel antisense compound targeted to nucleic acid molecule encoding  
PT clusterin, useful for treating animal having disease associated with  
PT clusterin such as hyperlipidemic disorder, cardiovascular disorder.  
XX  
PS Claim 3; Page 84; 125pp; English.  
XX  
CC The invention comprises antisense oligonucleotides that are capable of  
CC inhibiting expression of the human clusterin gene. The antisense  
CC oligonucleotides of the invention are useful for inhibiting the  
CC expression of clusterin in cells. The antisense oligonucleotides are also  
CC useful for treating an animal with a disease or condition associated with  
CC clusterin (e.g. hypercholesterolaemia; cardiovascular disorders;  
CC hyperproliferative disorders; and hyperlipidemic disorders). The present  
CC DNA sequence represents a clusterin antisense oligonucleotide of the  
CC invention. NOTE: The present DNA sequence has a phosphorothioate backbone  
CC and also contains 2'-O-methoxyethyl wings  
XX  
SQ Sequence 20 BP; 8 A; 6 C; 3 G; 3 T; 0 U; 0 Other;

Query Match 1.2%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 45;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 967 AGATCTTGTCTGTGGACTGT 986  
DB 20 AGATCTTGTCTGTGGACTGT 1  
|||||

RESULT 108  
ABN99718/c  
ID ABN99718 standard; DNA; 20 BP.  
XX  
AC ABN99718;  
XX  
DT 16-AUG-2002 (first entry)  
XX  
DE Human clusterin inhibiting antisense oligonucleotide 52.  
XX  
KW Human; antisense inhibition; antisense oligonucleotide; clusterin;  
KW hypercholesterolaemia; cardiovascular disorder; ss;  
KW hyperproliferative disorder; hyperlipidemic disorder;  
KW phosphorothioate backbone; 2'-O-methoxyethyl wing.  
XX  
OS Homo sapiens.  
XX  
FN WO200222635-A1.  
XX  
PD 21-MAR-2002.  
XX  
PF 10-SEP-2001; 2001WO-US028235.  
XX  
PR 11-SEP-2000; 2000US-00659791.  
XX  
PA (ISIS-) ISIS PHARM INC.  
XX  
PI Monia BP, Freier SM;  
XX  
DR WPI; 2002-404805/43.  
XX  
PT Novel antisense compound targeted to nucleic acid molecule encoding  
PT clusterin, useful for treating animal having disease associated with  
PT clusterin such as hyperlipidemic disorder, cardiovascular disorder.  
XX

PS Claim 3; Page 84; 125pp; English.  
XX  
CC The invention comprises antisense oligonucleotides that are capable of  
CC inhibiting expression of the human clusterin gene. The antisense  
CC oligonucleotides of the invention are useful for inhibiting the  
CC expression of clusterin in cells. The antisense oligonucleotides are also  
CC useful for treating an animal with a disease or condition associated with  
CC clusterin (e.g. hypercholesterolaemia; cardiovascular disorders;  
CC hyperproliferative disorders; and hyperlipidemic disorders). The present  
CC DNA sequence represents a clusterin antisense oligonucleotide of the  
CC invention. NOTE: The present DNA sequence has a phosphorothioate backbone  
CC and also contains 2'-O-methoxyethyl wings  
XX  
SQ Sequence 20 BP; 4 A; 8 C; 6 G; 2 T; 0 U; 0 Other;

Query Match 1.2%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 45;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1148 CTGGGTGTCCCGGTGGCAA 1167  
DB 20 CTGGGTGTCCCGGTGGCAA 1  
|||||

RESULT 109  
ABN99677/c  
ID ABN99677 standard; DNA; 20 BP.  
XX  
AC ABN99677;  
XX  
DT 16-AUG-2002 (first entry)  
XX  
DE Human clusterin inhibiting antisense oligonucleotide 11.  
XX  
KW Human; antisense inhibition; antisense oligonucleotide; clusterin;  
KW hypercholesterolaemia; cardiovascular disorder; ss;  
KW hyperproliferative disorder; hyperlipidemic disorder;  
KW phosphorothioate backbone; 2'-O-methoxyethyl wing.  
XX  
OS Homo sapiens.  
XX  
FN WO200222635-A1.  
XX  
PD 21-MAR-2002.  
XX  
PF 10-SEP-2001; 2001WO-US028235.  
XX  
PR 11-SEP-2000; 2000US-00659791.  
XX  
PA (ISIS-) ISIS PHARM INC.  
XX  
PI Monia BP, Freier SM;  
XX  
DR WPI; 2002-404805/43.  
XX  
PT Novel antisense compound targeted to nucleic acid molecule encoding  
PT clusterin, useful for treating animal having disease associated with  
PT clusterin such as hyperlipidemic disorder, cardiovascular disorder.  
XX  
PS Claim 3; Page 83; 125pp; English.  
XX  
CC The invention comprises antisense oligonucleotides that are capable of  
CC inhibiting expression of the human clusterin gene. The antisense  
CC oligonucleotides of the invention are useful for inhibiting the  
CC expression of clusterin in cells. The antisense oligonucleotides are also  
CC useful for treating an animal with a disease or condition associated with  
CC clusterin (e.g. hypercholesterolaemia; cardiovascular disorders;  
CC hyperproliferative disorders; and hyperlipidemic disorders). The present  
CC DNA sequence represents a clusterin antisense oligonucleotide of the  
CC invention. NOTE: The present DNA sequence has a phosphorothioate backbone  
CC and also contains 2'-O-methoxyethyl wings  
XX  
SQ Sequence 20 BP; 3 A; 5 C; 3 G; 9 T; 0 U; 0 Other;

```

Query Match          1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 45;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0

Qy      286 AGAAGAGGATGCCCTAAAT 305
Db      20 AGAAGAGGATGCCCTAAAT 1
      |||||||
RESULT 110
ABN99681/c
ID ABN99681 standard; DNA; 20 BP.
XX
AC ABN99681;
XX
DT 16-AUG-2002 (first entry)
XX
DE Human clusterin inhibiting antisense oligonucleotide 15.
XX
KW Human; antisense inhibition; antisense oligonucleotide; clusterin;
KW hypercholesterolaemia; cardiovascular disorder; ss;
KW hyperproliferative disorder; hyperlipidemic disorder;
KW phosphorothioate backbone; 2'-O-methoxyethyl wing.
XX
OS Homo sapiens.
XX
FN WO200222635-A1.
XX
PD 21-MAR-2002.
XX
PF 10-SEP-2001; 2001WO-US028235.
XX
PR 11-SEP-2000; 2000US-00659791.
XX
PI (ISIS-) ISIS PHARM INC.
XX
PI Monia BP, Freier SM;
XX
PI WPI; 2002-404805/43.
XX
DR
XX
PT Novel antisense compound targeted to nucleic acid molecule encoding
PT clusterin, useful for treating animal having disease associated with
PT clusterin such as hyperlipidemic disorder, cardiovascular disorder.
XX
PS Claim 3; Page 83; 125pp; English.
XX
CC The invention comprises antisense oligonucleotides that are capable of
CC inhibiting expression of the human clusterin gene. The antisense
CC oligonucleotides of the invention are useful for inhibiting the
CC expression of clusterin in cells. The antisense oligonucleotides are also
CC useful for treating an animal with a disease or condition associated with
CC clusterin (e.g. hypercholesterolaemia; cardiovascular disorders;
CC hyperproliferative disorders; and hyperlipidemic disorders). The present
CC DNA sequence represents a clusterin antisense oligonucleotide of the
CC invention. NOTE: The present DNA sequence has a phosphorothioate backbone
CC and also contains 2'-O-methoxyethyl wings
XX
SQ Sequence 20 BP; 4 A; 7 C; 6 G; 3 T; 0 U; 0 Other;

Query Match          1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 45;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0

Qy      359 GACCATGATGCCCTCTGGG 378
Db      20 GACCATGATGCCCTCTGGG 1
      |||||||
RESULT 111
ABN99668/c
ID ABN99668 standard; DNA; 20 BP.
XX

```

XX PD 21-MAR-2002.  
XX PF 10-SEP-2001; 2001WO-US028235.  
XX PR 11-SEP-2000; 2000US-00659791.  
XX PA (ISIS-) ISIS PHARM INC.  
XX PI Monia BP, Freier SM;  
XX WPI; 2002-404805/43.  
XX Novel antisense compound targeted to nucleic acid molecule encoding clusterin, useful for treating animal having disease associated with clusterin such as hyperlipidemic disorder, cardiovascular disorder.  
XX Claim 3; Page 83; 125pp; English.  
XX The invention comprises antisense oligonucleotides that are capable of inhibiting expression of the human clusterin gene. The antisense oligonucleotides of the invention are useful for inhibiting the expression of clusterin in cells. The antisense oligonucleotides are also useful for treating an animal with a disease or condition associated with clusterin (e.g. hypercholesterolaemia; cardiovascular disorders; hyperproliferative disorders; and hyperlipidemic disorders). The present DNA sequence represents a clusterin antisense oligonucleotide of the invention. NOTE: The present DNA sequence has a phosphorothioate backbone and also contains 2'-O-methoxyethyl wings  
XX Sequence 20 BP; 2 A; 7 C; 2 G; 9 T; 0 U; 0 Other;  
XX Query Match 1.2%; Score 20; DB 1; Length 20;  
XX Best Local Similarity 100.0%; Pred. No. 45;  
XX Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 201 GGGGTGAACACAGATAAAGAC 220  
DB 20 GGGGTGAACACAGATAAAGAC 1  
RESULT 113  
ABN99695/c  
ID ABN99695 standard; DNA; 20 BP.  
XX AC ABN99695;  
XX PD 16-AUG-2002 (first entry)  
XX DE Human clusterin inhibiting antisense oligonucleotide 29.  
XX KW Human; antisense inhibition; antisense oligonucleotide; clusterin;  
KW hypercholesterolaemia; cardiovascular disorder; ss;  
KW hyperproliferative disorder; hyperlipidemic disorder;  
KW phosphorothioate backbone; 2'-O-methoxyethyl wing.  
XX OS Homo sapiens.  
XX PN WO200222635-A1.  
XX PD 21-MAR-2002.  
XX PF 10-SEP-2001; 2001WO-US028235.  
XX PR 11-SEP-2000; 2000US-00659791.  
XX PA (ISIS-) ISIS PHARM INC.  
XX PI Monia BP, Freier SM;  
XX WPI; 2002-404805/43.  
XX Novel antisense compound targeted to nucleic acid molecule encoding

PT clusterin, useful for treating animal having disease associated with clusterin such as hyperlipidemic disorder, cardiovascular disorder.  
XX Claim 3; Page 83; 125pp; English.  
XX The invention comprises antisense oligonucleotides that are capable of inhibiting expression of the human clusterin gene. The antisense oligonucleotides of the invention are useful for inhibiting the expression of clusterin in cells. The antisense oligonucleotides are also useful for treating an animal with a disease or condition associated with clusterin (e.g. hypercholesterolaemia; cardiovascular disorders; hyperproliferative disorders; and hyperlipidemic disorders). The present DNA sequence represents a clusterin antisense oligonucleotide of the invention. NOTE: The present DNA sequence has a phosphorothioate backbone and also contains 2'-O-methoxyethyl wings  
XX Sequence 20 BP; 5 A; 5 C; 5 G; 5 T; 0 U; 0 Other;  
XX Query Match 1.2%; Score 20; DB 1; Length 20;  
XX Best Local Similarity 100.0%; Pred. No. 45;  
XX Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 567 GATGTCATGCAGGACCACCTT 586  
DB 20 GATGTCATGCAGGACCACCTT 1  
RESULT 114  
ABN99697/c  
ID ABN99697 standard; DNA; 20 BP.  
XX AC ABN99697;  
XX DT 16-AUG-2002 (first entry)  
XX DE Human clusterin inhibiting antisense oligonucleotide 31.  
XX KW Human; antisense inhibition; antisense oligonucleotide; clusterin;  
KW hypercholesterolaemia; cardiovascular disorder; ss;  
KW hyperproliferative disorder; hyperlipidemic disorder;  
KW phosphorothioate backbone; 2'-O-methoxyethyl wing.  
XX OS Homo sapiens.  
XX PN WO200222635-A1.  
XX PD 21-MAR-2002.  
XX PF 10-SEP-2001; 2001WO-US028235.  
XX PR 11-SEP-2000; 2000US-00659791.  
XX PA (ISIS-) ISIS PHARM INC.  
XX PI Monia BP, Freier SM;  
XX WPI; 2002-404805/43.  
XX Novel antisense compound targeted to nucleic acid molecule encoding clusterin, useful for treating animal having disease associated with clusterin such as hyperlipidemic disorder, cardiovascular disorder.  
XX Claim 3; Page 83; 125pp; English.  
XX The invention comprises antisense oligonucleotides that are capable of inhibiting expression of the human clusterin gene. The antisense oligonucleotides of the invention are useful for inhibiting the expression of clusterin in cells. The antisense oligonucleotides are also useful for treating an animal with a disease or condition associated with clusterin (e.g. hypercholesterolaemia; cardiovascular disorders; hyperproliferative disorders; and hyperlipidemic disorders). The present DNA sequence represents a clusterin antisense oligonucleotide of the invention. NOTE: The present DNA sequence has a phosphorothioate backbone and also contains 2'-O-methoxyethyl wings  
XX Sequence 20 BP; 5 A; 5 C; 5 G; 5 T; 0 U; 0 Other;  
XX Query Match 1.2%; Score 20; DB 1; Length 20;  
XX Best Local Similarity 100.0%; Pred. No. 45;  
XX Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 567 GATGTCATGCAGGACCACCTT 586  
DB 20 GATGTCATGCAGGACCACCTT 1  
RESULT 114  
ABN99697/c  
ID ABN99697 standard; DNA; 20 BP.  
XX AC ABN99697;  
XX DT 16-AUG-2002 (first entry)  
XX DE Human clusterin inhibiting antisense oligonucleotide 31.  
XX KW Human; antisense inhibition; antisense oligonucleotide; clusterin;  
KW hypercholesterolaemia; cardiovascular disorder; ss;  
KW hyperproliferative disorder; hyperlipidemic disorder;  
KW phosphorothioate backbone; 2'-O-methoxyethyl wing.  
XX OS Homo sapiens.  
XX PN WO200222635-A1.  
XX PD 21-MAR-2002.  
XX PF 10-SEP-2001; 2001WO-US028235.  
XX PR 11-SEP-2000; 2000US-00659791.  
XX PA (ISIS-) ISIS PHARM INC.  
XX PI Monia BP, Freier SM;  
XX WPI; 2002-404805/43.  
XX Novel antisense compound targeted to nucleic acid molecule encoding clusterin, useful for treating animal having disease associated with clusterin such as hyperlipidemic disorder, cardiovascular disorder.  
XX Claim 3; Page 83; 125pp; English.  
XX The invention comprises antisense oligonucleotides that are capable of inhibiting expression of the human clusterin gene. The antisense oligonucleotides of the invention are useful for inhibiting the expression of clusterin in cells. The antisense oligonucleotides are also useful for treating an animal with a disease or condition associated with clusterin (e.g. hypercholesterolaemia; cardiovascular disorders; hyperproliferative disorders; and hyperlipidemic disorders). The present DNA sequence represents a clusterin antisense oligonucleotide of the invention. NOTE: The present DNA sequence has a phosphorothioate backbone

```
CC and also contains 2'-O-methoxyethyl wings
XX
SQ Sequence 20 BP; 3 A; 5 C; 6 G; 6 T; 0 U; 0 Other;

Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 45;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 608 AGACGAGCTCTTCCAGGACA 627
Db 20 AGACGAGCTCTTCCAGGACA 1

RESULT 115
ABN99701/c
ID ABN99701 standard; DNA; 20 BP.
XX
AC ABN99701;
XX
DT 16-AUG-2002 (first entry)
XX
DE Human clusterin inhibiting antisense oligonucleotide 35.
XX
KW Human; antisense inhibition; antisense oligonucleotide; clusterin;
KW hypercholesterolaemia; cardiovascular disorder; ss;
KW hyperproliferative disorder; hyperlipidemic disorder;
KW phosphorothioate backbone; 2'-O-methoxyethyl wing.
XX
OS Homo sapiens.
XX
PN WO200222635-A1.
XX
PD 21-MAR-2002.
XX
PF 10-SEP-2001; 2001WO-US028235.
XX
PR 11-SEP-2000; 2000US-00659791.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Monia BP, Freier SM;
XX
DR WPI; 2002-404805/43.
XX
PT Novel antisense compound targeted to nucleic acid molecule encoding
PT clusterin, useful for treating animal having disease associated with
PT clusterin such as hyperlipidemic disorder, cardiovascular disorder.
XX
PS Claim 3; Page 83; 125pp; English.
XX
CC The invention comprises antisense oligonucleotides that are capable of
CC inhibiting expression of the human clusterin gene. The antisense
CC oligonucleotides of the invention are useful for inhibiting the
CC expression of clusterin in cells. The antisense oligonucleotides are also
CC useful for treating an animal with a disease or condition associated with
CC clusterin (e.g. hypercholesterolaemia; cardiovascular disorders;
CC hyperproliferative disorders; and hyperlipidemic disorders). The present
CC DNA sequence represents a clusterin antisense oligonucleotide of the
CC invention. NOTE: The present DNA sequence has a phosphorothioate backbone
CC and also contains 2'-O-methoxyethyl wings
XX
SQ Sequence 20 BP; 7 A; 4 C; 7 G; 2 T; 0 U; 0 Other;

Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 45;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 775 TGTTCAGCCCTTCCTTGAG 794
Db 20 TGTTCAGCCCTTCCTTGAG 1

RESULT 116
ABN99702/c
ID ABN99702 standard; DNA; 20 BP.
XX
AC ABN99702;
XX
DT 16-AUG-2002 (first entry)
XX
DE Human clusterin inhibiting antisense oligonucleotide 36.
XX
KW Human; antisense inhibition; antisense oligonucleotide; clusterin;
KW hypercholesterolaemia; cardiovascular disorder; ss;
KW hyperproliferative disorder; hyperlipidemic disorder;
KW phosphorothioate backbone; 2'-O-methoxyethyl wing.
XX
OS Homo sapiens.
XX
PN WO200222635-A1.
XX
PD 21-MAR-2002.
XX
PF 10-SEP-2001; 2001WO-US028235.
XX
PR 11-SEP-2000; 2000US-00659791.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Monia BP, Freier SM;
XX
DR WPI; 2002-404805/43.
XX
PT Novel antisense compound targeted to nucleic acid molecule encoding
PT clusterin, useful for treating animal having disease associated with
PT clusterin such as hyperlipidemic disorder, cardiovascular disorder.
XX
PS Claim 3; Page 83; 125pp; English.
XX
CC The invention comprises antisense oligonucleotides that are capable of
CC inhibiting expression of the human clusterin gene. The antisense
CC oligonucleotides of the invention are useful for inhibiting the
CC expression of clusterin in cells. The antisense oligonucleotides are also
CC useful for treating an animal with a disease or condition associated with
CC clusterin (e.g. hypercholesterolaemia; cardiovascular disorders;
CC hyperproliferative disorders; and hyperlipidemic disorders). The present
CC DNA sequence represents a clusterin antisense oligonucleotide of the
CC invention. NOTE: The present DNA sequence has a phosphorothioate backbone
CC and also contains 2'-O-methoxyethyl wings
XX
SQ Sequence 20 BP; 6 A; 4 C; 7 G; 3 T; 0 U; 0 Other;

Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 45;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 776 GTTCAGCCCTTCCTTGAGA 795
Db 20 GTTCAGCCCTTCCTTGAGA 1

RESULT 117
ABN99704/c
ID ABN99704 standard; DNA; 20 BP.
XX
AC ABN99704;
XX
DT 16-AUG-2002 (first entry)
XX
DE Human clusterin inhibiting antisense oligonucleotide 38.
XX
KW Human; antisense inhibition; antisense oligonucleotide; clusterin;
KW hypercholesterolaemia; cardiovascular disorder; ss;
KW hyperproliferative disorder; hyperlipidemic disorder;
KW phosphorothioate backbone; 2'-O-methoxyethyl wing.
XX
```

OS Homo sapiens.  
XX WO200222635-A1.  
PN  
XX 21-MAR-2002.  
PD  
XX  
XX 10-SEP-2001; 2001WO-US028235.  
PF  
XX  
XX 11-SEP-2000; 2000US-00659791.  
PR  
XX  
XX (ISIS-) ISIS PHARM INC.  
PA  
XX Monia BP, Freier SM;  
PI  
XX WPI; 2002-404805/43.  
XX  
XX Novel antisense compound targeted to nucleic acid molecule encoding  
PT clusterin, useful for treating animal having disease associated with  
PT clusterin such as hyperlipidemic disorder, cardiovascular disorder.  
XX  
XX Claim 3; Page 83; 125pp; English.  
PS  
XX The invention comprises antisense oligonucleotides that are capable of  
CC inhibiting expression of the human clusterin gene. The antisense  
CC oligonucleotides of the invention are useful for inhibiting the  
CC expression of clusterin in cells. The antisense oligonucleotides are also  
CC useful for treating an animal with a disease or condition associated with  
CC clusterin (e.g. hypercholesterolaemia; cardiovascular disorders;  
CC hyperproliferative disorders; and hyperlipidemic disorders). The present  
CC DNA sequence represents a clusterin antisense oligonucleotide of the  
CC invention. NOTE: The present DNA sequence has a phosphorothioate backbone  
CC and also contains 2'-O-methoxyethyl wings  
XX  
XX Sequence 20 BP; 4 A; 3 C; 8 G; 5 T; 0 U; 0 Other;  
SQ

Query Match 1.2%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. NO. 45;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 820 TGGACATCCACTTCCACAGC 839  
Db 20 TGGACATCCACTTCCACAGC 1

RESULT 118  
ABN99716/C  
ID ABN99716 standard; DNA; 20 BP.  
AC  
XX ABN99716;  
XX  
DT 16-AUG-2002 (first entry)  
XX  
DE Human clusterin inhibiting antisense oligonucleotide 50.  
XX  
XX Human; antisense inhibition; antisense oligonucleotide; clusterin;  
XX hypercholesterolaemia; cardiovascular disorder; ss;  
XX hyperproliferative disorder; hyperlipidemic disorder;  
XX phosphorothioate backbone; 2'-O-methoxyethyl wing.  
XX  
XX Homo sapiens.  
XX  
XX WO200222635-A1.  
PN  
XX  
XX 21-MAR-2002.  
PD  
XX  
XX 10-SEP-2001; 2001WO-US028235.  
PF  
XX  
XX 11-SEP-2000; 2000US-00659791.  
PR  
XX (ISIS-) ISIS PHARM INC.  
PA  
XX Monia BP, Freier SM;  
PI  
XX

DR WPI; 2002-404805/43.  
XX  
XX Novel antisense compound targeted to nucleic acid molecule encoding  
PT clusterin, useful for treating animal having disease associated with  
PT clusterin such as hyperlipidemic disorder, cardiovascular disorder.  
XX  
XX Claim 3; Page 84; 125pp; English.  
PS  
XX The invention comprises antisense oligonucleotides that are capable of  
CC inhibiting expression of the human clusterin gene. The antisense  
CC oligonucleotides of the invention are useful for inhibiting the  
CC expression of clusterin in cells. The antisense oligonucleotides are also  
CC useful for treating an animal with a disease or condition associated with  
CC clusterin (e.g. hypercholesterolaemia; cardiovascular disorders;  
CC hyperproliferative disorders; and hyperlipidemic disorders). The present  
CC DNA sequence represents a clusterin antisense oligonucleotide of the  
CC invention. NOTE: The present DNA sequence has a phosphorothioate backbone  
CC and also contains 2'-O-methoxyethyl wings  
XX  
XX Sequence 20 BP; 6 A; 5 C; 7 G; 2 T; 0 U; 0 Other;  
SQ

Query Match 1.2%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. NO. 45;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1113 TCCTCCTTGTCTGGAGCAGCT 1132  
Db 20 TCCTCCTTGTCTGGAGCAGCT 1

RESULT 119  
ABN99726/C  
ID ABN99726 standard; DNA; 20 BP.  
AC  
XX ABN99726;  
XX  
DT 16-AUG-2002 (first entry)  
XX  
XX Human clusterin inhibiting antisense oligonucleotide 60.  
DE  
XX Human; antisense inhibition; antisense oligonucleotide; clusterin;  
XX hypercholesterolaemia; cardiovascular disorder; ss;  
XX hyperproliferative disorder; hyperlipidemic disorder;  
XX phosphorothioate backbone; 2'-O-methoxyethyl wing.  
XX  
XX Homo sapiens.  
XX  
XX WO200222635-A1.  
PN  
XX  
XX 21-MAR-2002.  
PD  
XX  
XX 10-SEP-2001; 2001WO-US028235.  
PF  
XX  
XX 11-SEP-2000; 2000US-00659791.  
PR  
XX (ISIS-) ISIS PHARM INC.  
PA  
XX Monia BP, Freier SM;  
PI  
XX WPI; 2002-404805/43.  
XX  
XX Novel antisense compound targeted to nucleic acid molecule encoding  
PT clusterin, useful for treating animal having disease associated with  
PT clusterin such as hyperlipidemic disorder, cardiovascular disorder.  
XX  
XX Claim 3; Page 84; 125pp; English.  
PS  
XX The invention comprises antisense oligonucleotides that are capable of  
CC inhibiting expression of the human clusterin gene. The antisense  
CC oligonucleotides of the invention are useful for inhibiting the  
CC expression of clusterin in cells. The antisense oligonucleotides are also  
CC useful for treating an animal with a disease or condition associated with  
CC clusterin (e.g. hypercholesterolaemia; cardiovascular disorders;  
CC hyperproliferative disorders; and hyperlipidemic disorders). The present  
CC DNA sequence represents a clusterin antisense oligonucleotide of the  
CC invention. NOTE: The present DNA sequence has a phosphorothioate backbone  
CC and also contains 2'-O-methoxyethyl wings  
XX  
XX Sequence 20 BP; 6 A; 5 C; 7 G; 2 T; 0 U; 0 Other;  
SQ

CC hyperproliferative disorders; and hyperlipidemic disorders). The present  
CC DNA sequence represents a clusterin antisense oligonucleotide of the  
CC invention. NOTE: The present DNA sequence has a phosphorothioate backbone  
CC and also contains 2'-O-methoxyethyl wings

XX Sequence 20 BP; 6 A; 4 C; 7 G; 3 T; 0 U; 0 Other;

Query Match 1.2%; Score 20; DB 1; Length 20;

Best Local Similarity 100.0%; Pred. No. 45;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1545 GCTCTGGATCCCTGCACTCTA 1564

DB 20 GCTCTGGATCCCTGCACTCTA 1

RESULT 120

ABN99727/C

ID ABN99727 standard; DNA; 20 BP.

AC ABN99727;

XX 16-AUG-2002 (first entry)

DT 16-AUG-2002 (first entry)

XX Human clusterin inhibiting antisense oligonucleotide 61.

DE Human; antisense inhibition; antisense oligonucleotide; clusterin;

XX hypercholesterolaemia; cardiovascular disorder; ss;

KW hyperproliferative disorder; hyperlipidemic disorder;

KW phosphorothioate backbone; 2'-O-methoxyethyl wing.

XX Homo sapiens.

OS WO200222635-A1.

XX 21-MAR-2002.

XX 10-SEP-2001; 2001WO-US028235.

XX 11-SEP-2000; 2000US-00659791.

XX (ISIS-) ISIS PHARM INC.

XX Monia BP, Freier SM;

XX WPI; 2002-404805/43.

XX Novel antisense compound targeted to nucleic acid molecule encoding

PT clusterin, useful for treating animal having disease associated with

PT clusterin such as hyperlipidemic disorder, cardiovascular disorder.

XX Claim 3; Page 84; 125pp; English.

XX The invention comprises antisense oligonucleotides that are capable of

CC inhibiting expression of the human clusterin gene. The antisense

CC oligonucleotides of the invention are useful for inhibiting the

CC expression of clusterin in cells. The antisense oligonucleotides are also

CC useful for treating an animal with a disease or condition associated with

CC clusterin (e.g. hypercholesterolaemia; cardiovascular disorders;

CC hyperproliferative disorders; and hyperlipidemic disorders). The present

CC DNA sequence represents a clusterin antisense oligonucleotide of the

CC invention. NOTE: The present DNA sequence has a phosphorothioate backbone

CC and also contains 2'-O-methoxyethyl wings

XX Sequence 20 BP; 6 A; 3 C; 6 G; 5 T; 0 U; 0 Other;

Query Match 1.2%; Score 20; DB 1; Length 20;

Best Local Similarity 100.0%; Pred. No. 45;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1600 TGCTCTGATGCACTAAT 1619

DB 20 TGCTCTGATGCACTAAT 1

RESULT 121

ABN99670/C

ID ABN99670 standard; DNA; 20 BP.

XX AC ABN99670;

XX 16-AUG-2002 (first entry)

DT 16-AUG-2002 (first entry)

XX Human clusterin inhibiting antisense oligonucleotide 4.

DE Human; antisense inhibition; antisense oligonucleotide; clusterin;

XX hypercholesterolaemia; cardiovascular disorder; ss;

KW hyperproliferative disorder; hyperlipidemic disorder;

KW phosphorothioate backbone; 2'-O-methoxyethyl wing.

XX Homo sapiens.

OS WO200222635-A1.

XX 21-MAR-2002.

XX 10-SEP-2001; 2001WO-US028235.

XX 11-SEP-2000; 2000US-00659791.

XX (ISIS-) ISIS PHARM INC.

XX Monia BP, Freier SM;

XX WPI; 2002-404805/43.

XX Novel antisense compound targeted to nucleic acid molecule encoding

PT clusterin, useful for treating animal having disease associated with

PT clusterin such as hyperlipidemic disorder, cardiovascular disorder.

XX Example 15; Page 83; 125pp; English.

XX The invention comprises antisense oligonucleotides that are capable of

CC inhibiting expression of the human clusterin gene. The antisense

CC oligonucleotides of the invention are useful for inhibiting the

CC expression of clusterin in cells. The antisense oligonucleotides are also

CC useful for treating an animal with a disease or condition associated with

CC clusterin (e.g. hypercholesterolaemia; cardiovascular disorders;

CC hyperproliferative disorders; and hyperlipidemic disorders). The present

CC DNA sequence represents a clusterin antisense oligonucleotide of the

CC invention. NOTE: The present DNA sequence has a phosphorothioate backbone

CC and also contains 2'-O-methoxyethyl wings

XX Sequence 20 BP; 4 A; 8 C; 5 G; 3 T; 0 U; 0 Other;

Query Match 1.2%; Score 20; DB 1; Length 20;

Best Local Similarity 100.0%; Pred. No. 45;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 77 GCTGCTGCTGACCTGGGAGA 96

DB 20 GCTGCTGCTGACCTGGGAGA 1

RESULT 122

ABN99683/C

ID ABN99683 standard; DNA; 20 BP.

XX AC ABN99683;

XX 16-AUG-2002 (first entry)

DT 16-AUG-2002 (first entry)

XX Human clusterin inhibiting antisense oligonucleotide 17.

DE Human; antisense inhibition; antisense oligonucleotide; clusterin;

XX hypercholesterolaemia; cardiovascular disorder; ss;

```
KW hyperproliferative disorder; hyperlipidemic disorder;
KW phosphorothioate backbone; 2'-O-methoxyethyl wing.
XX
XX Homo sapiens.
XX
XX WO200222635-A1.
XX
XX 21-MAR-2002.
XX
XX 10-SEP-2001; 2001WO-US028235.
XX
XX 11-SEP-2000; 2000US-00659791.
XX
XX (ISIS-) ISIS PHARM INC.
XX
XX Monia BP, Freier SM;
XX
XX WPI; 2002-404805/43.
XX
XX Novel antisense compound targeted to nucleic acid molecule encoding
XX clusterin, useful for treating animal having disease associated with
XX clusterin such as hyperlipidemic disorder, cardiovascular disorder.
XX
XX Claim 3; Page 83; 125pp; English.
XX
XX The invention comprises antisense oligonucleotides that are capable of
XX inhibiting expression of the human clusterin gene. The antisense
XX oligonucleotides of the invention are useful for inhibiting the
XX expression of clusterin in cells. The antisense oligonucleotides are also
XX useful for treating an animal with a disease or condition associated with
XX clusterin (e.g. hypercholesterolaemia; cardiovascular disorders;
XX hyperproliferative disorders; and hyperlipidemic disorders). The present
XX DNA sequence represents a clusterin antisense oligonucleotide of the
XX invention. NOTE: The present DNA sequence has a phosphorothioate backbone
XX and also contains 2'-O-methoxyethyl wings
XX
XX Sequence 20 BP; 4 A; 6 C; 5 G; 5 T; 0 U; 0 Other;
XX
XX Query Match 1.2%; Score 20; DB 1; Length 20;
XX Best Local Similarity 100.0%; Pred. No. 45;
XX Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 380 AGAGTGTAAGCCCTGCTGA 399
XX |||||||
XX 20 AGAGTGTAAGCCCTGCTGA 1
XX
XX RESULT 123
XX ABN9722/C
XX ID ABN99722 standard; DNA; 20 BP.
XX
XX AC ABN99722;
XX
XX 16-AUG-2002 (first entry)
XX
XX Human clusterin inhibiting antisense oligonucleotide 56.
XX
XX Human; antisense inhibition; antisense oligonucleotide; clusterin;
XX hypercholesterolaemia; cardiovascular disorder; ss;
XX hyperproliferative disorder; hyperlipidemic disorder;
XX phosphorothioate backbone; 2'-O-methoxyethyl wing.
XX
XX Homo sapiens.
XX
XX WO200222635-A1.
XX
XX 21-MAR-2002.
XX
XX 10-SEP-2001; 2001WO-US028235.
XX
XX 11-SEP-2000; 2000US-00659791.
XX
XX (ISIS-) ISIS PHARM INC.
XX
XX Monia BP, Freier SM;
XX
XX WPI; 2002-404805/43.
XX
XX Novel antisense compound targeted to nucleic acid molecule encoding
XX clusterin, useful for treating animal having disease associated with
XX clusterin such as hyperlipidemic disorder, cardiovascular disorder.
XX
XX Claim 3; Page 83; 125pp; English.
XX
XX The invention comprises antisense oligonucleotides that are capable of
XX inhibiting expression of the human clusterin gene. The antisense
XX oligonucleotides of the invention are useful for inhibiting the
XX expression of clusterin in cells. The antisense oligonucleotides are also
XX useful for treating an animal with a disease or condition associated with
XX clusterin (e.g. hypercholesterolaemia; cardiovascular disorders;
XX hyperproliferative disorders; and hyperlipidemic disorders). The present
XX DNA sequence represents a clusterin antisense oligonucleotide of the
XX invention. NOTE: The present DNA sequence has a phosphorothioate backbone
XX and also contains 2'-O-methoxyethyl wings
XX
XX Sequence 20 BP; 4 A; 6 C; 5 G; 5 T; 0 U; 0 Other;
XX
XX Query Match 1.2%; Score 20; DB 1; Length 20;
XX Best Local Similarity 100.0%; Pred. No. 45;
XX Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 380 AGAGTGTAAGCCCTGCTGA 399
XX |||||||
XX 20 AGAGTGTAAGCCCTGCTGA 1
XX
XX RESULT 124
XX ABN99667/C
XX ID ABN99667 standard; DNA; 20 BP.
XX
XX AC ABN99667;
XX
XX 16-AUG-2002 (first entry)
XX
XX Human clusterin inhibiting antisense oligonucleotide 1.
XX
XX Human; antisense inhibition; antisense oligonucleotide; clusterin;
XX hypercholesterolaemia; cardiovascular disorder; ss;
XX hyperproliferative disorder; hyperlipidemic disorder;
XX phosphorothioate backbone; 2'-O-methoxyethyl wing.
XX
XX Homo sapiens.
XX
XX WO200222635-A1.
XX
XX 21-MAR-2002.
XX
XX 10-SEP-2001; 2001WO-US028235.
XX
XX 11-SEP-2000; 2000US-00659791.
XX
XX (ISIS-) ISIS PHARM INC.
XX
XX Monia BP, Freier SM;
XX
XX WPI; 2002-404805/43.
XX
XX Novel antisense compound targeted to nucleic acid molecule encoding
XX clusterin, useful for treating animal having disease associated with
XX clusterin such as hyperlipidemic disorder, cardiovascular disorder.
XX
XX Example 15; Page 83; 125pp; English.
XX
XX The invention comprises antisense oligonucleotides that are capable of
XX inhibiting expression of the human clusterin gene. The antisense
XX oligonucleotides of the invention are useful for inhibiting the
```



CC expression of clusterin in cells. The antisense oligonucleotides are also  
 CC useful for treating an animal with a disease or condition associated with  
 CC clusterin (e.g. hypercholesterolaemia; cardiovascular disorders;  
 CC hyperproliferative disorders; and hyperlipidemic disorders). The present  
 CC DNA sequence represents a clusterin antisense oligonucleotide of the  
 CC invention. NOTE: The present DNA sequence has a phosphorothioate backbone  
 CC and also contains 2'-O-methoxyethyl wings  
 XX  
 SQ Sequence 20 BP; 2 A; 7 C; 5 G; 6 T; 0 U; 0 Other;

Query Match 1.2%; Score 20; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 45;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 TGACCGAGCGGTGCAAGAC 32  
 |||||  
 DB 20 TGACCGAGCGGTGCAAGAC 1

## RESULT 125

ABN99687/C  
 ID ABN99687 standard; DNA; 20 BP.

XX  
 AC ABN99687;

DT 16-AUG-2002 (first entry)

XX Human clusterin inhibiting antisense oligonucleotide 21.

XX Human; antisense inhibition; antisense oligonucleotide; clusterin;  
 KW hypercholesterolaemia; cardiovascular disorder; ss;  
 KW hyperproliferative disorder; hyperlipidemic disorder;  
 KW phosphorothioate backbone; 2'-O-methoxyethyl wing.

XX Homo sapiens.

XX WO200222635-A1.

XX 21-MAR-2002.

XX 10-SEP-2001; 2001WO-US028235.

XX 11-SEP-2000; 2000US-00659791.

XX (ISIS-) ISIS PHARM INC.

XX Monia BP, Freier SM;

XX WPI; 2002-404805/43.

XX Novel antisense compound targeted to nucleic acid molecule encoding  
 PT clusterin, useful for treating animal having disease associated with  
 PT clusterin such as hyperlipidemic disorder, cardiovascular disorder.

XX Claim 3; Page 83; 125pp; English.

XX The invention comprises antisense oligonucleotides that are capable of  
 CC inhibiting expression of the human clusterin gene. The antisense  
 CC oligonucleotides of the invention are useful for inhibiting the  
 CC expression of clusterin in cells. The antisense oligonucleotides are also  
 CC useful for treating an animal with a disease or condition associated with  
 CC clusterin (e.g. hypercholesterolaemia; cardiovascular disorders;  
 CC hyperproliferative disorders; and hyperlipidemic disorders). The present  
 CC DNA sequence represents a clusterin antisense oligonucleotide of the  
 CC invention. NOTE: The present DNA sequence has a phosphorothioate backbone  
 CC and also contains 2'-O-methoxyethyl wings

XX Sequence 20 BP; 4 A; 8 C; 5 G; 3 T; 0 U; 0 Other;

Query Match 1.2%; Score 20; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 45;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 455 TCGCCGCCACGCTTGAGGACT 474  
 |||||  
 DB 20 TCGCCGCCACGCTTGAGGACT 1

## RESULT 126

ABN99712/C

XX ID ABN99712 standard; DNA; 20 BP.

XX AC ABN99712;

XX 16-AUG-2002 (first entry)

XX Human clusterin inhibiting antisense oligonucleotide 46.

XX Human; antisense inhibition; antisense oligonucleotide; clusterin;  
 KW hypercholesterolaemia; cardiovascular disorder; ss;  
 KW hyperproliferative disorder; hyperlipidemic disorder;  
 KW phosphorothioate backbone; 2'-O-methoxyethyl wing.

XX Homo sapiens.

XX WO200222635-A1.

XX 21-MAR-2002.

XX 10-SEP-2001; 2001WO-US028235.

XX 11-SEP-2000; 2000US-00659791.

XX (ISIS-) ISIS PHARM INC.

XX Monia BP, Freier SM;

XX WPI; 2002-404805/43.

XX Novel antisense compound targeted to nucleic acid molecule encoding  
 PT clusterin, useful for treating animal having disease associated with  
 PT clusterin such as hyperlipidemic disorder, cardiovascular disorder.

XX Claim 3; Page 84; 125pp; English.

XX The invention comprises antisense oligonucleotides that are capable of  
 CC inhibiting expression of the human clusterin gene. The antisense  
 CC oligonucleotides of the invention are useful for inhibiting the  
 CC expression of clusterin in cells. The antisense oligonucleotides are also  
 CC useful for treating an animal with a disease or condition associated with  
 CC clusterin (e.g. hypercholesterolaemia; cardiovascular disorders;  
 CC hyperproliferative disorders; and hyperlipidemic disorders). The present  
 CC DNA sequence represents a clusterin antisense oligonucleotide of the  
 CC invention. NOTE: The present DNA sequence has a phosphorothioate backbone  
 CC and also contains 2'-O-methoxyethyl wings

XX Sequence 20 BP; 3 A; 8 C; 6 G; 3 T; 0 U; 0 Other;

Query Match 1.2%; Score 20; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 45;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1009 CTAAGCTGCGCGGAGCTC 1028  
 |||||  
 DB 20 CTAAGCTGCGCGGAGCTC 1

## RESULT 127

ABN99725/C

XX ID ABN99725 standard; DNA; 20 BP.

XX AC ABN99725;

XX 16-AUG-2002 (first entry)

XX Human clusterin inhibiting antisense oligonucleotide 59.

XX Human; antisense inhibition; antisense oligonucleotide; clusterin;  
KW hypercholesterolaemia; cardiovascular disorder; ss;  
KN hyperproliferative disorder; hyperlipidemic disorder;  
KW phosphorothioate backbone; 2'-O-methoxyethyl wing.  
XX Homo sapiens.  
OS  
XX WO200222635-A1.  
PN  
XX 21-MAR-2002.  
PD  
XX 10-SEP-2001; 2001WO-US028235.  
PF  
XX 11-SEP-2000; 2000US-00659791.  
PR  
XX (ISIS-) ISIS PHARM INC.  
PA  
XX Monia BP, Freier SM;  
PI  
XX WPI; 2002-404805/43.  
DR  
XX Novel antisense compound targeted to nucleic acid molecule encoding  
PT clusterin, useful for treating animal having disease associated with  
PT clusterin such as hyperlipidemic disorder, cardiovascular disorder.  
XX  
PS Claim 3; Page 84; 125pp; English.  
XX The invention comprises antisense oligonucleotides that are capable of  
CC inhibiting expression of the human clusterin gene. The antisense  
CC oligonucleotides of the invention are useful for inhibiting the  
CC expression of clusterin in cells. The antisense oligonucleotides are also  
CC useful for treating an animal with a disease or condition associated with  
CC clusterin (e.g. hypercholesterolaemia; cardiovascular disorders;  
CC hyperproliferative disorders; and hyperlipidemic disorders). The present  
CC DNA sequence represents a clusterin antisense oligonucleotide of the  
CC invention. NOTE: The present DNA sequence has a phosphorothioate backbone  
CC and also contains 2'-O-methoxyethyl wings  
XX  
SQ Sequence 20 BP; 9 A; 7 C; 2 G; 2 T; 0 U; 0 Other;  
PS  
XX Query Match 1.2%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 45;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
XX  
QY 1398 GATGTGGATGTTGCTTTTGC 1417  
Db 20 GATGTGGATGTTGCTTTTGC 1  
XX  
RESULT 128  
ABN99671/C  
ID ABN99671 standard; DNA; 20 BP.  
XX  
AC ABN99671;  
XX  
XX 16-AUG-2002 (first entry)  
DT  
XX Human clusterin inhibiting antisense oligonucleotide 5.  
DE  
XX Human; antisense inhibition; antisense oligonucleotide; clusterin;  
KW hypercholesterolaemia; cardiovascular disorder; ss;  
KW hyperproliferative disorder; hyperlipidemic disorder;  
KW phosphorothioate backbone; 2'-O-methoxyethyl wing.  
XX  
XX Homo sapiens.  
OS  
XX WO200222635-A1.  
PN  
XX 21-MAR-2002.  
PD  
XX 10-SEP-2001; 2001WO-US028235.  
PF  
XX

PR 11-SEP-2000; 2000US-00659791.  
XX (ISIS-) ISIS PHARM INC.  
PA  
XX Monia BP, Freier SM;  
PI  
XX WPI; 2002-404805/43.  
DR  
XX Novel antisense compound targeted to nucleic acid molecule encoding  
PT clusterin, useful for treating animal having disease associated with  
PT clusterin such as hyperlipidemic disorder, cardiovascular disorder.  
XX  
PS Claim 3; Page 83; 125pp; English.  
XX The invention comprises antisense oligonucleotides that are capable of  
CC inhibiting expression of the human clusterin gene. The antisense  
CC oligonucleotides of the invention are useful for inhibiting the  
CC expression of clusterin in cells. The antisense oligonucleotides are also  
CC useful for treating an animal with a disease or condition associated with  
CC clusterin (e.g. hypercholesterolaemia; cardiovascular disorders;  
CC hyperproliferative disorders; and hyperlipidemic disorders). The present  
CC DNA sequence represents a clusterin antisense oligonucleotide of the  
CC invention. NOTE: The present DNA sequence has a phosphorothioate backbone  
CC and also contains 2'-O-methoxyethyl wings  
XX  
SQ Sequence 20 BP; 2 A; 9 C; 5 G; 4 T; 0 U; 0 Other;  
PS  
XX Query Match 1.2%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 45;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
XX  
QY 101 GCAGGTCTCTGGGGACCAGA 120  
Db 20 GCAGGTCTCTGGGGACCAGA 1  
XX  
RESULT 129  
ABN99678/C  
ID ABN99678 standard; DNA; 20 BP.  
XX  
AC ABN99678;  
XX  
XX 16-AUG-2002 (first entry)  
DT  
XX Human clusterin inhibiting antisense oligonucleotide 12.  
DE  
XX Human; antisense inhibition; antisense oligonucleotide; clusterin;  
KW hypercholesterolaemia; cardiovascular disorder; ss;  
KW hyperproliferative disorder; hyperlipidemic disorder;  
KW phosphorothioate backbone; 2'-O-methoxyethyl wing.  
XX  
XX Homo sapiens.  
OS  
XX WO200222635-A1.  
PN  
XX 21-MAR-2002.  
PD  
XX 10-SEP-2001; 2001WO-US028235.  
PF  
XX 11-SEP-2000; 2000US-00659791.  
PR  
XX (ISIS-) ISIS PHARM INC.  
PA  
XX Monia BP, Freier SM;  
PI  
XX WPI; 2002-404805/43.  
DR  
XX Novel antisense compound targeted to nucleic acid molecule encoding  
PT clusterin, useful for treating animal having disease associated with  
PT clusterin such as hyperlipidemic disorder, cardiovascular disorder.  
XX  
PS Claim 3; Page 83; 125pp; English.  
XX

CC The invention comprises antisense oligonucleotides that are capable of  
 CC inhibiting expression of the human clusterin gene. The antisense  
 CC oligonucleotides of the invention are useful for inhibiting the  
 CC expression of clusterin in cells. The antisense oligonucleotides are also  
 CC useful for treating an animal with a disease or condition associated with  
 CC clusterin (e.g. hypercholesterolaemia; cardiovascular disorders;  
 CC hyperproliferative disorders; and hyperlipidemic disorders). The present  
 CC DNA sequence represents a clusterin antisense oligonucleotide of the  
 CC invention. NOTE: The present DNA sequence has a phosphorothioate backbone  
 CC and also contains 2'-O-methoxyethyl wings  
 XX  
 SQ Sequence 20 BP; 2 A; 5 C; 5 G; 8 T; 0 U; 0 Other;

Query Match 1.2%; Score 20; DB 1; Length 20;

Best Local Similarity 100.0%; Pred. No. 45;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 298 CCTTAATGAGACCGGAA 317  
 DB 20 CCTTAATGAGACCGGAA 1  
 |||||

RESULT 130

ABN99694/c

ID ABN99694 standard; DNA; 20 BP.

XX AC

XX ABN99694;

DT 16-AUG-2002 (first entry)

XX DE

XX Human clusterin inhibiting antisense oligonucleotide 28.

XX KW

XX Human; antisense inhibition; antisense oligonucleotide; clusterin;

XX KW hypercholesterolaemia; cardiovascular disorder; ss;

XX KW hyperproliferative disorder; hyperlipidemic disorder;

XX KW phosphorothioate backbone; 2'-O-methoxyethyl wing.

XX OS

XX Homo sapiens.

XX PN

XX WO200222635-A1.

XX PD

XX 21-MAR-2002.

XX PF

XX 10-SEP-2001; 2001WO-US028235.

XX PR

XX 11-SEP-2000; 2000US-00659791.

XX PA

XX (ISIS-) ISIS PHARM INC.

XX PI

XX Monia BP, Freier SM;

XX PI

XX WPI; 2002-404805/43.

XX DR

XX Novel antisense compound targeted to nucleic acid molecule encoding

XX PT clusterin, useful for treating animal having disease associated with

XX PT clusterin such as hyperlipidemic disorder, cardiovascular disorder.

XX PS

XX Claim 3; Page 83; 125pp; English.

XX XX

XX The invention comprises antisense oligonucleotides that are capable of

XX CC inhibiting expression of the human clusterin gene. The antisense

XX CC oligonucleotides of the invention are useful for inhibiting the

XX CC expression of clusterin in cells. The antisense oligonucleotides are also

XX CC useful for treating an animal with a disease or condition associated with

XX CC clusterin (e.g. hypercholesterolaemia; cardiovascular disorders;

XX CC hyperproliferative disorders; and hyperlipidemic disorders). The present

XX CC DNA sequence represents a clusterin antisense oligonucleotide of the

XX CC invention. NOTE: The present DNA sequence has a phosphorothioate backbone

XX CC and also contains 2'-O-methoxyethyl wings

XX XX

SQ Sequence 20 BP; 4 A; 6 C; 5 G; 5 T; 0 U; 0 Other;

Query Match

1.2%; Score 20; DB 1; Length 20;

Best Local Similarity 100.0%; Pred. No. 45;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 565 TGGATGTCATGCAGGACCAC 584

DB 20 TGGATGTCATGCAGGACCAC 1  
 |||||

RESULT 131

ABN99700/c

ID ABN99700 standard; DNA; 20 BP.

XX AC

XX ABN99700;

DT 16-AUG-2002 (first entry)

XX DE

XX Human clusterin inhibiting antisense oligonucleotide 34.

XX KW

XX Human; antisense inhibition; antisense oligonucleotide; clusterin;

XX KW hypercholesterolaemia; cardiovascular disorder; ss;

XX KW hyperproliferative disorder; hyperlipidemic disorder;

XX KW phosphorothioate backbone; 2'-O-methoxyethyl wing.

XX OS

XX Homo sapiens.

XX PN

XX WO200222635-A1.

XX PD

XX 21-MAR-2002.

XX PF

XX 10-SEP-2001; 2001WO-US028235.

XX PR

XX 11-SEP-2000; 2000US-00659791.

XX PA

XX (ISIS-) ISIS PHARM INC.

XX PI

XX Monia BP, Freier SM;

XX PI

XX WPI; 2002-404805/43.

XX DR

XX Novel antisense compound targeted to nucleic acid molecule encoding

XX PT clusterin, useful for treating animal having disease associated with

XX PT clusterin such as hyperlipidemic disorder, cardiovascular disorder.

XX PS

XX Claim 3; Page 83; 125pp; English.

XX XX

XX The invention comprises antisense oligonucleotides that are capable of

XX CC inhibiting expression of the human clusterin gene. The antisense

XX CC oligonucleotides of the invention are useful for inhibiting the

XX CC expression of clusterin in cells. The antisense oligonucleotides are also

XX CC useful for treating an animal with a disease or condition associated with

XX CC clusterin (e.g. hypercholesterolaemia; cardiovascular disorders;

XX CC hyperproliferative disorders; and hyperlipidemic disorders). The present

XX CC DNA sequence represents a clusterin antisense oligonucleotide of the

XX CC invention. NOTE: The present DNA sequence has a phosphorothioate backbone

XX CC and also contains 2'-O-methoxyethyl wings

XX XX

SQ Sequence 20 BP; 5 A; 5 C; 8 G; 2 T; 0 U; 0 Other;

Query Match

1.2%; Score 20; DB 1; Length 20;

Best Local Similarity 100.0%; Pred. No. 45;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 721 TCGTCCGAGCTTGATGCC 740

DB 20 TCGTCCGAGCTTGATGCC 1  
 |||||

RESULT 132

ABN99721/c

ID ABN99721 standard; DNA; 20 BP.

XX AC

XX ABN99721;

XX XX

```
DT 16-AUG-2002 (first entry)
XX Human clusterin inhibiting antisense oligonucleotide 55.
DE
XX
XX Human; antisense inhibition; antisense oligonucleotide; clusterin;
KW hypercholesterolaemia; cardiovascular disorder; ss;
KW hyperproliferative disorder; hyperlipidemic disorder;
KW phosphorothioate backbone; 2'-O-methoxyethyl wing.
XX
XX Homo sapiens.
OS
XX WO200222635-A1.
XX
XX 21-MAR-2002.
PD
XX
XX 10-SEP-2001; 2001WO-US028235.
XX
XX 11-SEP-2000; 2000US-00659791.
XX
XX (ISIS-) ISIS PHARM INC.
XX
XX Monia BP, Freier SM;
XX
XX WPI; 2002-404805/43.
XX
XX Novel antisense compound targeted to nucleic acid molecule encoding
PT clusterin, useful for treating animal having disease associated with
PT clusterin such as hyperlipidemic disorder, cardiovascular disorder.
XX
XX Claim 3; Page 84; 125pp; English.
XX
XX The invention comprises antisense oligonucleotides that are capable of
XX inhibiting expression of the human clusterin gene. The antisense
XX oligonucleotides of the invention are useful for inhibiting the
XX expression of clusterin in cells. The antisense oligonucleotides are also
XX useful for treating an animal with a disease or condition associated with
XX clusterin (e.g. hypercholesterolaemia; cardiovascular disorders;
XX hyperproliferative disorders; and hyperlipidemic disorders). The present
XX DNA sequence represents a clusterin antisense oligonucleotide of the
XX invention. NOTE: The present DNA sequence has a phosphorothioate backbone
XX and also contains 2'-O-methoxyethyl wings
XX
XX Sequence 20 BP; 6 A; 2 C; 9 G; 3 T; 0 U; 0 Other;
XX
XX Query Match 1.2%; Score 20; DB 1; Length 20;
XX Best Local Similarity 100.0%; Pred. No. 45;
XX Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1216 CTTCCACACTTCTGACTCG 1235
XX
XX Db 20 CTTCCACACTTCTGACTCG 1
XX
XX RESULT 133
XX ABN99669/C
XX ID ABN99669 standard; DNA; 20 BP.
XX
XX AC ABN99669;
XX
XX 16-AUG-2002 (first entry)
XX
XX Human clusterin inhibiting antisense oligonucleotide 3.
XX
XX Human; antisense inhibition; antisense oligonucleotide; clusterin;
KW hypercholesterolaemia; cardiovascular disorder; ss;
KW hyperproliferative disorder; hyperlipidemic disorder;
KW phosphorothioate backbone; 2'-O-methoxyethyl wing.
XX
XX Homo sapiens.
OS
XX WO200222635-A1.
XX
XX 21-MAR-2002.
PD
```

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XX 10-SEP-2001; 2001WO-US028235.
XX
XX 11-SEP-2000; 2000US-00659791.
XX
XX (ISIS-) ISIS PHARM INC.
XX
XX Monia BP, Freier SM;
XX
XX WPI; 2002-404805/43.
XX
XX Novel antisense compound targeted to nucleic acid molecule encoding
PT clusterin, useful for treating animal having disease associated with
PT clusterin such as hyperlipidemic disorder, cardiovascular disorder.
XX
XX Example 15; Page 83; 125pp; English.
XX
XX The invention comprises antisense oligonucleotides that are capable of
XX inhibiting expression of the human clusterin gene. The antisense
XX oligonucleotides of the invention are useful for inhibiting the
XX expression of clusterin in cells. The antisense oligonucleotides are also
XX useful for treating an animal with a disease or condition associated with
XX clusterin (e.g. hypercholesterolaemia; cardiovascular disorders;
XX hyperproliferative disorders; and hyperlipidemic disorders). The present
XX DNA sequence represents a clusterin antisense oligonucleotide of the
XX invention. NOTE: The present DNA sequence has a phosphorothioate backbone
XX and also contains 2'-O-methoxyethyl wings
XX
XX Sequence 20 BP; 4 A; 7 C; 2 G; 7 T; 0 U; 0 Other;
XX
XX Query Match 1.2%; Score 20; DB 1; Length 20;
XX Best Local Similarity 100.0%; Pred. No. 45;
XX Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 39 ATTGGAGGCGCATGATGAAGAC 58
XX
XX Db 20 ATTGGAGGCGCATGATGAAGAC 1
XX
XX RESULT 134
XX ABN99685/C
XX ID ABN99685 standard; DNA; 20 BP.
XX
XX AC ABN99685;
XX
XX 16-AUG-2002 (first entry)
XX
XX Human clusterin inhibiting antisense oligonucleotide 19.
XX
XX Human; antisense inhibition; antisense oligonucleotide; clusterin;
KW hypercholesterolaemia; cardiovascular disorder; ss;
KW hyperproliferative disorder; hyperlipidemic disorder;
KW phosphorothioate backbone; 2'-O-methoxyethyl wing.
XX
XX Homo sapiens.
OS
XX WO200222635-A1.
XX
XX 21-MAR-2002.
PD
XX
XX 10-SEP-2001; 2001WO-US028235.
XX
XX 11-SEP-2000; 2000US-00659791.
XX
XX (ISIS-) ISIS PHARM INC.
XX
XX Monia BP, Freier SM;
XX
XX WPI; 2002-404805/43.
XX
XX Novel antisense compound targeted to nucleic acid molecule encoding
PT clusterin, useful for treating animal having disease associated with
PT clusterin such as hyperlipidemic disorder, cardiovascular disorder.
XX
```

XX PS Claim 3; Page 83; 125pp; English.  
XX CC The invention comprises antisense oligonucleotides that are capable of  
XX CC inhibiting expression of the human clusterin gene. The antisense  
XX CC oligonucleotides of the invention are useful for inhibiting the  
XX CC expression of clusterin in cells. The antisense oligonucleotides are also  
XX CC useful for treating an animal with a disease or condition associated with  
XX CC clusterin (e.g. hypercholesterolaemia; cardiovascular disorders;  
XX CC hyperproliferative disorders; and hyperlipidemic disorders). The present  
XX CC DNA sequence represents a clusterin antisense oligonucleotide of the  
XX CC invention. NOTE: The present DNA sequence has a phosphorothioate backbone  
XX CC and also contains 2'-O-methoxyethyl wings  
XX SQ Sequence 20 BP; 4 A; 7 C; 8 G; 1 T; 0 U; 0 Other;  
  
Query Match 1.2%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 45;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 443 CTCAGGCTGGTTGGCGGCC 462  
DB 20 CTCAGGCTGGTTGGCGGCC 1  
  
RESULT 135  
ABN99689/c  
ID ABN99689 standard; DNA; 20 BP.  
XX AC ABN99689;  
XX DT 16-AUG-2002 (first entry)  
XX DE Human clusterin inhibiting antisense oligonucleotide 23.  
XX KW Human; antisense inhibition; antisense oligonucleotide; clusterin;  
XX KW hypercholesterolaemia; cardiovascular disorder; ss;  
XX KW hyperproliferative disorder; hyperlipidemic disorder;  
XX KW phosphorothioate backbone; 2'-O-methoxyethyl wing.  
XX OS Homo sapiens.  
XX PN WO200222635-A1.  
XX PD 21-MAR-2002.  
XX PF 10-SEP-2001; 2001WO-US028235.  
XX PR 11-SEP-2000; 2000US-00659791.  
XX PA (ISIS-) ISIS PHARM INC.  
XX PI Monia BP, Freier SM;  
XX DR WPI; 2002-404805/43.  
XX PT Novel antisense compound targeted to nucleic acid molecule encoding  
XX PT clusterin, useful for treating animal having disease associated with  
XX PT clusterin such as hyperlipidemic disorder, cardiovascular disorder.  
XX PS Claim 3; Page 83; 125pp; English.  
XX CC The invention comprises antisense oligonucleotides that are capable of  
XX CC inhibiting expression of the human clusterin gene. The antisense  
XX CC oligonucleotides of the invention are useful for inhibiting the  
XX CC expression of clusterin in cells. The antisense oligonucleotides are also  
XX CC useful for treating an animal with a disease or condition associated with  
XX CC clusterin (e.g. hypercholesterolaemia; cardiovascular disorders;  
XX CC hyperproliferative disorders; and hyperlipidemic disorders). The present  
XX CC DNA sequence represents a clusterin antisense oligonucleotide of the  
XX CC invention. NOTE: The present DNA sequence has a phosphorothioate backbone  
XX CC and also contains 2'-O-methoxyethyl wings  
XX SQ Sequence 20 BP; 4 A; 7 C; 8 G; 1 T; 0 U; 0 Other;  
  
Query Match 1.2%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 45;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 443 CTCAGGCTGGTTGGCGGCC 462  
DB 20 CTCAGGCTGGTTGGCGGCC 1  
  
RESULT 135  
ABN99689/c  
ID ABN99689 standard; DNA; 20 BP.  
XX AC ABN99689;  
XX DT 16-AUG-2002 (first entry)  
XX DE Human clusterin inhibiting antisense oligonucleotide 23.  
XX KW Human; antisense inhibition; antisense oligonucleotide; clusterin;  
XX KW hypercholesterolaemia; cardiovascular disorder; ss;  
XX KW hyperproliferative disorder; hyperlipidemic disorder;  
XX KW phosphorothioate backbone; 2'-O-methoxyethyl wing.  
XX OS Homo sapiens.  
XX PN WO200222635-A1.  
XX PD 21-MAR-2002.  
XX PF 10-SEP-2001; 2001WO-US028235.  
XX PR 11-SEP-2000; 2000US-00659791.  
XX PA (ISIS-) ISIS PHARM INC.  
XX PI Monia BP, Freier SM;  
XX DR WPI; 2002-404805/43.  
XX PT Novel antisense compound targeted to nucleic acid molecule encoding  
XX PT clusterin, useful for treating animal having disease associated with  
XX PT clusterin such as hyperlipidemic disorder, cardiovascular disorder.  
XX PS Claim 3; Page 83; 125pp; English.  
XX CC The invention comprises antisense oligonucleotides that are capable of  
XX CC inhibiting expression of the human clusterin gene. The antisense  
XX CC oligonucleotides of the invention are useful for inhibiting the  
XX CC expression of clusterin in cells. The antisense oligonucleotides are also  
XX CC useful for treating an animal with a disease or condition associated with  
XX CC clusterin (e.g. hypercholesterolaemia; cardiovascular disorders;  
XX CC hyperproliferative disorders; and hyperlipidemic disorders). The present  
XX CC DNA sequence represents a clusterin antisense oligonucleotide of the  
XX CC invention. NOTE: The present DNA sequence has a phosphorothioate backbone  
XX CC and also contains 2'-O-methoxyethyl wings  
XX SQ Sequence 20 BP; 4 A; 7 C; 8 G; 1 T; 0 U; 0 Other;

SQ Sequence 20 BP; 7 A; 3 C; 6 G; 4 T; 0 U; 0 Other;  
  
Query Match 1.2%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 45;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 492 CCCTTCTACTTCTGGATGAA 511  
DB 20 CCCTTCTACTTCTGGATGAA 1  
  
RESULT 136  
ABN99703/c  
ID ABN99703 standard; DNA; 20 BP.  
XX AC ABN99703;  
XX DT 16-AUG-2002 (first entry)  
XX DE Human clusterin inhibiting antisense oligonucleotide 37.  
XX KW Human; antisense inhibition; antisense oligonucleotide; clusterin;  
XX KW hypercholesterolaemia; cardiovascular disorder; ss;  
XX KW hyperproliferative disorder; hyperlipidemic disorder;  
XX KW phosphorothioate backbone; 2'-O-methoxyethyl wing.  
XX OS Homo sapiens.  
XX PN WO200222635-A1.  
XX PD 21-MAR-2002.  
XX PF 10-SEP-2001; 2001WO-US028235.  
XX PR 11-SEP-2000; 2000US-00659791.  
XX PA (ISIS-) ISIS PHARM INC.  
XX PI Monia BP, Freier SM;  
XX DR WPI; 2002-404805/43.  
XX PT Novel antisense compound targeted to nucleic acid molecule encoding  
XX PT clusterin, useful for treating animal having disease associated with  
XX PT clusterin such as hyperlipidemic disorder, cardiovascular disorder.  
XX PS Claim 3; Page 83; 125pp; English.  
XX CC The invention comprises antisense oligonucleotides that are capable of  
XX CC inhibiting expression of the human clusterin gene. The antisense  
XX CC oligonucleotides of the invention are useful for inhibiting the  
XX CC expression of clusterin in cells. The antisense oligonucleotides are also  
XX CC useful for treating an animal with a disease or condition associated with  
XX CC clusterin (e.g. hypercholesterolaemia; cardiovascular disorders;  
XX CC hyperproliferative disorders; and hyperlipidemic disorders). The present  
XX CC DNA sequence represents a clusterin antisense oligonucleotide of the  
XX CC invention. NOTE: The present DNA sequence has a phosphorothioate backbone  
XX CC and also contains 2'-O-methoxyethyl wings  
XX SQ Sequence 20 BP; 6 A; 3 C; 6 G; 5 T; 0 U; 0 Other;  
  
Query Match 1.2%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 45;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 783 CCCTTCTCTTGAGATGATACA 802  
DB 20 CCCTTCTCTTGAGATGATACA 1  
  
RESULT 137  
ABN99720/c  
ID ABN99720 standard; DNA; 20 BP.

```
XX AC ABN99720;
XX DT 16-AUG-2002 (first entry)
XX DE Human clusterin inhibiting antisense oligonucleotide 54.
XX DE
XX KW Human; antisense inhibition; antisense oligonucleotide; clusterin;
XX KW hypercholesterolaemia; cardiovascular disorder; ss;
XX KW hyperproliferative disorder; hyperlipidemic disorder;
XX KW phosphorothioate backbone; 2'-O-methoxyethyl wing.
XX OS Homo sapiens.
XX PN WO200222635-A1.
XX PD 21-MAR-2002.
XX PF 10-SEP-2001; 2001WO-US028235.
XX PR 11-SEP-2000; 2000US-00659791.
XX PA (ISIS-) ISIS PHARM INC.
XX PI Monia BP, Freier SM;
XX XX WPI; 2002-404805/43.
XX PT Novel antisense compound targeted to nucleic acid molecule encoding
XX PT clusterin, useful for treating animal having disease associated with
XX PT clusterin such as hyperlipidemic disorder, cardiovascular disorder.
XX PS Claim 3; Page 84; 125pp; English.
XX CC The invention comprises antisense oligonucleotides that are capable of
XX CC inhibiting expression of the human clusterin gene. The antisense
XX CC oligonucleotides of the invention are useful for inhibiting the
XX CC expression of clusterin in cells. The antisense oligonucleotides are also
XX CC useful for treating an animal with a disease or condition associated with
XX CC clusterin (e.g. hypercholesterolaemia; cardiovascular disorders;
XX CC hyperproliferative disorders; and hyperlipidemic disorders). The present
XX CC DNA sequence represents a clusterin antisense oligonucleotide of the
XX CC invention. NOTE: The present DNA sequence has a phosphorothioate backbone
XX CC and also contains 2'-O-methoxyethyl wings
XX SQ Sequence 20 BP; 5 A; 6 C; 6 G; 3 T; 0 U; 0 Other;

Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 45;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1194 TATCTGCGGTACACACGGT 1213
Db 20 TATCTGCGGTACACACGGT 1

RESULT 138
ABN99691/C
ID ABN99691 standard; DNA; 20 BP.
XX AC ABN99691;
XX DT 16-AUG-2002 (first entry)
XX DE Human clusterin inhibiting antisense oligonucleotide 25.
XX DE
XX KW Human; antisense inhibition; antisense oligonucleotide; clusterin;
XX KW hypercholesterolaemia; cardiovascular disorder; ss;
XX KW hyperproliferative disorder; hyperlipidemic disorder;
XX KW phosphorothioate backbone; 2'-O-methoxyethyl wing.
XX OS Homo sapiens.
XX XX
```

```
PN WO200222635-A1.
XX PD 21-MAR-2002.
XX PF 10-SEP-2001; 2001WO-US028235.
XX PR 11-SEP-2000; 2000US-00659791.
XX PA (ISIS-) ISIS PHARM INC.
XX PI Monia BP, Freier SM;
XX XX WPI; 2002-404805/43.
XX PT Novel antisense compound targeted to nucleic acid molecule encoding
XX PT clusterin, useful for treating animal having disease associated with
XX PT clusterin such as hyperlipidemic disorder, cardiovascular disorder.
XX PS Claim 3; Page 83; 125pp; English.
XX CC The invention comprises antisense oligonucleotides that are capable of
XX CC inhibiting expression of the human clusterin gene. The antisense
XX CC oligonucleotides of the invention are useful for inhibiting the
XX CC expression of clusterin in cells. The antisense oligonucleotides are also
XX CC useful for treating an animal with a disease or condition associated with
XX CC clusterin (e.g. hypercholesterolaemia; cardiovascular disorders;
XX CC hyperproliferative disorders; and hyperlipidemic disorders). The present
XX CC DNA sequence represents a clusterin antisense oligonucleotide of the
XX CC invention. NOTE: The present DNA sequence has a phosphorothioate backbone
XX CC and also contains 2'-O-methoxyethyl wings
XX SQ Sequence 20 BP; 1 A; 8 C; 6 G; 5 T; 0 U; 0 Other;

Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 45;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 533 GCTGAGAACGACCGGCAGC 552
Db 20 GCTGAGAACGACCGGCAGC 1

RESULT 139
ABN99713/C
ID ABN99713 standard; DNA; 20 BP.
XX AC ABN99713;
XX DT 16-AUG-2002 (first entry)
XX DE Human clusterin inhibiting antisense oligonucleotide 47.
XX DE
XX KW Human; antisense inhibition; antisense oligonucleotide; clusterin;
XX KW hypercholesterolaemia; cardiovascular disorder; ss;
XX KW hyperproliferative disorder; hyperlipidemic disorder;
XX KW phosphorothioate backbone; 2'-O-methoxyethyl wing.
XX OS Homo sapiens.
XX XX WO200222635-A1.
XX XX PD 21-MAR-2002.
XX PF 10-SEP-2001; 2001WO-US028235.
XX PR 11-SEP-2000; 2000US-00659791.
XX PA (ISIS-) ISIS PHARM INC.
XX PI Monia BP, Freier SM;
XX XX WPI; 2002-404805/43.
XX XX
```

PT Novel antisense compound targeted to nucleic acid molecule encoding  
 PT clusterin, useful for treating animal having disease associated with  
 PT clusterin such as hyperlipidemic disorder, cardiovascular disorder.  
 XX  
 XX  
 PS Claim 3; Page 84; 125pp; English.

XX The invention comprises antisense oligonucleotides that are capable of  
 CC inhibiting expression of the human clusterin gene. The antisense  
 CC oligonucleotides of the invention are useful for inhibiting the  
 CC expression of clusterin in cells. The antisense oligonucleotides are also  
 CC useful for treating an animal with a disease or condition associated with  
 CC clusterin (e.g. hypercholesterolaemia; cardiovascular disorders;  
 CC hyperproliferative disorders; and hyperlipidemic disorders). The present  
 CC DNA sequence represents a clusterin antisense oligonucleotide of the  
 CC invention. NOTE: The present DNA sequence has a phosphorothioate backbone  
 CC and also contains 2'-O-methoxyethyl wings

XX Sequence 20 BP; 3 A; 5 C; 8 G; 4 T; 0 U; 0 Other;

Query Match 1.2%; Score 20; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 45;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1022 GGAGCTCGAGCAATCCCTCC 1041

Db 20 GGAGCTCGAGCAATCCCTCC 1

RESULT 140

ABN99724/C

ID ABN99724 standard; DNA; 20 BP.

XX

AC ABN99724;

XX

DT 16-AUG-2002 (first entry)

XX

DE Human clusterin inhibiting antisense oligonucleotide 58.

XX

KW Human; antisense inhibition; antisense oligonucleotide; clusterin;

KW hypercholesterolaemia; cardiovascular disorder; ss;

KW hyperproliferative disorder; hyperlipidemic disorder;

KW phosphorothioate backbone; 2'-O-methoxyethyl wing.

XX

OS Homo sapiens.

XX

PN WO200222635-A1.

XX

XX PD 21-MAR-2002.

XX

PF 10-SEP-2001; 2001WO-US028235.

XX

XX PR 11-SEP-2000; 2000US-00659791.

XX

PA (ISIS-) ISIS PHARM INC.

XX

PI Monia BP, Freier SM;

XX

XX WPI; 2002-404805/43.

XX

XX Novel antisense compound targeted to nucleic acid molecule encoding  
 PT clusterin, useful for treating animal having disease associated with  
 PT clusterin such as hyperlipidemic disorder, cardiovascular disorder.

XX Claim 3; Page 84; 125pp; English.

XX

XX The invention comprises antisense oligonucleotides that are capable of  
 CC inhibiting expression of the human clusterin gene. The antisense  
 CC oligonucleotides of the invention are useful for inhibiting the  
 CC expression of clusterin in cells. The antisense oligonucleotides are also  
 CC useful for treating an animal with a disease or condition associated with  
 CC clusterin (e.g. hypercholesterolaemia; cardiovascular disorders;  
 CC hyperproliferative disorders; and hyperlipidemic disorders). The present  
 CC DNA sequence represents a clusterin antisense oligonucleotide of the

CC invention. NOTE: The present DNA sequence has a phosphorothioate backbone  
 CC and also contains 2'-O-methoxyethyl wings

XX

SQ Sequence 20 BP; 5 A; 6 C; 3 G; 6 T; 0 U; 0 Other;

Query Match 1.2%; Score 20; DB 1; Length 20;

Best Local Similarity 100.0%; Pred. No. 45;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1332 AAATTTATGGAGACCGTGGC 1351

Db 20 AAATTTATGGAGACCGTGGC 1

RESULT 141

ABN99690/C

ID ABN99690 standard; DNA; 20 BP.

XX

AC ABN99690;

XX

DT 16-AUG-2002 (first entry)

XX

DE Human clusterin inhibiting antisense oligonucleotide 24.

XX

KW Human; antisense inhibition; antisense oligonucleotide; clusterin;

KW hypercholesterolaemia; cardiovascular disorder; ss;

KW hyperproliferative disorder; hyperlipidemic disorder;

KW phosphorothioate backbone; 2'-O-methoxyethyl wing.

XX

OS Homo sapiens.

XX

PN WO200222635-A1.

XX

PD 21-MAR-2002.

XX

PF 10-SEP-2001; 2001WO-US028235.

XX

PR 11-SEP-2000; 2000US-00659791.

XX

PA (ISIS-) ISIS PHARM INC.

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PI Monia BP, Freier SM;

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XX WPI; 2002-404805/43.

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XX Novel antisense compound targeted to nucleic acid molecule encoding  
 PT clusterin, useful for treating animal having disease associated with  
 PT clusterin such as hyperlipidemic disorder, cardiovascular disorder.

XX Claim 3; Page 83; 125pp; English.

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 CC expression of clusterin in cells. The antisense oligonucleotides are also  
 CC useful for treating an animal with a disease or condition associated with  
 CC clusterin (e.g. hypercholesterolaemia; cardiovascular disorders;  
 CC hyperproliferative disorders; and hyperlipidemic disorders). The present  
 CC DNA sequence represents a clusterin antisense oligonucleotide of the  
 CC invention. NOTE: The present DNA sequence has a phosphorothioate backbone  
 CC and also contains 2'-O-methoxyethyl wings

XX Sequence 20 BP; 4 A; 4 C; 9 G; 3 T; 0 U; 0 Other;

Query Match 1.2%; Score 20; DB 1; Length 20;

Best Local Similarity 100.0%; Pred. No. 45;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 517 ACCGATCGACTCCCTGCTG 536

Db 20 ACCGATCGACTCCCTGCTG 1

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Tue Sep 13 10:53:20 2005

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XX OS Homo sapiens.
XX PN WO200222635-A1.
XX PD 21-MAR-2002.
XX XX
XX XX 10-SEP-2001; 2001WO-US028235.
XX XX 11-SEP-2000; 2000US-00659791.
XX PR (ISIS-) ISIS PHARM INC.
XX PA Monia BP, Freier SM;
XX PI WPI; 2002-404805/43.
XX DR
XX OS Novel antisense compound targeted to nucleic acid molecule encoding
XX PN clusterin, useful for treating animal having disease associated with
XX PD clusterin such as hyperlipidemic disorder, cardiovascular disorder.
XX XX
XX PS Claim 3; Page 84; 125pp; English.
XX CC The invention comprises antisense oligonucleotides that are capable of
XX CC inhibiting expression of the human clusterin gene. The antisense
XX CC oligonucleotides of the invention are useful for inhibiting the
XX CC expression of clusterin in cells. The antisense oligonucleotides are also
XX CC useful for treating an animal with a disease or condition associated with
XX CC clusterin (e.g. hypercholesterolaemia; cardiovascular disorders;
XX CC hyperproliferative disorders; and hyperlipidemic disorders). The present
XX CC DNA sequence represents a clusterin antisense oligonucleotide of the
XX CC invention. NOTE: The present DNA sequence has a phosphorothioate backbone
XX CC and also contains 2'-O-methoxyethyl wings
XX SQ Sequence 20 BP; 2 A; 8 C; 5 G; 5 T; 0 U; 0 Other;

Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 45;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1121 GCTGAGCAGCTGAACGAGC 1140
Db 20 GCTGAGCAGCTGAACGAGC 1

RESULT 144
ABN99672/C
ID ABN99672 standard; DNA; 20 BP.
XX AC ABN99672;
XX DT 16-AUG-2002 (first entry)
XX DE Human clusterin inhibiting antisense oligonucleotide 6.
XX XX
XX KW Human; antisense inhibition; antisense oligonucleotide; clusterin;
XX KW hypercholesterolaemia; cardiovascular disorder; ss;
XX KW hyperproliferative disorder; hyperlipidemic disorder;
XX KW phosphorothioate backbone; 2'-O-methoxyethyl wing.
XX OS
XX OS Homo sapiens.
XX PN WO200222635-A1.
XX PD 21-MAR-2002.
XX XX
XX XX 10-SEP-2001; 2001WO-US028235.
XX PF 11-SEP-2000; 2000US-00659791.
XX PR (ISIS-) ISIS PHARM INC.
XX PA Monia BP, Freier SM;
XX PI WPI; 2002-404805/43.
XX DR
XX OS Novel antisense compound targeted to nucleic acid molecule encoding
XX PN clusterin, useful for treating animal having disease associated with
XX PD clusterin such as hyperlipidemic disorder, cardiovascular disorder.
XX XX
XX PS Claim 3; Page 83; 125pp; English.
XX CC The invention comprises antisense oligonucleotides that are capable of
XX CC inhibiting expression of the human clusterin gene. The antisense
XX CC oligonucleotides of the invention are useful for inhibiting the
XX CC expression of clusterin in cells. The antisense oligonucleotides are also
XX CC useful for treating an animal with a disease or condition associated with
XX CC clusterin (e.g. hypercholesterolaemia; cardiovascular disorders;
XX CC hyperproliferative disorders; and hyperlipidemic disorders). The present
XX CC DNA sequence represents a clusterin antisense oligonucleotide of the
XX CC invention. NOTE: The present DNA sequence has a phosphorothioate backbone
XX CC and also contains 2'-O-methoxyethyl wings
XX SQ Sequence 20 BP; 4 A; 8 C; 5 G; 3 T; 0 U; 0 Other;

Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 45;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 894 ACTGTGTGCGGAGATCCG 913
Db 20 ACTGTGTGCGGAGATCCG 1

RESULT 143
ABN99717/C
ID ABN99717 standard; DNA; 20 BP.
XX AC ABN99717;
XX DT 16-AUG-2002 (first entry)
XX DE Human clusterin inhibiting antisense oligonucleotide 51.
XX XX
XX KW Human; antisense inhibition; antisense oligonucleotide; clusterin;
XX KW hypercholesterolaemia; cardiovascular disorder; ss;
XX KW hyperproliferative disorder; hyperlipidemic disorder;
XX KW phosphorothioate backbone; 2'-O-methoxyethyl wing.

```



XX DR WPI; 2002-404805/43.  
 XX PT Novel antisense compound targeted to nucleic acid molecule encoding  
 PT clusterin, useful for treating animal having disease associated with  
 PT clusterin such as hyperlipidemic disorder, cardiovascular disorder.  
 XX PS Claim 3; Page 83; 125pp; English.  
 XX CC The invention comprises antisense oligonucleotides that are capable of  
 CC inhibiting expression of the human clusterin gene. The antisense  
 CC oligonucleotides of the invention are useful for inhibiting the  
 CC expression of clusterin in cells. The antisense oligonucleotides are also  
 CC useful for treating an animal with a disease or condition associated with  
 CC clusterin (e.g. hypercholesterolaemia; cardiovascular disorders;  
 CC hyperproliferative disorders; and hyperlipidemic disorders). The present  
 CC DNA sequence represents a clusterin antisense oligonucleotide of the  
 CC invention. NOTE: The present DNA sequence has a phosphorothioate backbone  
 CC and also contains 2'-O-methoxyethyl wings  
 XX SQ Sequence 20 BP; 4 A; 5 C; 6 G; 5 T; 0 U; 0 Other;  
 Query Match 1.2%; Score 20; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 45;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 122 GGTCTCAGACATGAGCTCC 141  
 Db 20 GGTCTCAGACATGAGCTCC 1  
 RESULT 145  
 ABN99693/C  
 ID ABN99693 standard; DNA; 20 BP.  
 XX AC ABN99693;  
 XX DT 16-AUG-2002 (first entry)  
 XX DE Human clusterin inhibiting antisense oligonucleotide 27.  
 XX KW Human; antisense inhibition; antisense oligonucleotide; clusterin;  
 KW hypercholesterolaemia; cardiovascular disorder; ss;  
 KW hyperproliferative disorder; hyperlipidemic disorder;  
 KW phosphorothioate backbone; 2'-O-methoxyethyl wing.  
 XX OS Homo sapiens.  
 XX PN WO200222635-A1.  
 XX PD 21-MAR-2002.  
 XX PF 10-SEP-2001; 2001WO-US028235.  
 XX PR 11-SEP-2000; 2000US-00659791.  
 XX PA (ISIS-) ISIS PHARM INC.  
 XX PI Monia BP, Freier SM;  
 XX PS WPI; 2002-404805/43.  
 XX PT Novel antisense compound targeted to nucleic acid molecule encoding  
 PT clusterin, useful for treating animal having disease associated with  
 PT clusterin such as hyperlipidemic disorder, cardiovascular disorder.  
 XX PS Claim 3; Page 83; 125pp; English.  
 XX CC The invention comprises antisense oligonucleotides that are capable of  
 CC inhibiting expression of the human clusterin gene. The antisense  
 CC oligonucleotides of the invention are useful for inhibiting the  
 CC expression of clusterin in cells. The antisense oligonucleotides are also  
 CC useful for treating an animal with a disease or condition associated with

CC clusterin (e.g. hypercholesterolaemia; cardiovascular disorders;  
 CC hyperproliferative disorders; and hyperlipidemic disorders). The present  
 CC DNA sequence represents a clusterin antisense oligonucleotide of the  
 CC invention. NOTE: The present DNA sequence has a phosphorothioate backbone  
 CC and also contains 2'-O-methoxyethyl wings  
 XX SQ Sequence 20 BP; 4 A; 6 C; 5 G; 5 T; 0 U; 0 Other;  
 Query Match 1.2%; Score 20; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 45;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 553 AGACGCACATGCTGGATGTC 572  
 Db 20 AGACGCACATGCTGGATGTC 1  
 RESULT 146  
 ABN99698/C  
 ID ABN99698 standard; DNA; 20 BP.  
 XX AC ABN99698;  
 XX DT 16-AUG-2002 (first entry)  
 XX DE Human clusterin inhibiting antisense oligonucleotide 32.  
 XX KW Human; antisense inhibition; antisense oligonucleotide; clusterin;  
 KW hypercholesterolaemia; cardiovascular disorder; ss;  
 KW hyperproliferative disorder; hyperlipidemic disorder;  
 KW phosphorothioate backbone; 2'-O-methoxyethyl wing.  
 XX OS Homo sapiens.  
 XX PN WO200222635-A1.  
 XX PD 21-MAR-2002.  
 XX PF 10-SEP-2001; 2001WO-US028235.  
 XX PR 11-SEP-2000; 2000US-00659791.  
 XX PA (ISIS-) ISIS PHARM INC.  
 XX PI Monia BP, Freier SM;  
 XX PS WPI; 2002-404805/43.  
 XX PT Novel antisense compound targeted to nucleic acid molecule encoding  
 PT clusterin, useful for treating animal having disease associated with  
 PT clusterin such as hyperlipidemic disorder, cardiovascular disorder.  
 XX PS Claim 3; Page 83; 125pp; English.  
 XX CC The invention comprises antisense oligonucleotides that are capable of  
 CC inhibiting expression of the human clusterin gene. The antisense  
 CC oligonucleotides of the invention are useful for inhibiting the  
 CC expression of clusterin in cells. The antisense oligonucleotides are also  
 CC useful for treating an animal with a disease or condition associated with  
 CC clusterin (e.g. hypercholesterolaemia; cardiovascular disorders;  
 CC hyperproliferative disorders; and hyperlipidemic disorders). The present  
 CC DNA sequence represents a clusterin antisense oligonucleotide of the  
 CC invention. NOTE: The present DNA sequence has a phosphorothioate backbone  
 CC and also contains 2'-O-methoxyethyl wings  
 XX SQ Sequence 20 BP; 5 A; 5 C; 6 G; 4 T; 0 U; 0 Other;  
 Query Match 1.2%; Score 20; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 45;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 613 AGCTTTCAGACAGGTTTC 632  
 |||||

Db 20 AGCTCTTCCAGGACAGGTTTC 1

RESULT 147  
ABN99715/c  
ID ABN99715 standard; DNA; 20 BP.  
XX  
AC ABN99715;  
XX  
DT 16-AUG-2002 (first entry)  
XX  
DE Human clusterin inhibiting antisense oligonucleotide 49.  
XX  
KW Human; antisense inhibition; antisense oligonucleotide; clusterin;  
KW hypercholesterolaemia; cardiovascular disorder; ss;  
KW hyperproliferative disorder; hyperlipidemic disorder;  
KW phosphorothioate backbone; 2'-O-methoxyethyl wing.  
XX  
OS Homo sapiens.  
XX  
PN WO200222635-A1.  
XX  
PD 21-MAR-2002.  
XX  
PF 10-SEP-2001; 2001WO-US028235.  
XX  
PR 11-SEP-2000; 2000US-00659791.  
XX  
PA (ISIS-) ISIS PHARM INC.  
XX  
PI Monia BP, Freier SM;  
XX  
DR WPI; 2002-404805/43.  
XX  
XX Novel antisense compound targeted to nucleic acid molecule encoding clusterin, useful for treating animal having disease associated with clusterin such as hyperlipidemic disorder, cardiovascular disorder.  
PT  
PT  
PS Claim 3; Page 84; 125pp; English.  
XX  
XX The invention comprises antisense oligonucleotides that are capable of inhibiting expression of the human clusterin gene. The antisense oligonucleotides of the invention are useful for inhibiting the expression of clusterin in cells. The antisense oligonucleotides are also useful for treating an animal with a disease or condition associated with clusterin (e.g. hypercholesterolaemia; cardiovascular disorders; hyperproliferative disorders; and hyperlipidemic disorders). The present DNA sequence represents a clusterin antisense oligonucleotide of the invention. NOTE: The present DNA sequence has a phosphorothioate backbone and also contains 2'-O-methoxyethyl wings  
XX  
SQ Sequence 20 BP; 3 A; 5 C; 5 G; 7 T; 0 U; 0 Other;  
XX  
XX Query Match 1.2%; Score 20; DB 1; Length 20;  
XX Best Local Similarity 100.0%; Pred. No. 45;  
XX Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
XX  
Qy 1091 CCAGTGGAGATGCTCAACA 1110  
Db 20 CCAGTGGAGATGCTCAACA 1  
XX  
XX RESULT 148  
XX ABN99715/c  
XX ID ABN99719 standard; DNA; 20 BP.  
XX  
AC ABN99719;  
XX  
DT 16-AUG-2002 (first entry)  
XX  
DE Human clusterin inhibiting antisense oligonucleotide 53.  
XX  
KW Human; antisense inhibition; antisense oligonucleotide; clusterin;

KW hypercholesterolaemia; cardiovascular disorder; ss;  
KW hyperproliferative disorder; hyperlipidemic disorder;  
KW phosphorothioate backbone; 2'-O-methoxyethyl wing.  
XX  
OS Homo sapiens.  
XX  
PN WO200222635-A1.  
XX  
PD 21-MAR-2002.  
XX  
PF 10-SEP-2001; 2001WO-US028235.  
XX  
PR 11-SEP-2000; 2000US-00659791.  
XX  
PA (ISIS-) ISIS PHARM INC.  
XX  
PI Monia BP, Freier SM;  
XX  
DR WPI; 2002-404805/43.  
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PT  
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XX  
SQ Sequence 20 BP; 4 A; 5 C; 5 G; 6 T; 0 U; 0 Other;  
XX  
XX Query Match 1.2%; Score 20; DB 1; Length 20;  
XX Best Local Similarity 100.0%; Pred. No. 45;  
XX Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
XX  
Qy 1182 GAAGACCAAGTACTATCTGCG 1201  
Db 20 GAAGACCAAGTACTATCTGCG 1  
XX  
XX RESULT 149  
XX ABN99728/c  
XX ID ABN99728 standard; DNA; 20 BP.  
XX  
AC ABN99728;  
XX  
DT 16-AUG-2002 (first entry)  
XX  
DE Human clusterin inhibiting antisense oligonucleotide 62.  
XX  
KW Human; antisense inhibition; antisense oligonucleotide; clusterin;  
KW hypercholesterolaemia; cardiovascular disorder; ss;  
KW hyperproliferative disorder; hyperlipidemic disorder;  
KW phosphorothioate backbone; 2'-O-methoxyethyl wing.  
XX  
OS Homo sapiens.  
XX  
PN WO200222635-A1.  
XX  
PD 21-MAR-2002.  
XX  
PF 10-SEP-2001; 2001WO-US028235.  
XX  
PR 11-SEP-2000; 2000US-00659791.  
XX

PA (ISIS-) ISIS PHARM INC.  
XX Monia BP, Freier SM;  
DR WPI; 2002-404805/43.  
XX Novel antisense compound targeted to nucleic acid molecule encoding  
PT clusterin, useful for treating animal having disease associated with  
PT clusterin such as hyperlipidemic disorder, cardiovascular disorder.  
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CC DNA sequence represents a clusterin antisense oligonucleotide of the  
CC invention. NOTE: The present DNA sequence has a phosphorothioate backbone  
CC and also contains 2'-O-methoxyethyl wings  
XX  
SQ Sequence 20 BP; 7 A; 1 C; 4 G; 8 T; 0 U; 0 Other;  
  
Query Match 1.2%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 45;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1615 CTAAATCAATAAAGTCTCT 1634  
DB 20 CTAAATCAATAAAGTCTCT 1  
|||||  
RESULT 150  
ABN99733/c  
ID ABN99733 standard; DNA; 20 BP.  
AC ABN99733;  
XX  
XX 16-AUG-2002 (first entry)  
DT  
DE Human clusterin inhibiting antisense oligonucleotide 67.  
XX  
XX Human; antisense inhibition; antisense oligonucleotide; clusterin;  
KW hypercholesterolaemia; cardiovascular disorder; ss;  
KW hyperproliferative disorder; hyperlipidemic disorder;  
KW phosphorothioate backbone; 2'-O-methoxyethyl wing.  
XX  
OS Homo sapiens.  
XX  
XX WO200222635-A1.  
AC  
XX  
XX 21-MAR-2002.  
PD  
PF 10-SEP-2001; 2001WO-US028235.  
PR  
PR 11-SEP-2000; 2000US-00659791.  
XX  
XX (ISIS-) ISIS PHARM INC.  
PA  
PI Monia BP, Freier SM;  
PI WPI; 2002-404805/43.  
XX  
XX Novel antisense compound targeted to nucleic acid molecule encoding  
PT clusterin, useful for treating animal having disease associated with  
PT clusterin such as hyperlipidemic disorder, cardiovascular disorder.  
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CC hyperproliferative disorders; and hyperlipidemic disorders). The present  
CC DNA sequence represents a clusterin antisense oligonucleotide of the  
CC invention. NOTE: The present DNA sequence has a phosphorothioate backbone  
CC and also contains 2'-O-methoxyethyl wings  
XX  
SQ Sequence 20 BP; 3 A; 9 C; 3 G; 5 T; 0 U; 0 Other;  
  
Query Match 1.2%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 45;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1383 CACCGGAGGAGTGAGATGT 1402  
DB 20 CACCGGAGGAGTGAGATGT 1  
|||||  
RESULT 151  
ABN99673/c  
ID ABN99673 standard; DNA; 20 BP.  
XX  
XX ABN99673;  
AC  
XX  
XX 16-AUG-2002 (first entry)  
DT  
DE Human clusterin inhibiting antisense oligonucleotide 7.  
XX  
XX Human; antisense inhibition; antisense oligonucleotide; clusterin;  
KW hypercholesterolaemia; cardiovascular disorder; ss;  
KW hyperproliferative disorder; hyperlipidemic disorder;  
KW phosphorothioate backbone; 2'-O-methoxyethyl wing.  
XX  
OS Homo sapiens.  
XX  
XX WO200222635-A1.  
AC  
XX  
XX 21-MAR-2002.  
PD  
PF 10-SEP-2001; 2001WO-US028235.  
PR  
PR 11-SEP-2000; 2000US-00659791.  
XX  
XX (ISIS-) ISIS PHARM INC.  
PA  
PI Monia BP, Freier SM;  
PI WPI; 2002-404805/43.  
XX  
XX Novel antisense compound targeted to nucleic acid molecule encoding  
PT clusterin, useful for treating animal having disease associated with  
PT clusterin such as hyperlipidemic disorder, cardiovascular disorder.  
XX  
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CC clusterin (e.g. hypercholesterolaemia; cardiovascular disorders;  
CC hyperproliferative disorders; and hyperlipidemic disorders). The present  
CC DNA sequence represents a clusterin antisense oligonucleotide of the  
CC invention. NOTE: The present DNA sequence has a phosphorothioate backbone  
CC and also contains 2'-O-methoxyethyl wings  
XX  
SQ Sequence 20 BP; 4 A; 6 C; 3 G; 7 T; 0 U; 0 Other;  
  
Query Match 1.2%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 45;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
QY 149 GTCCAATCAGGAAGTAAGT 168
Db 20 GTCCAATCAGGAAGTAAGT 1

RESULT 152
ABN99679/c
ID ABN99679 standard; DNA; 20 BP.
AC ABN99679;
XX
XX
XX 16-AUG-2002 (first entry)
XX
XX Human clusterin inhibiting antisense oligonucleotide 13.
XX
XX Human; antisense inhibition; antisense oligonucleotide; clusterin;
KW hypercholesterolaemia; cardiovascular disorder; ss;
KW hyperproliferative disorder; hyperlipidemic disorder;
KW phosphorothioate backbone; 2'-O-methoxyethyl wing.
XX
XX Homo sapiens.
OS
XX WO200222635-A1.
PN
XX
XX 21-MAR-2002.
PD
XX
XX 10-SEP-2001; 2001WO-US028235.
PF
XX
XX 11-SEP-2000; 2000US-00659791.
PR
XX (ISIS-) ISIS PHARM INC.
PA
XX Monia BP, Freier SM;
PI
XX WPI; 2002-404805/43.
DR
XX
XX Novel antisense compound targeted to nucleic acid molecule encoding
PT clusterin, useful for treating animal having disease associated with
PT clusterin such as hyperlipidemic disorder, cardiovascular disorder.
XX
XX Claim 3; Page 83; 125pp; English.
XX
XX The invention comprises antisense oligonucleotides that are capable of
CC inhibiting expression of the human clusterin gene. The antisense
CC oligonucleotides of the invention are useful for inhibiting the
CC expression of clusterin in cells. The antisense oligonucleotides are also
CC useful for treating an animal with a disease or condition associated with
CC clusterin (e.g. hypercholesterolaemia; cardiovascular disorders;
CC hyperproliferative disorders; and hyperlipidemic disorders). The present
CC DNA sequence represents a clusterin antisense oligonucleotide of the
CC invention. NOTE: The present DNA sequence has a phosphorothioate backbone
CC and also contains 2'-O-methoxyethyl wings
XX
XX Sequence 20 BP; 1 A; 6 C; 4 G; 9 T; 0 U; 0 Other;
XX
XX The invention comprises antisense oligonucleotides that are capable of
CC inhibiting expression of the human clusterin gene. The antisense
CC oligonucleotides of the invention are useful for inhibiting the
CC expression of clusterin in cells. The antisense oligonucleotides are also
CC useful for treating an animal with a disease or condition associated with
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CC hyperproliferative disorders; and hyperlipidemic disorders). The present
CC DNA sequence represents a clusterin antisense oligonucleotide of the
CC invention. NOTE: The present DNA sequence has a phosphorothioate backbone
CC and also contains 2'-O-methoxyethyl wings
XX
XX Query Match 1.2%; Score 20; DB 1; Length 20;
XX Best Local Similarity 100.0%; Pred. No. 45;
XX Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 307 AGACCAGGGAATCAGAGACA 326
Db 20 AGACCAGGGAATCAGAGACA 1

RESULT 153
ABN99696/c
ID ABN99696 standard; DNA; 20 BP.
AC ABN99696;
XX
XX
XX 16-AUG-2002 (first entry)
XX
XX Human clusterin inhibiting antisense oligonucleotide 39.
XX
XX Human; antisense inhibition; antisense oligonucleotide; clusterin;
KW hypercholesterolaemia; cardiovascular disorder; ss;
KW hyperproliferative disorder; hyperlipidemic disorder;
KW phosphorothioate backbone; 2'-O-methoxyethyl wing.
XX
XX Homo sapiens.
OS
XX WO200222635-A1.
PN
XX
XX 21-MAR-2002.
PD
XX
XX 10-SEP-2001; 2001WO-US028235.
PF
XX
XX 11-SEP-2000; 2000US-00659791.
PR
XX (ISIS-) ISIS PHARM INC.
PA
XX Monia BP, Freier SM;
PI
XX WPI; 2002-404805/43.
DR
XX
XX Novel antisense compound targeted to nucleic acid molecule encoding
PT clusterin, useful for treating animal having disease associated with
PT clusterin such as hyperlipidemic disorder, cardiovascular disorder.
XX
XX Claim 3; Page 83; 125pp; English.
XX
XX The invention comprises antisense oligonucleotides that are capable of
CC inhibiting expression of the human clusterin gene. The antisense
CC oligonucleotides of the invention are useful for inhibiting the
CC expression of clusterin in cells. The antisense oligonucleotides are also
CC useful for treating an animal with a disease or condition associated with
CC clusterin (e.g. hypercholesterolaemia; cardiovascular disorders;
CC hyperproliferative disorders; and hyperlipidemic disorders). The present
CC DNA sequence represents a clusterin antisense oligonucleotide of the
CC invention. NOTE: The present DNA sequence has a phosphorothioate backbone
CC and also contains 2'-O-methoxyethyl wings
XX
XX Query Match 1.2%; Score 20; DB 1; Length 20;
XX Best Local Similarity 100.0%; Pred. No. 45;
XX Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 307 AGACCAGGGAATCAGAGACA 326
Db 20 AGACCAGGGAATCAGAGACA 1

RESULT 154
ABN99705/c
ID ABN99705 standard; DNA; 20 BP.
AC ABN99705;
XX
XX
XX 16-AUG-2002 (first entry)
XX
XX Human clusterin inhibiting antisense oligonucleotide 39.
XX
XX Human; antisense inhibition; antisense oligonucleotide; clusterin;
KW hypercholesterolaemia; cardiovascular disorder; ss;
KW hyperproliferative disorder; hyperlipidemic disorder;
KW phosphorothioate backbone; 2'-O-methoxyethyl wing.
XX
XX Homo sapiens.
OS
XX WO200222635-A1.
PN
XX
XX 21-MAR-2002.
PD
XX
XX 10-SEP-2001; 2001WO-US028235.
PF
```

XX 11-SEP-2000; 2000US-00659791.  
XX (ISIS-) ISIS PHARM INC.  
XX Monia BP, Freier SM;  
XX WPI; 2002-404805/43.  
XX Novel antisense compound targeted to nucleic acid molecule encoding  
PT clusterin, useful for treating animal having disease associated with  
PT clusterin such as hyperlipidemic disorder, cardiovascular disorder.  
XX Claim 3; Page 83; 125pp; English.  
XX The invention comprises antisense oligonucleotides that are capable of  
CC inhibiting expression of the human clusterin gene. The antisense  
CC oligonucleotides of the invention are useful for inhibiting the  
CC expression of clusterin in cells. The antisense oligonucleotides are also  
CC useful for treating an animal with a disease or condition associated with  
CC clusterin (e.g. hypercholesterolaemia; cardiovascular disorders;  
CC hyperproliferative disorders; and hyperlipidemic disorders). The present  
CC DNA sequence represents a clusterin antisense oligonucleotide of the  
CC invention. NOTE: The present DNA sequence has a phosphorothioate backbone  
CC and also contains 2'-O-methoxyethyl wings  
XX Sequence 20 BP; 1 A; 3 C; 9 G; 7 T; 0 U; 0 Other;  
SQ

Query Match 1.2%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 45;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 848 CCAGCACCCGCCCAACAGAAT 867  
DB 20 CCAGCACCCGCCCAACAGAAT 1  
|||||

RESULT 155  
ABN9706/c  
ID ABN9706 standard; DNA; 20 BP.  
XX  
AC ABN9706;  
XX  
DT 16-AUG-2002 (first entry)  
XX  
DE Human clusterin inhibiting antisense oligonucleotide 40.  
XX  
KW Human; antisense inhibition; antisense oligonucleotide; clusterin;  
KW hypercholesterolaemia; cardiovascular disorder; ss;  
KW hyperproliferative disorder; hyperlipidemic disorder;  
KW phosphorothioate backbone; 2'-O-methoxyethyl wing.  
XX  
OS Homo sapiens.  
XX  
PN WO200222635-A1.  
XX  
AC ABN9706;  
XX  
DT 16-AUG-2002 (first entry)  
XX  
DE Human clusterin inhibiting antisense oligonucleotide 40.  
XX  
KW Human; antisense inhibition; antisense oligonucleotide; clusterin;  
KW hypercholesterolaemia; cardiovascular disorder; ss;  
KW hyperproliferative disorder; hyperlipidemic disorder;  
KW phosphorothioate backbone; 2'-O-methoxyethyl wing.  
XX  
OS Homo sapiens.  
XX  
PN WO200222635-A1.  
XX  
PD 21-MAR-2002.  
XX  
PF 10-SEP-2001; 2001WO-US028235.  
XX  
PR 11-SEP-2000; 2000US-00659791.  
XX  
PA (ISIS-) ISIS PHARM INC.  
XX  
PI Monia BP, Freier SM;  
XX  
WPI; 2002-404805/43.  
XX  
Novel antisense compound targeted to nucleic acid molecule encoding  
PT clusterin, useful for treating animal having disease associated with  
PT clusterin such as hyperlipidemic disorder, cardiovascular disorder.  
XX Claim 3; Page 83; 125pp; English.

XX The invention comprises antisense oligonucleotides that are capable of  
CC inhibiting expression of the human clusterin gene. The antisense  
CC oligonucleotides of the invention are useful for inhibiting the  
CC expression of clusterin in cells. The antisense oligonucleotides are also  
CC useful for treating an animal with a disease or condition associated with  
CC clusterin (e.g. hypercholesterolaemia; cardiovascular disorders;  
CC hyperproliferative disorders; and hyperlipidemic disorders). The present  
CC DNA sequence represents a clusterin antisense oligonucleotide of the  
CC invention. NOTE: The present DNA sequence has a phosphorothioate backbone  
CC and also contains 2'-O-methoxyethyl wings  
XX Sequence 20 BP; 3 A; 2 C; 7 G; 8 T; 0 U; 0 Other;  
SQ

Query Match 1.2%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 45;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 853 ACCCGCCCAACAGATTTCATA 872  
DB 20 ACCCGCCCAACAGATTTCATA 1  
|||||

RESULT 156  
ABN9723/c  
ID ABN9723 standard; DNA; 20 BP.  
XX  
AC ABN9723;  
XX  
DT 16-AUG-2002 (first entry)  
XX  
DE Human clusterin inhibiting antisense oligonucleotide 57.  
XX  
KW Human; antisense inhibition; antisense oligonucleotide; clusterin;  
KW hypercholesterolaemia; cardiovascular disorder; ss;  
KW hyperproliferative disorder; hyperlipidemic disorder;  
KW phosphorothioate backbone; 2'-O-methoxyethyl wing.  
XX  
OS Homo sapiens.  
XX  
PN WO200222635-A1.  
XX  
PD 21-MAR-2002.  
XX  
PF 10-SEP-2001; 2001WO-US028235.  
XX  
PR 11-SEP-2000; 2000US-00659791.  
XX  
PA (ISIS-) ISIS PHARM INC.  
XX  
PI Monia BP, Freier SM;  
XX  
WPI; 2002-404805/43.  
XX  
Novel antisense compound targeted to nucleic acid molecule encoding  
PT clusterin, useful for treating animal having disease associated with  
PT clusterin such as hyperlipidemic disorder, cardiovascular disorder.  
XX Claim 3; Page 84; 125pp; English.  
XX The invention comprises antisense oligonucleotides that are capable of  
CC inhibiting expression of the human clusterin gene. The antisense  
CC oligonucleotides of the invention are useful for inhibiting the  
CC expression of clusterin in cells. The antisense oligonucleotides are also  
CC useful for treating an animal with a disease or condition associated with  
CC clusterin (e.g. hypercholesterolaemia; cardiovascular disorders;  
CC hyperproliferative disorders; and hyperlipidemic disorders). The present  
CC DNA sequence represents a clusterin antisense oligonucleotide of the  
CC invention. NOTE: The present DNA sequence has a phosphorothioate backbone  
CC and also contains 2'-O-methoxyethyl wings  
XX Sequence 20 BP; 5 A; 5 C; 7 G; 3 T; 0 U; 0 Other;  
SQ

```

Query Match      1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred.No. 45;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1300 CGGTCCCTGTAGAGTCTCC 1319
        |||||
DB       20 CGGTCCCTGTAGAGTCTCC 1

RESULT 157
ABN99731/c
ID ABN99731 standard; DNA; 20 BP.
XX AC
XX AC ABN99731;
XX DT
XX DE 16-AUG-2002 (first entry)
XX DE Human clusterin inhibiting antisense oligonucleotide 65.
XX KW Human; antisense inhibition; antisense oligonucleotide; clusterin;
XX KW hypercholesterolaemia; cardiovascular disorder; ss;
KW KW hyperproliferative disorder; hyperlipidemic disorder;
KW KW phosphorothioate backbone; 2'-O-methoxyethyl wing.
XX KW
OS Homo sapiens.
XX PN WO200222635-A1.
XX PN 21-MAR-2002.
XX PF 10-SEP-2001; 2001WO-US028235.
XX PR 11-SEP-2000; 2000US-00659791.
XX PA (ISIS-) ISIS PHARM INC.
XX PA Monia BP, Freier SM;
XX PI WPI; 2002-404805/43.
XX DR
XX PT Novel antisense compound targeted to nucleic acid molecule encoding
PT PT clusterin, useful for treating animal having disease associated with
PT PT clusterin such as hyperlipidemic disorder, cardiovascular disorder.
XX PS
XX PS Claim 3; Page 84; 125pp; English.
XX CC The invention comprises antisense oligonucleotides that are capable of
CC CC inhibiting expression of the human clusterin gene. The antisense
CC CC oligonucleotides of the invention are useful for inhibiting the
CC CC expression of clusterin in cells. The antisense oligonucleotides are also
CC CC useful for treating an animal with a disease or condition associated with
CC CC clusterin (e.g. hypercholesterolaemia; cardiovascular disorders;
CC CC hyperproliferative disorders; and hyperlipidemic disorders). The present
CC CC DNA sequence represents a clusterin antisense oligonucleotide of the
CC CC invention. NOTE: The present DNA sequence has a phosphorothioate backbone
CC CC and also contains 2'-O-methoxyethyl wings
XX SQ Sequence 20 BP; 4 A; 3 C; 7 G; 6 T; 0 U; 0 Other;

Query Match      1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred.No. 45;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      979 TGGACTGTTCCACCAACAAC 998
        |||||
DB       20 TGGACTGTTCCACCAACAAC 1

RESULT 158
ABN99699/c
ID ABN99699 standard; DNA; 20 BP.
XX AC
XX AC ABN99699;

```

PD 21-MAR-2002.  
XX  
PF 10-SEP-2001; 2001WO-US028235.  
XX  
PR 11-SEP-2000; 2000US-00659791.  
XX  
PA (ISIS-) ISIS PHARM INC.  
XX  
PI Monia BP, Freier SM;  
XX  
DR WPI; 2002-404805/43.  
XX  
PT Novel antisense compound targeted to nucleic acid molecule encoding  
PT clusterin, useful for treating animal having disease associated with  
PT clusterin such as hyperlipidemic disorder, cardiovascular disorder.  
XX  
PS Claim 3; Page 84; 125pp; English.  
XX  
CC The invention comprises antisense oligonucleotides that are capable of  
CC inhibiting expression of the human clusterin gene. The antisense  
CC oligonucleotides of the invention are useful for inhibiting the  
CC expression of clusterin in cells. The antisense oligonucleotides are also  
CC useful for treating an animal with a disease or condition associated with  
CC clusterin (e.g. hypercholesterolaemia; cardiovascular disorders;  
CC hyperproliferative disorders; and hyperlipidemic disorders). The present  
CC DNA sequence represents a clusterin antisense oligonucleotide of the  
CC invention. NOTE: The present DNA sequence has a phosphorothioate backbone  
CC and also contains 2'-O-methoxyethyl wings  
XX  
SQ Sequence 20 BP; 4 A; 5 C; 4 G; 7 T; 0 U; 0 Other;  
  
Query Match 1.2%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 45;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1083 AGTCTTACCAGTGGGAAGAT 1102  
DB 20 AAGTCTTACCAGTGGGAAGAT 1  
|||||  
RESULT 160  
ABN99674/C  
ID ABN99674 standard; DNA; 20 BP.  
XX  
AC ABN99674;  
XX  
DT 16-AUG-2002 (first entry)  
XX  
DE Human clusterin inhibiting antisense oligonucleotide 8.  
XX  
KW Human; antisense inhibition; antisense oligonucleotide; clusterin;  
KW hypercholesterolaemia; cardiovascular disorder; ss;  
KW hyperproliferative disorder; hyperlipidemic disorder;  
KW phosphorothioate backbone; 2'-O-methoxyethyl wing.  
XX  
OS Homo sapiens.  
XX  
PN WO200222635-A1.  
XX  
AC ABN99674;  
XX  
DT 16-AUG-2002 (first entry)  
XX  
DE Human clusterin inhibiting antisense oligonucleotide 8.  
XX  
KW Human; antisense inhibition; antisense oligonucleotide; clusterin;  
KW hypercholesterolaemia; cardiovascular disorder; ss;  
KW hyperproliferative disorder; hyperlipidemic disorder;  
KW phosphorothioate backbone; 2'-O-methoxyethyl wing.  
XX  
OS Homo sapiens.  
XX  
PN WO200222635-A1.  
XX  
PD 21-MAR-2002.  
XX  
PF 10-SEP-2001; 2001WO-US028235.  
XX  
PR 11-SEP-2000; 2000US-00659791.  
XX  
PA (ISIS-) ISIS PHARM INC.  
XX  
PI Monia BP, Freier SM;  
XX  
DR WPI; 2002-404805/43.  
XX  
PT Novel antisense compound targeted to nucleic acid molecule encoding  
PT clusterin, useful for treating animal having disease associated with

PT clusterin such as hyperlipidemic disorder, cardiovascular disorder.  
XX  
PS Claim 3; Page 83; 125pp; English.  
XX  
CC The invention comprises antisense oligonucleotides that are capable of  
CC inhibiting expression of the human clusterin gene. The antisense  
CC oligonucleotides of the invention are useful for inhibiting the  
CC expression of clusterin in cells. The antisense oligonucleotides are also  
CC useful for treating an animal with a disease or condition associated with  
CC clusterin (e.g. hypercholesterolaemia; cardiovascular disorders;  
CC hyperproliferative disorders; and hyperlipidemic disorders). The present  
CC DNA sequence represents a clusterin antisense oligonucleotide of the  
CC invention. NOTE: The present DNA sequence has a phosphorothioate backbone  
CC and also contains 2'-O-methoxyethyl wings  
XX  
SQ Sequence 20 BP; 5 A; 4 C; 2 G; 9 T; 0 U; 0 Other;  
  
Query Match 1.2%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 45;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 166 AGTACGTCAATAAGGAATT 185  
DB 20 AGTACGTCAATAAGGAATT 1  
|||||  
RESULT 161  
ABN99688/C  
ID ABN99688 standard; DNA; 20 BP.  
XX  
AC ABN99688;  
XX  
DT 16-AUG-2002 (first entry)  
XX  
DE Human clusterin inhibiting antisense oligonucleotide 22.  
XX  
KW Human; antisense inhibition; antisense oligonucleotide; clusterin;  
KW hypercholesterolaemia; cardiovascular disorder; ss;  
KW hyperproliferative disorder; hyperlipidemic disorder;  
KW phosphorothioate backbone; 2'-O-methoxyethyl wing.  
XX  
OS Homo sapiens.  
XX  
PN WO200222635-A1.  
XX  
PD 21-MAR-2002.  
XX  
PF 10-SEP-2001; 2001WO-US028235.  
XX  
PR 11-SEP-2000; 2000US-00659791.  
XX  
PA (ISIS-) ISIS PHARM INC.  
XX  
PI Monia BP, Freier SM;  
XX  
DR WPI; 2002-404805/43.  
XX  
PT Novel antisense compound targeted to nucleic acid molecule encoding  
PT clusterin, useful for treating animal having disease associated with  
PT clusterin such as hyperlipidemic disorder, cardiovascular disorder.  
XX  
PS Claim 3; Page 83; 125pp; English.  
XX  
CC The invention comprises antisense oligonucleotides that are capable of  
CC inhibiting expression of the human clusterin gene. The antisense  
CC oligonucleotides of the invention are useful for inhibiting the  
CC expression of clusterin in cells. The antisense oligonucleotides are also  
CC useful for treating an animal with a disease or condition associated with  
CC clusterin (e.g. hypercholesterolaemia; cardiovascular disorders;  
CC hyperproliferative disorders; and hyperlipidemic disorders). The present  
CC DNA sequence represents a clusterin antisense oligonucleotide of the  
CC invention. NOTE: The present DNA sequence has a phosphorothioate backbone  
CC and also contains 2'-O-methoxyethyl wings

```
XX Sequence 20 BP; 5 A; 3 C; 9 G; 3 T; 0 U; 0 Other;
SQ Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 45;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 482 CCAGAGCTCGCCCTTCTACT 501
DB 20 CCAGAGCTCGCCCTTCTACT 1

RESULT 162
ABN99710/c
ID ABN99710 standard; DNA; 20 BP.
XX AC ABN99710;
XX DT 16-AUG-2002 (first entry)
XX DE Human clusterin inhibiting antisense oligonucleotide 44.
XX DE Human; antisense inhibition; antisense oligonucleotide; clusterin;
XX KW hypercholesterolaemia; cardiovascular disorder; ss;
XX KW hyperproliferative disorder; hyperlipidemic disorder;
XX KW phosphorothioate backbone; 2'-O-methoxyethyl wing.
XX OS Homo sapiens.
XX WO200222635-A1.
XX PD 21-MAR-2002.
XX PF 10-SEP-2001; 2001WO-US028235.
XX PR 11-SEP-2000; 2000US-00659791.
XX PA (ISIS-) ISIS PHARM INC.
XX PI Monia BP, Freier SM;
XX PI WPI; 2002-404805/43.
XX DR Novel antisense compound targeted to nucleic acid molecule encoding
XX PT clusterin, useful for treating animal having disease associated with
XX PT clusterin such as hyperlipidemic disorder, cardiovascular disorder.
XX PS Claim 3; Page 84; 125pp; English.
XX CC The invention comprises antisense oligonucleotides that are capable of
XX CC inhibiting expression of the human clusterin gene. The antisense
XX CC oligonucleotides of the invention are useful for inhibiting the
XX CC expression of clusterin in cells. The antisense oligonucleotides are also
XX CC useful for treating an animal with a disease or condition associated with
XX CC clusterin (e.g. hypercholesterolaemia; cardiovascular disorders;
XX CC hyperproliferative disorders; and hyperlipidemic disorders). The present
XX CC DNA sequence represents a clusterin antisense oligonucleotide of the
XX CC invention. NOTE: The present DNA sequence has a phosphorothioate backbone
XX CC and also contains 2'-O-methoxyethyl wings
XX SQ Sequence 20 BP; 3 A; 8 C; 5 G; 4 T; 0 U; 0 Other;

Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 45;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 928 GCTGCTCGCGATGAAGGAC 947
DB 20 GCTGCTCGCGATGAAGGAC 1

RESULT 163
ABN99676/c
```

```
ID ABN99676 standard; DNA; 20 BP.
XX AC ABN99676;
XX DT 16-AUG-2002 (first entry)
XX DE Human clusterin inhibiting antisense oligonucleotide 10.
XX DE Human; antisense inhibition; antisense oligonucleotide; clusterin;
XX KW hypercholesterolaemia; cardiovascular disorder; ss;
XX KW hyperproliferative disorder; hyperlipidemic disorder;
XX KW phosphorothioate backbone; 2'-O-methoxyethyl wing.
XX OS Homo sapiens.
XX WO200222635-A1.
XX PD 21-MAR-2002.
XX PF 10-SEP-2001; 2001WO-US028235.
XX PR 11-SEP-2000; 2000US-00659791.
XX PA (ISIS-) ISIS PHARM INC.
XX PI Monia BP, Freier SM;
XX PI WPI; 2002-404805/43.
XX DR Novel antisense compound targeted to nucleic acid molecule encoding
XX PT clusterin, useful for treating animal having disease associated with
XX PT clusterin such as hyperlipidemic disorder, cardiovascular disorder.
XX PS Claim 3; Page 83; 125pp; English.
XX CC The invention comprises antisense oligonucleotides that are capable of
XX CC inhibiting expression of the human clusterin gene. The antisense
XX CC oligonucleotides of the invention are useful for inhibiting the
XX CC expression of clusterin in cells. The antisense oligonucleotides are also
XX CC useful for treating an animal with a disease or condition associated with
XX CC clusterin (e.g. hypercholesterolaemia; cardiovascular disorders;
XX CC hyperproliferative disorders; and hyperlipidemic disorders). The present
XX CC DNA sequence represents a clusterin antisense oligonucleotide of the
XX CC invention. NOTE: The present DNA sequence has a phosphorothioate backbone
XX CC and also contains 2'-O-methoxyethyl wings
XX SQ Sequence 20 BP; 1 A; 7 C; 3 G; 9 T; 0 U; 0 Other;

Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 45;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 281 GAAGAAGAAAGAGATGCC 300
DB 20 GAAGAAGAAAGAGATGCC 1

RESULT 164
ABN99692/c
ID ABN99692 standard; DNA; 20 BP.
XX AC ABN99692;
XX DT 16-AUG-2002 (first entry)
XX DE Human clusterin inhibiting antisense oligonucleotide 26.
XX DE Human; antisense inhibition; antisense oligonucleotide; clusterin;
XX KW hypercholesterolaemia; cardiovascular disorder; ss;
XX KW hyperproliferative disorder; hyperlipidemic disorder;
XX KW phosphorothioate backbone; 2'-O-methoxyethyl wing.
XX OS Homo sapiens.
```



XX WO200222635-A1.  
 XX 21-MAR-2002.  
 XX 10-SEP-2001; 2001WO-US028235.  
 XX 11-SEP-2000; 2000US-00659791.  
 XX (ISIS-) ISIS PHARM INC.  
 XX Monia BP, Freier SM;  
 XX WPI; 2002-404805/43.  
 XX Novel antisense compound targeted to nucleic acid molecule encoding clusterin, useful for treating animal having disease associated with clusterin such as hyperlipidemic disorder, cardiovascular disorder.  
 XX Claim 3; Page 83; 125pp; English.  
 XX The invention comprises antisense oligonucleotides that are capable of inhibiting expression of the human clusterin gene. The antisense oligonucleotides of the invention are useful for inhibiting the expression of clusterin in cells. The antisense oligonucleotides are also useful for treating an animal with a disease or condition associated with clusterin (e.g. hypercholesterolaemia; cardiovascular disorders; hyperproliferative disorders; and hyperlipidemic disorders). The present DNA sequence represents a clusterin antisense oligonucleotide of the invention. NOTE: The present DNA sequence has a phosphorothioate backbone and also contains 2'-O-methoxyethyl wings  
 XX Sequence 20 BP; 3 A; 7 C; 5 G; 5 T; 0 U; 0 Other;  
 XX Query Match 1.2%; Score 20; DB 1; Length 20;  
 XX Best Local Similarity 100.0%; Pred. No. 45;  
 XX Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 551 GCAGACGCACATGCTGGATG 570  
 DB 20 GCAGACGCACATGCTGGATG 1  
 RESULT 165  
 ABN99707/c  
 ID ABN99707 standard; DNA; 20 BP.  
 XX AC ABN99707;  
 XX 16-AUG-2002 (first entry)  
 XX Human clusterin inhibiting antisense oligonucleotide 41.  
 XX Human; antisense inhibition; antisense oligonucleotide; clusterin;  
 KW hypercholesterolaemia; cardiovascular disorder; ss;  
 KW hyperproliferative disorder; hyperlipidemic disorder;  
 KW phosphorothioate backbone; 2'-O-methoxyethyl wing.  
 XX Homo sapiens.  
 OS WPI; 2002-404805/43.  
 XX WO200222635-A1.  
 XX 21-MAR-2002.  
 XX 10-SEP-2001; 2001WO-US028235.  
 XX 11-SEP-2000; 2000US-00659791.  
 XX (ISIS-) ISIS PHARM INC.  
 XX Monia BP, Freier SM;  
 XX WPI; 2002-404805/43.

XX Novel antisense compound targeted to nucleic acid molecule encoding clusterin, useful for treating animal having disease associated with clusterin such as hyperlipidemic disorder, cardiovascular disorder.  
 XX Claim 3; Page 83; 125pp; English.  
 XX The invention comprises antisense oligonucleotides that are capable of inhibiting expression of the human clusterin gene. The antisense oligonucleotides of the invention are useful for inhibiting the expression of clusterin in cells. The antisense oligonucleotides are also useful for treating an animal with a disease or condition associated with clusterin (e.g. hypercholesterolaemia; cardiovascular disorders; hyperproliferative disorders; and hyperlipidemic disorders). The present DNA sequence represents a clusterin antisense oligonucleotide of the invention. NOTE: The present DNA sequence has a phosphorothioate backbone and also contains 2'-O-methoxyethyl wings  
 XX Sequence 20 BP; 4 A; 8 C; 5 G; 3 T; 0 U; 0 Other;  
 XX Query Match 1.2%; Score 20; DB 1; Length 20;  
 XX Best Local Similarity 100.0%; Pred. No. 45;  
 XX Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 893 GACTGTGTGCGCGGAGATCC 912  
 DB 20 GACTGTGTGCGCGGAGATCC 1  
 RESULT 166  
 ADO07105  
 ID ADO07105 standard; DNA; 20 BP.  
 XX AC ADO07105;  
 XX 15-JUL-2004 (first entry)  
 XX CLU gene forward PCR primer.  
 XX Rheumatoid arthritis; osteoarthritis; microarray; molecular profiling;  
 KW diagnosis; antiarthritic; CLU; PCR; primer; human; ss.  
 XX Homo sapiens.  
 OS WO2004035827-A2.  
 XX 29-APR-2004.  
 XX 20-OCT-2003; 2003WO-IB005143.  
 XX 18-OCT-2002; 2002US-0419650P.  
 XX (INRM ) INSERM INST NAT SANTE & RECH MEDICALE.  
 XX (ASSI-) ASSISTANCE PUBLIQUE HOPITAUX PARIS.  
 XX (COMS ) COMMISSARIAT ENERGIE ATOMIQUE.  
 XX Breban M, Gidrol X, Marion S, Chiocchia G;  
 XX WPI; 2004-348476/32.  
 XX New library of polynucleotide sequences expressed in cells from synovial tissues, useful for diagnosing and treating rheumatoid arthritis or osteoarthritis.  
 XX Disclosure; SEQ ID NO 5; 71pp; English.  
 XX The present invention concerns an analysis of genes differentially expressed in synovial tissues from rheumatoid arthritis (RA) and osteoarthritis (OA) patients. Microarray technology was used to compare gene expression profiles, and sets of genes were identified based on over-expression or under-expression in RA samples compared to OA samples. Results for 6 of the selected genes (GBP1, CLU, RH70, GLO1, DXS and CTSL) were verified by real-time, quantitative PCR using samples identical to

CC those used in the microarray experiments and also entirely separate  
CC samples. The present sequence is that of a forward PCR primer for CLU; a  
CC reverse primer is also provided ADO07106. CLU was shown to be under-  
CC expressed in RA relative to OA samples. The invention provides libraries  
CC and arrays of polynucleotide sequences useful for prognosticating or  
CC diagnosing RA or OA. Methods are also provided for following the  
CC efficiency of a treatment against RA or OA, and for screening potential  
CC therapeutic agents for treating RA or OA.  
SQ Sequence 20 BP; 6 A; 5 C; 5 G; 4 T; 0 U; 0 Other;  
  
Query Match 1.2%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 45;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1180 GCGAGACCAGTACTATCTG 1199  
Db 1 GCGAGACCAGTACTATCTG 20  
  
RESULT 167  
ADO07106/c  
ID ADO07106 standard; DNA; 20 BP.  
XX  
AC ADO07106;  
DT 15-JUL-2004 (first entry)  
XX  
DE CLU gene reverse PCR primer.  
XX  
KW Rheumatoid arthritis; osteoarthritis; microarray; molecular profiling;  
KW diagnosis; antiarthritic; CLU; PCR; primer; human; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO2004035827-A2.  
XX  
PD 29-APR-2004.  
XX  
PF 20-OCT-2003; 2003WO-IB005143.  
XX  
PR 18-OCT-2002; 2002US-0419650P.  
XX  
PA (INRM ) INSERM INST NAT SANTE & RECH MEDICALE.  
PA (ASSI-) ASSISTANCE PUBLIQUE HOPITAUX PARIS.  
PA (COMS ) COMMISSARIAT ENERGIE ATOMIQUE.  
XX  
PI Breban M, Gidrol X, Marion S, Chiocchia G;  
XX  
DR WPI; 2004-348476/32.  
XX  
PT New library of polynucleotide sequences expressed in cells from synovial  
PT tissues, useful for diagnosing and treating rheumatoid arthritis or  
PT osteoarthritis.  
XX  
PS Disclosure; SEQ ID NO 6; 71pp; English.  
XX  
CC The present invention concerns an analysis of genes differentially  
CC expressed in synovial tissues from rheumatoid arthritis (RA) and  
CC osteoarthritis (OA) patients. Microarray technology was used to compare  
CC gene expression profiles, and sets of genes were identified based on over  
CC expression or under-expression in RA samples compared to OA samples.  
CC Results for 6 of the selected genes (GEP1, CLU, RH70, GLO1, DAX and CTSL)  
CC were verified by real-time, quantitative PCR using samples identical to  
CC those used in the microarray experiments and also entirely separate  
CC samples. The present sequence is that of a reverse PCR primer for CLU; a  
CC forward primer is also provided ADO07105. CLU was shown to be under-  
CC expressed in RA relative to OA samples. The invention provides libraries  
CC and arrays of polynucleotide sequences useful for prognosticating or  
CC diagnosing RA or OA. Methods are also provided for following the  
CC efficiency of a treatment against RA or OA, and for screening potential  
CC therapeutic agents for treating RA or OA.  
XX

SQ Sequence 20 BP; 2 A; 5 C; 5 G; 8 T; 0 U; 0 Other;  
  
Query Match 1.2%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 45;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1361 GCTGCAGGAATACCGCAAAA 1380  
Db 20 GCTGCAGGAATACCGCAAAA 1  
  
RESULT 168  
ADL70464  
ID ADL70464 standard; RNA; 21 BP.  
XX  
AC ADL70464;  
XX  
DT 20-MAY-2004 (first entry)  
XX  
DE RNAi for human clusterin.  
XX  
KW RNA interference; RNAi; short interfering RNA; siRNA; human; clusterin;  
KW cytosolic; neuroprotective; nootropic; gene silencing; DNA-RNA hybrid;  
KW ss.  
XX  
OS Homo sapiens.  
OS Synthetic.  
XX  
FH Key Location/Qualifiers  
FT modified\_base 20..21 /\*tag= a  
FT /mod\_base= OTHER  
FT /note= "OTHER= dtdt"  
XX  
FN WO2004018676-A2.  
XX  
PD 04-MAR-2004.  
XX  
PF 21-AUG-2003; 2003WO-CA001277.  
XX  
PR 21-AUG-2002; 2002US-0405193P.  
PR 03-SEP-2002; 2002US-0408152P.  
PR 20-MAY-2003; 2003US-0472387P.  
XX  
PA (UYBR-) UNIV BRITISH COLUMBIA.  
XX  
PI Jansen B, Gleave ME, Signaevsky M, Beraldi E, Trougakos IP;  
PI Gonos ES;  
XX  
DR WPI; 2004-226852/21.  
XX  
PT New RNA molecule less than 49 bases and having a sequence effective to  
PT mediate degradation or block translation of mRNA that is the  
PT transcriptional product of a target gene, useful for treating Alzheimer's  
PT disease or cancer.  
XX  
PS Claim 4; SEQ ID NO 9; 63pp; English.  
XX  
CC The present sequence is the sense strand of a short interfering RNA  
CC (siRNA) targeted to human clusterin. The antisense strand is also  
CC provided ADL70465. The siRNA can be used to interfere with the expression  
CC of clusterin. Clusterin, also known as testosterone-repressed prostate  
CC message-2 (TRPM-2) or sulfated glycoprotein-2 (SGP-2), is expressed in  
CC increased amounts by prostate tumour cells following androgen withdrawal,  
CC and has also been shown to be critical for neuritic toxicity in mouse  
CC models of Alzheimer's disease. siRNAs of the invention can be used alone  
CC or in combination with other chemotherapy or apoptosis inducing  
CC treatments for the treatment of prostate cancer, sarcomas such as  
CC osteosarcoma, renal cell carcinoma, breast cancer, bladder cancer, lung  
CC cancer, colon cancer, ovarian cancer, anaplastic large cell lymphoma and  
CC melanoma, and also for the treatment of Alzheimer's disease.  
XX  
SQ Sequence 21 BP; 5 A; 4 C; 5 G; 2 T; 5 U; 0 Other;





XX AC ADL70444;  
XX DT 20-MAY-2004 (first entry)  
XX DE RNAi for human clusterin.  
XX KW Human; clusterin; RNAi; melanoma; cytostatic; gene silencing;  
XX DE short interfering RNA; siRNA; DNA-RNA hybrid; ss.  
XX OS Homo sapiens.  
XX OS Synthetic.  
XX FH Key Location/Qualifiers  
FT modified\_base 18..19  
FT /\*tag= a  
FT /mod\_base= OTHER  
FT /note= "OTHER= TT"  
XX PN WO2004018675-A1.  
XX PD 04-MAR-2004.  
XX PF 21-AUG-2003; 2003WO-CA001276.  
XX PR 21-AUG-2002; 2002US-0405193P.  
XX PR 03-SEP-2002; 2002US-0408152P.  
XX PR 02-DEC-2002; 2002US-0319748P.  
XX PR 20-MAY-2003; 2003US-0472387P.  
XX PA (UYBR-) UNIV BRITISH COLUMBIA.  
XX PA (GLEA/) GLEAVE M E.  
XX PI Jansen B;  
XX DR WPI; 2004-226851/21.  
XX PT Treating melanoma in a mammalian subject comprises administering to the  
XX PT subject a therapeutic agent effective to reduce the effective amount of  
XX PT clusterin in the melanoma cells.  
XX PS Claim 20; SEQ ID NO 42; 32pp; English.  
XX CC The present sequence is that of a short interfering RNA (siRNA) molecule  
XX CC targeted to human clusterin ADL70403. The invention relates to the  
XX CC treatment of melanoma through reduction in the effective amount of  
XX CC clusterin. The therapeutic agent may be an antisense oligonucleotide  
XX CC ADL70404-ADL70421 or short interfering RNA (siRNA) ADL70422-ADL70445  
XX CC targeted to clusterin. The siRNAs molecules direct cleavage of clusterin  
XX CC mRNA. A method for regulating expression of bcl-xL in a subject or cell  
XX CC line comprises administering an agent effective to modulate the amount of  
XX CC clusterin expression. In clusterin-expressing cells, expression of bcl-xL  
XX CC is down-regulated when the effective amount of clusterin is reduced. Such  
XX CC inhibition is significant because bcl-xL is known to act as an inhibitor  
XX CC of apoptosis.  
XX SQ Sequence 19 BP; 5 A; 4 C; 5 G; 0 T; 5 U; 0 Other;  
XX  
XX Query Match 1.2%; Score 19; DB 1; Length 19;  
XX Best Local Similarity 73.7%; Pred. No. 52;  
XX Matches 14; Conservative 5; Mismatches 0; Indels 0; Gaps 0;  
XX  
XX QY 48 ATGATGAAGACTCTGCTGC 66  
XX Db 1 AUGAUGAGACUCUGCUGC 19  
XX  
XX RESULT 174  
XX ADL70445/c  
XX ID ADL70445 standard; RNA; 19 BP.  
XX AC ADL70445;  
XX XX

DT 20-MAY-2004 (first entry)  
XX RNAi for human clusterin.  
XX DE Human; clusterin; RNAi; melanoma; cytostatic; gene silencing;  
XX KW short interfering RNA; siRNA; DNA-RNA hybrid; ss.  
XX OS Homo sapiens.  
XX OS Synthetic.  
XX FH Key Location/Qualifiers  
FT modified\_base 18..19  
FT /\*tag= a  
FT /mod\_base= OTHER  
FT /note= "OTHER= TT"  
XX PN WO2004018675-A1.  
XX PD 04-MAR-2004.  
XX PF 21-AUG-2003; 2003WO-CA001276.  
XX PR 21-AUG-2002; 2002US-0405193P.  
XX PR 03-SEP-2002; 2002US-0408152P.  
XX PR 02-DEC-2002; 2002US-0319748P.  
XX PR 20-MAY-2003; 2003US-0472387P.  
XX PA (UYBR-) UNIV BRITISH COLUMBIA.  
XX PA (GLEA/) GLEAVE M E.  
XX PI Jansen B;  
XX DR WPI; 2004-226851/21.  
XX PT Treating melanoma in a mammalian subject comprises administering to the  
XX PT subject a therapeutic agent effective to reduce the effective amount of  
XX PT clusterin in the melanoma cells.  
XX PS Claim 20; SEQ ID NO 43; 32pp; English.  
XX CC The present sequence is that of a short interfering RNA (siRNA) molecule  
XX CC targeted to human clusterin ADL70403. The invention relates to the  
XX CC treatment of melanoma through reduction in the effective amount of  
XX CC clusterin. The therapeutic agent may be an antisense oligonucleotide  
XX CC ADL70404-ADL70421 or short interfering RNA (siRNA) ADL70422-ADL70445  
XX CC targeted to clusterin. The siRNAs molecules direct cleavage of clusterin  
XX CC mRNA. A method for regulating expression of bcl-xL in a subject or cell  
XX CC line comprises administering an agent effective to modulate the amount of  
XX CC clusterin expression. In clusterin-expressing cells, expression of bcl-xL  
XX CC is down-regulated when the effective amount of clusterin is reduced. Such  
XX CC inhibition is significant because bcl-xL is known to act as an inhibitor  
XX CC of apoptosis.  
XX SQ Sequence 19 BP; 5 A; 5 C; 4 G; 0 T; 5 U; 0 Other;  
XX  
XX Query Match 1.2%; Score 19; DB 1; Length 19;  
XX Best Local Similarity 100.0%; Pred. No. 52;  
XX Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
XX  
XX QY 48 ATGATGAAGACTCTGCTGC 66  
XX Db 19 ATGATGAAGACTCTGCTGC 1  
XX  
XX RESULT 175  
XX ADL70465/c  
XX ID ADL70465 standard; RNA; 21 BP.  
XX AC ADL70465;  
XX XX  
XX DT 20-MAY-2004 (first entry)  
XX DE RNAi for human clusterin.

RNA interference; RNAi; short interfering RNA; siRNA; human; clusterin; cystostatic; neuroprotective; nootropic; gene silencing; DNA-RNA hybrid; ss.	Key	Location/Qualifiers
Homo sapiens.	modified_base	20..21
Synthetic.	/*tag= a	
	/mod_base= OTHER	
	/note= "OTHER= dTdT"	
W02004018676-R2.		
04-MAR-2004.		
21-AUG-2003; 2003WO-CA001277.		
21-AUG-2002; 2002US-0405193P.		
03-SEP-2002; 2002US-0408152P.		
20-MAY-2003; 2003US-0472387P.		
(UYBR-) UNIV BRITISH COLUMBIA.		
Jansen B, Gleave ME, Signaevsky M, Beraldi E, Trougakos IP; Gonos ES;		
WPI; 2004-226852/21.		
New RNA molecule less than 49 bases and having a sequence effective to mediate degradation or block translation of mRNA that is the transcriptional product of a target gene, useful for treating Alzheimer's disease or cancer.		
Claim 4; SEQ ID NO 10; 63pp; English.		
The present sequence is the antisense strand of a short interfering RNA (siRNA) targeted to human clusterin. The sense strand is also provided ADL70464. The siRNA can be used to interfere with the expression of clusterin. Clusterin, also known as testosterone-repressed prostate message-2 (TRPM-2) or sulfated glycoprotein-2 (SGP-2), is expressed in increased amounts by prostate tumour cells following androgen withdrawal, and has also been shown to be critical for neuritic toxicity in mouse models of Alzheimer's disease. siRNAs of the invention can be used alone or in combination with other chemotherapy or apoptosis inducing treatments for the treatment of prostate cancer, sarcomas such as osteosarcoma, renal cell carcinoma, breast cancer, bladder cancer, lung cancer, colon cancer, ovarian cancer, anaplastic large cell lymphoma and melanoma, and also for the treatment of Alzheimer's disease.		
Sequence 21 BP; 5 A; 5 C; 4 G; 2 T; 5 U; 0 Other;		
Query Match	1.2%;	Score 19; DB 1; Length 21;
Best Local Similarity	100.0%;	Pred. No. 75;
Matches	19; Conservative	0; Mismatches
	0; Indels	0; Gaps
48	ATGATGAAGACTCTGCTGC	66
19	ATGATGAAGACTCTGCTGC	1
RESULT 176		
ADL70431/c		
ADL70431	standard; RNA; 21 BP.	
ADL70431;		
20-MAY-2004	(first entry)	
RNAi for human clusterin.		

KW endocrine disorder; CNS disorder; inflammatory disorder;  
KW chromosome mapping; tissue typing; predictive medicine.  
XX Homo sapiens.

OS  
XX WO200300842-A2.  
FN  
XX

XX  
PD  
XX

XX  
03-JAN-2003.

XX  
04-JUN-2002; 2002WO-US017443.

XX  
04-JUN-2001; 2001US-0295607P.

XX  
04-JUN-2001; 2001US-0295661P.

XX  
06-JUN-2001; 2001US-0296404P.

XX  
06-JUN-2001; 2001US-0296418P.

XX  
07-JUN-2001; 2001US-0296575P.

XX  
11-JUN-2001; 2001US-0297414P.

XX  
12-JUN-2001; 2001US-0295573P.

XX  
12-JUN-2001; 2001US-0297567P.

XX  
14-JUN-2001; 2001US-0298285P.

XX  
15-JUN-2001; 2001US-0298528P.

XX  
18-JUN-2001; 2001US-0299133P.

XX  
19-JUN-2001; 2001US-0299230P.

XX  
21-JUN-2001; 2001US-0299949P.

XX  
22-JUN-2001; 2001US-0300177P.

XX  
26-JUN-2001; 2001US-0300883P.

XX  
28-JUN-2001; 2001US-0301530P.

XX  
28-JUN-2001; 2001US-0301550P.

XX  
03-JUL-2001; 2001US-0302951P.

XX  
31-JUL-2001; 2001US-0308909P.

XX  
14-SEP-2001; 2001US-0322297P.

XX  
25-SEP-2001; 2001US-0324669P.

XX  
03-DEC-2001; 2001US-0337477P.

XX  
14-DEC-2001; 2001US-0341562P.

XX  
21-FEB-2002; 2002US-0358656P.

XX  
21-FEB-2002; 2002US-0359122P.

XX  
22-FEB-2002; 2002US-0358978P.

XX  
22-FEB-2002; 2002US-0359034P.

XX  
22-FEB-2002; 2002US-0359035P.

XX  
22-FEB-2002; 2002US-0359121P.

XX  
27-FEB-2002; 2002US-0359864P.

XX  
01-MAR-2002; 2002US-0360858P.

XX  
12-MAR-2002; 2002US-0363430P.

XX  
12-MAR-2002; 2002US-0363676P.

XX  
10-APR-2002; 2002US-0371346P.

XX  
10-MAY-2002; 2002US-0379444P.

XX  
04-JUN-2002; 2002US-00379444.  
XX  
(CURA-) CURAGEN CORP.

XX  
Agee ML, Anderson DW, Berghs C, Casman SJ, Catterton B;  
PI Dipippo VA, Edinger SR, Eisen A, Ellerman K, Gangolli EA;  
PI Gerlach VL, Gorman L, Guo X, Herrmann JL, Hjalt T, Ji W, Kekuda R;  
PI Khrantsov NV, Li L, Liu X, Malyankar UM, Miller CE, Millet I;  
PI Ort T, Padigaru M, Patturajan M, Pena CEA, Rastelli L, Rieger DK;  
PI Rothenberg ME, Shenoy SG, Shimkets RA, Smithson G, Spaderna SK;  
PI Spytek KA, Stone DJ, Vernet CAM, Zhong H, Zhong M, Alsobrook JT;  
PI Burgess CE, Lepley DM;  
XX  
WPI; 2003-210149/20.

XX  
New isolated NOVX polypeptides and nucleic acid molecules useful for  
XX treating, preventing and diagnosing pathological conditions with NOVX-  
PT associated disorders, such as cancer, obesity, diabetes and inflammatory  
PT or CNS diseases.

XX  
Example B; SEQ ID NO 417; 772pp; English.

XX  
The invention relates to novel isolated polypeptides, mature form of the  
XX polypeptide, a sequence that is 95% identical to the polypeptide or the  
CC polypeptide comprising one or more conservative substitutions. The NOVX  
CC polypeptide is useful for treating or preventing a pathology associated  
CC with the polypeptide e.g. disorders associated with aberrant expression

CC or activity of the polypeptide, such as cancer, diabetes, obesity, and  
CC endocrine, CNS and inflammatory disorders. They can also be used in  
CC various detection and screening assays, chromosome mapping, tissue typing  
CC and predictive medicine. This sequence corresponds to a primer used to  
CC amplify and isolate the coding sequence for one of the polypeptides of  
CC the invention.  
XX

XX  
SQ Sequence 22 BP; 1 A; 7 C; 3 G; 11 T; 0 U; 0 Other;

XX  
Query Match 1.1%; Score 18.8; DB 1; Length 22;  
Best Local Similarity 90.9%; Pred. No. 94;  
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 264 AACCTAGAGAGCCCAAGAAGA 285

DB 22 AAGCTAGAGAGCCCAAGAAGA 1

RESULT 178

AAT41539/c

ID AAT41539 standard; DNA; 18 BP.

XX

AC AAT41539;

XX

DT 24-JUN-1997 (first entry)

XX

DE Human apolipoprotein-J gene exon 7-specific 3' PCR primer.

XX

KW Apolipoprotein J; ApoJ; polymorphism; detection; allele; exon; probe;

KW primer; specific; Alzheimer's disease; polymerase chain reaction; PCR;

XX

OS Synthetic.

XX

PN WO9632502-A1.

XX

PD 17-OCT-1996.

XX

PF 02-APR-1996; 96WO-US004510.

XX

PR 11-APR-1995; 95US-00420291.

XX

PA (UYCO ) UNIV COLUMBIA NEW YORK.

XX

PI Mayeux R, Tycko B;

XX

DR WPI; 1996-477152/47.

XX

PT

PT New oligo:nucleotide specific for apolipoprotein-J polymorphisms - used  
to identify patients susceptible to Alzheimer's disease or prostate  
cancer.

XX

PS Example 1; Page 20; 62pp; English.

XX  
AAT41527-T41541 are exon-specific PCR primers used for the amplification  
of exons 2-8 of the human apolipoprotein-J (ApoJ) gene. The primers were  
used in a method for detecting polymorphisms associated with an allelic  
variation in the ApoJ gene. The oligonucleotide (OG) detects the  
probability of a person developing Alzheimer's disease (AD), preferably  
in patients of African or Hispanic descent. The OG also detects the  
probability of a person developing a cognitive disorder, or a prostatic  
carcinoma. Transgenic mammals expressing an allelic variant of an ApoJ  
gene may be used as a prognostic and diagnostic means for studying AD,  
and to determine the effectiveness of therapeutic drugs

XX  
SQ Sequence 18 BP; 3 A; 4 C; 5 G; 6 T; 0 U; 0 Other;

XX  
Query Match 1.1%; Score 18; DB 1; Length 18;  
Best Local Similarity 100.0%; Pred. No. 60;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1070 CAACGAGTGTCTAAAGTC 1087

|||||

Db 18 CAACGAGCTGCTAAAGTC 1

RESULT 179  
AAT41527  
ID AAT41527 standard; DNA; 18 BP.  
XX  
AC AAT41527;  
XX  
DT 24-JUN-1997 (first entry)  
XX  
DE Human apolipoprotein-J gene exon 2-specific 5' PCR primer.  
XX  
KW Apolipoprotein J; ApoJ; polymorphism; detection; allele; exon; probe;  
KW primer; specific; Alzheimer's disease; polymerase chain reaction; PCR;  
KW diagnosis; ss.  
XX  
OS Synthetic.  
XX  
PN WO9632502-A1.  
XX  
PD 17-OCT-1996.  
XX  
PF 02-APR-1996; 96WO-US004510.  
XX  
PR 11-APR-1995; 95US-00420291.  
XX  
PA (UYCO ) UNIV COLUMBIA NEW YORK.  
XX  
PI Mayeux R, Tycko B;  
XX  
DR WPI; 1996-477152/47.  
XX  
PT New oligo:nucleotide specific for apolipoprotein-J polymorphisms - used  
PT to identify patients susceptible to Alzheimer's disease or prostate  
PT cancer.  
XX  
PS Example 1; Page 20; 62pp; English.  
XX  
CC AAT41527-T41541 are exon-specific PCR primers used for the amplification  
CC of exons 2-8 of the human apolipoprotein-J (ApoJ) gene. The primers were  
CC used in a method for detecting polymorphisms associated with an allelic  
CC variation in the ApoJ gene. The oligonucleotide (OG) detects the  
CC probability of a person developing Alzheimer's disease (AD), preferably  
CC in patients of African or Hispanic descent. The OG also detects the  
CC probability of a person developing a cognitive disorder, or a prostatic  
CC carcinoma. Transgenic mammals expressing an allelic variant of an ApoJ  
CC gene may be used as a prognostic and diagnostic means for studying AD,  
CC and to determine the effectiveness of therapeutic drugs  
XX  
SQ Sequence 18 BP; 7 A; 5 C; 4 G; 2 T; 0 U; 0 Other;  
Query Match 1.1%; Score 18; DB 1; Length 18;  
Best Local Similarity 100.0%; Pred. No. 60;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 22 CGTGCAAGACTCCAGAA 39  
Db 1 CGTGCAAGACTCCAGAA 18

RESULT 180  
AAT39501/c  
ID AAT39501 standard; DNA; 18 BP.  
XX  
AC AAT39501;  
XX  
DT 21-MAY-1997 (first entry)  
XX  
DE Chromosome 8p clustrin gene (CL1) specific primer (nt 2836-2854).  
XX  
KW Chromosome 8p; polymerase chain reaction; PCR; primer; CL1;  
KW clustrin gene; human; steroidogenesis; acute regulatory protein;  
KW

XX regional mapping; confirmation; hSTAR; ss.  
XX Synthetic.  
XX WO9629338-A1.  
XX  
PD 26-SEP-1996.  
XX  
PF 22-MAR-1996; 96WO-US003896.  
XX  
PR 23-MAR-1995; 95US-00410540.  
XX  
PA (REGC ) UNIV CALIFORNIA.  
XX (UYPE-) UNIV PENNSYLVANIA.  
XX  
PI Miller WL, Lin D, Strauss JF;  
XX  
DR WPI; 1996-443130/44.  
XX  
PT Isolated human steroidogenesis acute regulatory protein gene - used for  
PT detection of mutation(s) of this gene that cause congenital lipoid  
PT adrenal hyperplasia.  
XX  
PS Example 7; Page 51; 89pp; English.  
XX  
CC The present sequence is a human chromosome 8p clustrin gene (CL1)  
CC specific PCR primer, which was used in the confirmation of the regional  
CC mapping of the human steroidogenesis acute regulatory protein (hSTAR)  
XX  
SQ Sequence 18 BP; 3 A; 5 C; 6 G; 4 T; 0 U; 0 Other;  
Query Match 1.1%; Score 18; DB 1; Length 18;  
Best Local Similarity 100.0%; Pred. No. 60;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1475 GAGAGCTCTGCACGTCAC 1492  
Db 18 GAGAGCTCTGCACGTCAC 1

RESULT 181  
ABN99657  
ID ABN99657 standard; DNA; 18 BP.  
XX  
AC ABN99657;  
XX  
DT 16-AUG-2002 (first entry)  
XX  
DE Human clustrin PCR primer 1.  
XX  
KW Human; antisense inhibition; antisense oligonucleotide; clustrin;  
KW hypercholesterolaemia; cardiovascular disorder; ss; PCR; primer;  
KW hyperproliferative disorder; hyperlipidemic disorder.  
XX  
OS Homo sapiens.  
XX  
PN WO200222635-A1.  
XX  
PD 21-MAR-2002.  
XX  
PF 10-SEP-2001; 2001WO-US028235.  
XX  
PR 11-SEP-2000; 2000US-00659791.  
XX  
PA (ISIS-) ISIS PHARM INC.  
XX  
PI Monia BP, Freier SM;  
XX  
DR WPI; 2002-404805/43.  
XX  
PT Novel antisense compound targeted to nucleic acid molecule encoding  
PT clustrin, useful for treating animal having disease associated with  
PT clustrin such as hyperlipidemic disorder, cardiovascular disorder.



XX Example 13; Page 80; 125pp; English.

XX The invention comprises antisense oligonucleotides that are capable of

CC inhibiting expression of the human clusterin gene. The antisense

CC oligonucleotides of the invention are useful for inhibiting the

CC expression of clusterin in cells. The antisense oligonucleotides are also

CC useful for treating an animal with a disease or condition associated with

CC clusterin (e.g. hypercholesterolemia; cardiovascular disorders;

CC hyperproliferative disorders; and hyperlipidemic disorders). The present

CC DNA sequence represents a PCR primer used to amplify the human clusterin

CC gene

XX

SQ Sequence 18 BP; 4 A; 7 C; 4 G; 3 T; 0 U; 0 Other;

Query Match 1.1%; Score 18; DB 1; Length 18;

Best Local Similarity 100.0%; Pred. No. 60;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 746 TCCGTACGAGCCCTGAA 763

|||||

Db 1 TCCGTACGAGCCCTGAA 18

RESULT 182

ACF36409/C

ID ACF36409 standard; DNA; 21 BP.

XX

AC ACF36409;

XX

DT 18-DEC-2003 (first entry)

XX

DE DNA sequence of a TRPM-2 mismatch control oligonucleotide.

XX

TRPM-2; testosterone-repressed prostate message-2; cytostatic; androgen;

KW prostate cancer; anti-apoptotic protein; antisense; ss.

XX

OS Synthetic.

XX

PN WO2003072591-A1.

XX

PD 04-SEP-2003.

XX

PF 20-FEB-2003; 2003WO-US005305.

XX

PR 22-FEB-2002; 2002US-00080794.

XX

PA (UYBR-) UNIV BRITISH COLUMBIA.

XX

PI Gleave M, Rennie PS, Miyake H, Nelson C, Monia BP;

XX

DR WPI; 2003-689981/65.

XX

PT New modified antisense oligonucleotide, useful particularly for treating

PT prostatic cancer, inhibits the testosterone-repressed prostate message-2.

XX

PS Example 13; Page 20; 44pp; English.

XX

CC The invention relates to a compound consisting of an oligonucleotide with

CC a phosphorothioate backbone throughout, in which: (a) sugars on

CC nucleotide residues 1-4 and 18-21 are 2'-O-methoxyethyl modified, and the

CC remaining nucleotides 5-17 are 2'-deoxy; and (b) the cytosines at

CC positions 1, 4 and 19 are 5-methylated. Oligonucleotide shown in sequence

CC ACF36398 (I) is used: (a) to delay progression of androgen-sensitive

CC prostatic cancer cells to the androgen-independent state, in vivo or in

CC vitro; (b) to treat prostatic cancer (after initially withdrawing

CC androgens to induce apoptosis); and (c) to increase sensitivity of cancer

CC cells (prostatic, renal, non-small cell lung, urothelial transitional,

CC ovarian and some breast cancer cells) that express abnormal levels of

CC TRPM-2 to chemotherapy or radiation. The modifications present in (I)

CC increase stability in vivo and activity (both in vivo or in vitro) and

CC result in a synergistic increase in effect when (I) is used with

CC chemotherapeutic agents or other antisense oligonucleotides directed

CC against other antiapoptotic genes. The present sequence represents a

CC mismatch control oligonucleotide, used in antisense assays of anti-

CC apoptotic protein TRPM-2 (testosterone-repressed prostate message-2)

XX

SQ Sequence 21 BP; 7 A; 4 C; 4 G; 6 T; 0 U; 0 Other;

Query Match 1.1%; Score 17.8; DB 1; Length 21;

Best Local Similarity 90.5%; Pred. No. 1.1e+02;

Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 48 ATGATGAAGACTCTGCTGCTG 68

|||||

Db 21 ATGATAAATACTCTGCTGCTG 1

RESULT 183

ADM83080/C

ID ADM83080 standard; DNA; 21 BP.

XX

AC ADM83080;

XX

DT 03-JUN-2004 (first entry)

XX

DE Control TRPM-2 mismatch oligonucleotide.

XX

KW Testosterone-repressed prostate message-2; TRPM-2; chemo-sensitivity;

KW radiation-sensitivity; prostate cancer; bladder cancer; ovarian cancer;

KW lung cancer; renal cell carcinoma; RCC; antisense gene therapy; ss.

XX

OS Unidentified.

XX

PN US2003158130-A1.

XX

PD 21-AUG-2003.

XX

PF 28-SEP-2001; 2001US-00967726.

XX

PR 25-FEB-2000; 2000WO-US004875.

PR 28-SEP-2000; 2000US-0236301P.

PR 10-AUG-2001; 2001US-00913325.

XX

PA (GLEA/) GLEAVE M.

PA (RENN/) RENNIE P S.

PA (MIYA/) MIYAKE H.

PA (NELS/) NELSON C.

PA (ZELL/) ZELLWEGER T.

XX

PI Gleave M, Rennie PS, Miyake H, Nelson C, Zellweger T;

XX

DR WPI; 2003-778017/73.

XX

PT Enhancing the chemo-sensitivity or radiation-sensitivity of cancer cells

PT that expresses testosterone-repressed prostate message-2 (TRPM-2)

PT comprises administering a composition that inhibits expression of TRPM-2.

XX

PS Disclosure; SEQ ID NO 15; 14pp; English.

XX

CC The present invention provides a method for treating cancer in which

CC cancer cells express testosterone-repressed prostate message-2 (TRPM-2).

CC The invention is useful for enhancing the chemo-sensitivity or radiation-

CC sensitivity of cancer cells for treating cancer such as prostate cancer,

CC bladder cancer, ovarian cancer, lung cancer and renal cell carcinoma

CC (RCC). The invention is also useful in antisense gene therapy. The

CC present sequence is control testosterone-repressed prostate message-2

CC (TRPM-2) mismatch oligonucleotide. The oligonucleotide is used in the

CC exemplification of the invention.

XX

SQ Sequence 21 BP; 7 A; 4 C; 4 G; 6 T; 0 U; 0 Other;

Query Match 1.1%; Score 17.8; DB 1; Length 21;

Best Local Similarity 90.5%; Pred. No. 1.1e+02;

Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```

QY 48 ATGATGAAGACTCTGCTGCTG 68
Db 21 ATGATAAATACTCTGCTGCTG 1

RESULT 184
AAT41526
ID AAT41526 standard; DNA; 17 BP.
XX AAT41526;
AC AAT41526;
XX 24-JUN-1997 (first entry)
XX Human apolipoprotein-J gene J3-allelic variant primer/probe.
XX Apolipoprotein J; ApoJ; polymorphism; detection; allele; exon; probe;
KW primer; specific; Alzheimer's disease; polymerase chain reaction; PCR;
KW diagnosis; ss.
XX Synthetic.
XX OS Synthetic.
XX WO9632502-A1.
XX 17-OCT-1996.
XX 02-APR-1996; 96WO-US004510.
XX 11-APR-1995; 95US-00420291.
XX (UYCO ) UNIV COLUMBIA NEW YORK.
XX Mayeux R, Tycko B;
XX WPI; 1996-477152/47.
XX New oligo:nucleotide specific for apolipoprotein-J polymorphisms - used
PT to identify patients susceptible to Alzheimer's disease or prostate
PT cancer.
XX Claim 29; Page 41; 62pp; English.
XX AAT41526 is a primer/probe used to detect a J3 allelic variation in the
CC human apolipoprotein-J (ApoJ) gene. The primer/probe is used for
CC detecting polymorphisms associated with an allelic variation in the ApoJ
CC gene. The oligonucleotide (OG) detects the probability of a person
CC developing Alzheimer's disease (AD), preferably in patients of African or
CC Hispanic descent. The OG also detects the probability of a person
CC developing a cognitive disorder, or a prostatic carcinoma. Transgenic
CC mammals expressing an allelic variant of an ApoJ gene may be used as a
CC prognostic and diagnostic means for studying AD, and to determine the
CC effectiveness of therapeutic drugs
XX Sequence 17 BP; 4 A; 6 C; 4 G; 3 T; 0 U; 0 Other;

Query Match 1.0%; Score 17; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 68;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1023 GAGCTCGACGATCCCT 1039
Db 1 GAGCTCGACGATCCCT 17

RESULT 185
AAT41542
ID AAT41542 standard; DNA; 17 BP.
XX AAT41542;
AC AAT41542;
XX 24-JUN-1997 (first entry)
XX Human apolipoprotein-J gene J1-allelic specific primer/probe.
XX Apolipoprotein J; ApoJ; polymorphism; detection; allele; exon; probe;
KW primer; specific; Alzheimer's disease; polymerase chain reaction; PCR;
KW diagnosis; ss.
XX Synthetic.
XX OS Synthetic.
XX WO9632502-A1.
XX 17-OCT-1996.
XX 02-APR-1996; 96WO-US004510.
XX 11-APR-1995; 95US-00420291.
XX (UYCO ) UNIV COLUMBIA NEW YORK.
XX Mayeux R, Tycko B;
XX WPI; 1996-477152/47.
XX New oligo:nucleotide specific for apolipoprotein-J polymorphisms - used
PT to identify patients susceptible to Alzheimer's disease or prostate
PT cancer.
XX Claim 29; Page 41; 62pp; English.
XX AAT41542 and AAT41543 are J1 allele-specific primer/probes used as
CC controls in an example of a method for detecting polymorphisms associated
CC with an allelic variation in the human apolipoprotein-J (ApoJ) gene. The
CC oligonucleotide (OG) detects the probability of a person developing
CC Alzheimer's disease (AD), preferably in patients of African or Hispanic
CC descent. The OG also detects the probability of a person developing a
CC cognitive disorder, or a prostatic carcinoma. Transgenic mammals
CC expressing an allelic variant of an ApoJ gene may be used as a prognostic
CC and diagnostic means for studying AD, and to determine the effectiveness
CC of therapeutic drugs
XX Sequence 17 BP; 5 A; 8 C; 1 G; 3 T; 0 U; 0 Other;

Query Match 1.0%; Score 17; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 68;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 984 TGTTCACCAACCAACCC 1000
Db 1 TGTTCACCAACCAACCC 17

RESULT 186
ABT34616
ID ABT34616 standard; DNA; 17 BP.
XX ABT34616;
AC ABT34616;
XX 12-JUN-2003 (first entry)
XX Tumour suppression related human fukutin oligo SEQ ID No 253.
XX Cytostatic; virucide; neuroprotective; nootropic; neuroleptic; gene chip;
KW antisense; sense; tumour; cell degeneration; cancer; Alzheimer's disease;
KW schizophrenia; protein chip; gene therapy; tumour suppression;
KW human fukutin; ds.
XX Homo sapiens.
XX OS Homo sapiens.
XX WO2003025175-A2.
XX 27-MAR-2003.
XX 17-SEP-2002; 2002WO-IB004208.
XX 17-SEP-2001; 2001FR-00011978.
XX

```

PA (MOLE-) MOLECULAR ENGINES LAB.  
 XX  
 PI Telerman A, Amson R, Tuijnder M;  
 XX  
 DR WPI; 2003-313353/30.  
 XX  
 DR  
 XX  
 XX New isolated nucleic acid, useful for treating viral diseases associated  
 PT with tumors and cell degeneration, also related polypeptides, antibodies  
 PT and transfected cells.  
 PT  
 XX  
 XX Disclosure; Page 63; 720pp; French.  
 PS  
 XX  
 CC The invention relates to a novel isolated 17 mer nucleic acid sequence,  
 CC given in the specification, a sequence containing at least 15 consecutive  
 CC nucleotides from the 17 mer sequence, a sequence with, after optimal  
 CC alignment, at least 80 % identity to the 17 mer sequence, a sequence that  
 CC hybridizes to them under highly stringent conditions, or the complement  
 CC of any of them, or the corresponding RNA. The novel isolated nucleic  
 CC acids of the invention are useful as probes and primers for detecting,  
 CC identifying, quantifying and/or amplifying a nucleic acid, e.g. as one  
 CC component of a gene chip, in vitro as (anti)sense reagents, and for  
 CC production of recombinant polypeptides. Any of the nucleic acids,  
 CC polypeptides, vectors containing the nucleic acids, cells containing the  
 CC vector or antibodies directed against the polypeptides are useful for  
 CC preparation of pharmaceuticals for prevention and/or treatment of viral  
 CC diseases that are characterised by development of tumours or cell  
 CC degeneration, specifically cancer but also Alzheimer's disease and  
 CC schizophrenia. Analysis of the expression of the 17 mer nucleic acids in  
 CC patient samples is useful for diagnosis and/or prognosis of these  
 CC diseases. The polypeptides can also be used to generate antibodies, and  
 CC both the polypeptide and antibodies are useful as components of protein  
 CC chips. The nucleic acid sequences of the invention can be used in gene  
 CC therapy. This polynucleotide sequence represents a tumour suppression  
 CC related human fukutin oligonucleotide of the invention  
 CC  
 XX  
 SQ Sequence 17 BP; 5 A; 6 C; 2 G; 4 T; 0 U; 0 Other;  
 Query Match 1.0%; Score 17; DB 1; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 68;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1551 GATCCTGCACCTTAACA 1567  
 Db 1 GATCCTGCACCTTAACA 17  
 RESULT 187  
 ADB45708  
 ID ADB45708 standard; DNA; 17 BP.  
 XX  
 AC ADB45708;  
 XX  
 DT 18-DEC-2003 (first entry)  
 XX  
 DE Tumour suppression/reversion associated nucleotide #6031.  
 XX  
 KW cytotatic; antiviral; neuroprotective; nootropic; neuroleptic; ss;  
 KW Primer; probe; tumour suppression; tumour reversion; apoptosis;  
 KW virus resistance; transgenic animals; Alzheimer's disease; schizophrenia;  
 KW diagnosis.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO2003040369-A2.  
 XX  
 PD 15-MAY-2003.  
 XX  
 PF 17-SEP-2002; 2002WO-IB004219.  
 XX  
 PR 17-SEP-2001; 2001FR-00011981.  
 XX  
 PA (MOLE-) MOLECULAR ENGINES LAB.  
 XX  
 PI Telerman A, Amson R, Tuijnder M;  
 XX  
 DR WPI; 2003-441574/41.  
 XX  
 DR New nucleic acid encoding human prostate membrane-specific antigen,  
 PT useful e.g. for treatment of tumors and viral infection, also related  
 PT polypeptide and antibodies.  
 PT  
 XX  
 XX Disclosure; Page 737; 771pp; French.  
 PS  
 XX  
 CC The invention relates to the isolation of 6327 nucleotide sequences,  
 CC fragments of at least 15 consecutive nucleotides of these nucleotides, a  
 CC sequence having at least 80% identity, after optimal alignment, with the  
 CC nucleotides, a sequence that hybridizes under stringent conditions with  
 CC the nucleotides, or the complement, or corresponding RNA, of the  
 CC nucleotides. The nucleotides are used as probes or primers for detecting,  
 CC identifying, quantifying and/or amplifying nucleic acids, as in vitro  
 CC sense and antisense sequences, of nucleotides involved in tumour  
 CC suppression or reversion, apoptosis and or viral resistance, to produce  
 CC recombinant polypeptides, and to prepare transgenic animals, as  
 CC experimental models. The nucleotides (also vectors containing them and  
 CC cells containing the vectors), the encoded polypeptides and antibodies  
 CC (Ab) against the polypeptide are useful for prevention and/or treatment  
 CC of viral infections or diseases characterized by development of tumours  
 CC or cell degeneration (e.g. Alzheimer's disease or schizophrenia).  
 CC Analysis of the expression of the nucleotides can be used for diagnosis  
 CC and/or prognosis of these diseases. The nucleotides and polypeptides can  
 CC also be used to screen for their specific interactive molecules,  
 CC potentially useful for treating diseases associated with abnormal  
 CC expression of the nucleotides.  
 XX  
 SQ Sequence 17 BP; 5 A; 6 C; 2 G; 4 T; 0 U; 0 Other;  
 Query Match 1.0%; Score 17; DB 1; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 68;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1551 GATCCTGCACCTTAACA 1567  
 Db 1 GATCCTGCACCTTAACA 17  
 RESULT 188  
 AAQ58405/c  
 ID AAQ58405 standard; DNA; 20 BP.  
 XX  
 AC AAQ58405;  
 XX  
 DT 25-MAR-2003 (revised)  
 DT 04-OCT-1994 (first entry)  
 XX  
 DE Antisense oligonucleotide CAS-110-G-119 to HCV 5'-UTR.  
 XX  
 KW Hepatitis C virus; HCV; non-A, non-B hepatitis virus; NANBHV;  
 KW antisense oligonucleotide; translation inhibition; therapy; 5'-UTR;  
 KW 5'-untranslated region; loop C; ss.  
 XX  
 OS Synthetic.  
 XX  
 PN WO9405813-A1.  
 XX  
 PD 17-MAR-1994.  
 XX  
 PF 10-SEP-1993; 93WO-JP001293.  
 XX  
 PR 10-SEP-1992; 92US-00945289.  
 PR 14-APR-1993; 93JP-00087195.  
 XX  
 XX (MOCH ) MOCHIDA PHARM CO LTD.  
 PA (KACA ) CEMO SERO THERAPEUTIC RES INST.  
 PA (ISIS-) ISIS PHARM INC.  
 XX  
 XX Anderson KP, Hanecak RC, Hoshiko K, Nozaki C, Nishihara T;

PI Nakatake H, Hamada F, Eto T, Furukawa S;  
XX WPI; 1994-101217/12.  
XX Anti-sense oligo:nucleotide(s) complementary to hepatitis C viral genome  
PT - useful for inhibiting HCV replication, to treat related diseases.  
XX  
XX Example 7; Page 24; 91pp; English.  
XX  
XX Antisense oligonucleotides were synthesised which are complementary to  
CC target sequences located at 10-nucleotide intervals from nucleotide 1 to  
CC 339 in the HCV RNA 5'-untranslated region. Of these sequences (CAS-1 to  
CC CAS-320), oligonucleotide CAS-110 (AAQ58403), which is complementary to a  
CC portion of loop C, was found to cause greater than 80% inhibition of core  
CC protein translation. The nucleotide at position 119 in loop C has a high  
CC variation rate among HCV strains so oligonucleotide CAS-110-I-119 was  
CC synthesised in which inosine replaced the T (corresp. to A at position  
CC 119) in CAS-110. The CAS-110-I-119 showed an inhibitory activity of more  
CC than 70%. A control oligonucleotide (CAS-110-G-119) showed much lower  
CC activity. See AAQ58388-Q58422, AAQ44885-Q44892 and AAQ58383. (Updated on  
CC 25-MAR-2003 to correct PN field.)  
XX  
XX Sequence 20 BP; 2 A; 3 C; 14 G; 1 T; 0 U; 0 Other;  
SQ  
Query Match 1.0%; Score 16.8; DB 1; Length 20;  
Best Local Similarity 90.0%; Pred. No. 1.3e+02;  
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 1510 GCCTCAGGCCCCCACTCC 1529  
Db 20 GCCTCAGGCCCCCCCCCTCC 1  
RESULT 189  
ADN02449/C  
ID ADN02449 standard; DNA; 20 BP.  
XX  
XX ADN02449;  
XX  
XX 17-JUN-2004 (first entry)  
XX  
XX Western equine encephalomyelitis virus 26S region PCR primer WEEP2.  
XX  
XX ss; expression vector; western equine encephalitis; WEE;  
KW anti-encephalitis; Venezuelan equine encephalitis virus; encephalitis;  
KW PCR; primer.  
XX  
XX Western equine encephalomyelitis virus.  
XX  
XX CA2327189-A1.  
XX  
XX 21-JUN-2002.  
XX  
XX 21-DEC-2000; 2000CA-02327189.  
XX  
XX 21-DEC-2000; 2000CA-02327189.  
XX  
XX (MIND ) CANADA MIN NAT DEFENCE.  
XX  
XX Wong JP, Nagata LP;  
PI WPI; 2002-600289/65.  
DR  
XX A western equine encephalitis (WEE) virus strain used to develop DNA  
PT vaccines to WEE virus and related alphaviruses.  
PT  
XX Disclosure; Page 28; 52pp; English.  
XX  
XX The invention relates to a novel mammalian expression vector, under which  
CC expression of the structural genes of western equine encephalitis (WEE)  
CC virus strain 71V-1658 have been placed under the control of a eukaryotic  
CC promoter. The expression vector has anti-encephalitis activity. The  
CC invention provides a means of developing a vaccine to the WEE virus which

CC is important for protection against an aerosol challenge of WEE used in  
CC biological warfare. The prophylactic method of the invention is used for  
CC inducing a protective immune response to eastern equine encephalitis  
CC virus and Venezuelan equine encephalitis virus in a mammal. The present  
CC sequence represents a WEE virus 26S region PCR primer.  
XX  
XX Sequence 20 BP; 2 A; 7 C; 6 G; 5 T; 0 U; 0 Other;  
SQ  
Query Match 1.0%; Score 16.8; DB 1; Length 20;  
Best Local Similarity 90.0%; Pred. No. 1.3e+02;  
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 524 CGACTCCCTGCTCGAGAACG 543  
Db 20 CGACACGCTGCTCGAGAACG 1  
RESULT 190  
AAQ68062/C  
ID AAQ68062 standard; DNA; 16 BP.  
XX  
XX AAQ68062;  
XX  
XX 25-MAR-2003 (revised)  
DT 19-DEC-1994 (first entry)  
XX  
XX Antisense probe 155 for HCV LiPA typing.  
DE  
XX Hepatitis C virus; HCV; probe; genotyping; hybridisation;  
KW non-A, non-B hepatitis; NANBH; amplification; primer;  
KW polymerase chain reaction; PCR; line probe assay; LiPA; ss.  
XX  
XX Synthetic.  
OS  
XX WO9412670-A2.  
FN  
XX 09-JUN-1994.  
PD  
XX 26-NOV-1993; 93WO-EP003325.  
PF  
XX 27-NOV-1992; 92EP-00403222.  
PR  
XX 31-AUG-1993; 93EP-00402129.  
XX  
XX (INNO-) INNOGENETICS NV SA.  
PA  
XX Maertens G, Stuyver L, Rossau R, Van Heuverswyn H;  
PI WPI; 1994-200296/24.  
DR  
XX Process for genotyping Hepatitis C virus (HCV) isolates - utilises probes  
PT hybridising to HCV isolate domains.  
PT  
XX Disclosure; Page 29; 96pp; English.  
PS  
XX Genotyping HCV utilises probes hybridising to HCV isolate domains. HCV  
CC types 2, 3, 4, 5 or 6 and subtypes 1a, 1b, 2a, 2b, 3a, 3b, 3c, 4a, 4b,  
CC 4c, 4d, 4e, 4f, 4g and 4h can be typed. Antisense probe 155 was used in  
CC the identification of type 4 isolates. (Updated on 25-MAR-2003 to correct  
CC PN field.)  
XX  
XX Sequence 16 BP; 1 A; 3 C; 10 G; 2 T; 0 U; 0 Other;  
SQ  
Query Match 1.0%; Score 16; DB 1; Length 16;  
Best Local Similarity 100.0%; Pred. No. 75;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1508 CAGCCTCCAGGCCCCC 1523  
Db 16 CAGCCTCCAGGCCCCC 1  
RESULT 191  
AAQ14650

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ID AAX14650 standard; DNA; 17 BP.
XX
AC AAX14650;
XX
DT 24-MAR-1999 (first entry)
XX
DE Triple helix forming nucleotides 5967-5983 of the dystrophin gene.
XX
KW Triple-helix forming region; Triplex formation; DNA detection;
KW identification; bacteria; oncogene; virus; ds.
XX
OS Homo sapiens.
XX
PN US5861244-A.
XX
PD 19-JAN-1999.
XX
PF 22-DEC-1993; 93US-00173489.
XX
PR 29-OCT-1992; 92US-00968436.
XX
PA (PROF-) PROFILE DIAGNOSTIC SCI INC.
XX
PI Hepburn AG, Wang C;
XX
DR WPI; 1999-130384/11.
XX
PT Assay of genetic sequences based on triplex formation from double
PT stranded analyte - and hybrid of anchor and reporter sequences, with
PT reporter released if triplex formation occurs, used e.g. to identify
PT bacteria.
XX
PS Disclosure; Col 15-16; 168pp; English.
XX
CC The present sequence represents a potential triple-helix forming region.
CC It can be used to demonstrate the assay of the invention. The assay
CC comprises adding a sample containing double-stranded DNA test sequences,
CC e.g. containing the present sequence, to an aqueous medium containing at
CC least one complex of anchor DNA, attached to a solid support, and
CC reporter DNA, where either a part of the anchor DNA or reporter DNA is
CC designed to form a triple-strand structure with part of the test
CC sequence. Triplex formation results in displacement of the reporter DNA
CC which is detected as an indication of the presence of the DNA test
CC sequence. The method is used to detect DNA sequences, particularly for
CC identification of bacteria (by detecting genes for ribosomal RNA) in
CC clinical samples, but also detection of oncogenes and Hepatitis B virus
XX
SQ Sequence 17 BP; 10 A; 0 C; 7 G; 0 T; 0 U; 0 Other;

Query Match 1.0%; Score 16; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 94;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 280 AGAAGAGAGAGAGGGA 295
Db 1 AGAAGAGAGAGAGGGA 16

RESULT 192
ADS00161/c
ID ADS00161 standard; RNA; 19 BP.
XX
AC ADS00161;
XX
DT 16-DEC-2004 (first entry)
XX
DE Duchenne muscular dystrophy gene-specific antisense oligonucleotide #7.
XX
KW antisense oligonucleotide; Duchenne muscular dystrophy gene; DMD gene;
KW pre-mRNA recognition alteration; inherited disease;
KW pre-mRNA exon skipping induction; splicing machinery efficiency; ss.
XX
OS Unidentified.

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XX Key Location/Qualifiers
FH modified_base 1..19
FT /*tag= a
FT /mod_base= OTHER
FT /note= "OTHER = Phosphorothioate backbone"
XX
PN WO2004083432-A1.
XX
PD 30-SEP-2004.
XX
PF 21-MAR-2003; 2003WO-NL000214.
XX
PR 21-MAR-2003; 2003WO-NL000214.
XX
PA (ZIEK-) ACAD ZIEKENHUIS LEIDEN.
XX
PI Van Ommen GB, Van Deutekom JCT, Den Dunnen JT, Aartsma-Rus A;
XX
DR WPI; 2004-691055/67.
XX
PT Generating an oligonucleotide for treating diseases, comprises
PT determining from a structure of RNA from an exon, a region that assumes a
PT structure hybridized to another part of the RNA and a region that is not
PT hybridized in the structure.
XX
PS Example 2; Page 48; 71pp; English.
XX
CC The invention comprises a method for generating an oligonucleotide
CC involving: determining from a secondary structure of RNA from an exon, a
CC region that assumes a structure that is hybridized to another part of the
CC RNA (closed structure) and a region that is not hybridized in the
CC structure (open structure); and subsequently generating an
CC oligonucleotide, where at least one part of the oligonucleotide is
CC complementary to the closed structure and at least one part of the
CC oligonucleotide is complementary to the open structure. The gene from
CC which the RNA comprising the exon is transcribed, may be selected from:
CC an aberrant Duchenne muscular dystrophy gene (DMD), a collagen VI alpha 1
CC gene (COL6A1), a myotubular myopathy 1 gene (MTM1), a dysferlin gene
CC (DYSF), a laminin-alpha 2 gene (LAMA2), an emery-dreyfuss muscular
CC dystrophy gene (EMD), and/or a calpain 3 gene (CAPN3). The
CC oligonucleotides produced by the method of the invention are useful for:
CC for the treatment of an inherited disease; for inducing exon skipping in
CC a pre-mRNA; for altering exon-recognition in a pre-mRNA; and for altering
CC the efficiency with which a splice donor or splice acceptor sequence is
CC used by a splicing machinery. The present RNA sequence represents an
CC antisense oligonucleotide that is targeted to the DMD gene.
XX
SQ Sequence 19 BP; 0 A; 8 C; 1 G; 0 T; 10 U; 0 Other;

Query Match 1.0%; Score 16; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 280 AGAAGAGAGAGAGGGA 295
Db 17 AGAAGAGAGAGAGGGA 2

RESULT 193
ADS73873/c
ID ADS73873 standard; RNA; 19 BP.
XX
AC ADS73873;
XX
DT 16-DEC-2004 (first entry)
XX
DE DMD gene specific antisense oligonucleotide h41A0N1.
XX
KW DMD; Duchenne muscular dystrophy; collagen VI alpha 1; COL6A1;
KW myotubular myopathy 1; MTM1; dysferlin; DYSF; laminin-alpha 2; LAMA2;
KW emery-dreyfuss muscular dystrophy; EMD; calpain 3; CAPN3; antisense; ss.
XX

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OS Synthetic.  
FN WO2004083446-A2.  
XX  
PD 30-SEP-2004.  
XX  
PF 22-MAR-2004; 2004WO-NL000196.  
XX  
XX 21-MAR-2003; 2003WO-NL000214.  
XX  
XX (ZIEK-) ACAD ZIEKENHUIS LEIDEN.  
XX  
XX Van Ommeren GB, Van Deutekom JCT, Den Dunnen JT, Aartsma-Rus A;  
PI WPI; 2004-691060/67.  
XX  
DR Generating an oligonucleotide for treating diseases, comprises  
XX determining from a structure of RNA from an exon, a region that assumes a  
PT structure hybridized to another part of the RNA and a region that is not  
PT hybridized in the structure.  
XX  
PS Example 1; Page 88; 117pp; English.  
XX  
XX The invention relates to generating an oligonucleotide and involves  
CC determining from a secondary structure of RNA from an exon, a region that  
CC assumes a structure that is hybridized to another part of the RNA (closed  
CC structure) and a region that is not hybridized in the structure (open  
CC structure), and subsequently generating an oligonucleotide, where at  
CC least a part of the oligonucleotide is complementary to the closed  
CC structure and at least another part of the oligonucleotide is  
CC complementary to the open structure. In generating an oligonucleotide,  
CC the open and closed structures are adjacent to each other. The  
CC oligonucleotide is complementary to a consecutive part of 14-50  
CC nucleotides of the RNA. It also comprises RNA, where the RNA contains a  
CC modification, preferably a 2'-O-methyl modified ribose (RNA) or  
CC deoxyribose (DNA) modification. The pre-mRNA comprising the exon exhibits  
CC undesired splicing in a subject. The absence of the exon from mRNA  
CC produced from the pre-mRNA generates a coding region for a protein. The  
CC gene from which the RNA comprising the exon is transcribed encodes an  
CC aberrant Duchenne muscular dystrophy gene (DMD), a collagen VI alpha 1  
CC gene (COL6A1), a myotubular myopathy 1 gene (MTM1), a dysferlin gene  
CC (DYSPF), a laminin-alpha 2 gene (LAMA2), an emery-dreyfuss muscular  
CC dystrophy gene (EMD), and/or a calpain 3 gene (CAPN3). Preferably, the  
CC gene is the DMD gene. The oligonucleotide, its equivalent, or the  
CC compound is useful for at least in part altering recognition of the exon  
CC or exons in a pre-mRNA; for the preparation of a medicament for the  
CC treatment of an inherited disease; for inducing exon skipping in a pre-  
CC mRNA; for altering exon-recognition in a pre-mRNA; for altering the  
CC efficiency with which a splice donor or splice acceptor sequence is used  
CC by a splicing machinery; for inducing exon-skipping of two, three, or  
CC more exons in a pre-mRNA; or for inducing skipping of the at least two  
CC exons and a sequence located between the at least two exons (intervening  
CC sequence) on the pre-mRNA, where intervening sequence further comprises  
CC exon or exons. Sequences ADS73865-ADS73903 represent antisense  
CC oligonucleotides (AONs) used to study targeted skipping of 15 different  
CC DMD exons.  
XX  
SQ Sequence 19 BP; 0 A; 8 C; 1 G; 0 T; 10 U; 0 Other;  
Query Match 1.0%; Score 16; DB 1; Length 19;  
Best Local Similarity 100.0%; Pred. No. 1.4e+02;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
XX  
QY 280 AGAAGAAGAAAGAGGA 295  
Db 17 AGAAGAAGAAAGAGGA 2  
|||||  
RESULT 194  
ADI19217/c  
ID ADI19217 standard; DNA; 20 BP.  
XX  
XX ADI19217;  
AC

XX 22-APR-2004 (first entry)  
XX Human PCTAIRE protein kinase 2 antisense oligonucleotide #71.  
DE  
XX gene therapy; antisense technology; PCTAIRE protein kinase 2;  
XX neurological disorder; human; PCTAIRE protein kinase 2; ss.  
KW  
XX Homo sapiens.  
OS  
XX  
XX  
PH Location/Qualifiers  
FT modified\_base 1..20  
FT /tag= b  
FT /mod\_base= OTHER  
FT /note= "OTHER= Phosphorothioate backbone. All cytidines  
FT are 5-methylcytidines"  
FT modified\_base 1..5  
FT /tag= a  
FT /mod\_base= OTHER  
FT /note= "OTHER= 2'-O-Methoxyethyl (2'-MOE) nucleotides"  
FT modified\_base 15..20  
FT /tag= c  
FT /mod\_base= OTHER  
FT /note= "OTHER= 2'-O-Methoxyethyl (2'-MOE) nucleotides"  
XX  
XX US2003225256-A1.  
XX  
XX 04-DEC-2003.  
XX  
XX 31-MAY-2002; 2002US-00160787.  
XX  
XX 31-MAY-2002; 2002US-00160787.  
XX (ISIS-) ISIS PHARM INC.  
XX Watt AT;  
XX WPI; 2004-022085/02.  
XX  
XX New antisense oligonucleotide, having a sequence targeted to a nucleic  
PT acid encoding PCTAIRE protein kinase 2, useful for preparing a  
PT composition for treating neurological disorders.  
XX  
XX Claim 1; SEQ ID NO 84; 58pp; English.  
XX  
XX The invention describes a new antisense oligonucleotide, having a  
CC sequence comprising 8-80 bp targeted to a nucleic acid encoding PCTAIRE  
CC protein kinase 2, that specifically hybridises with the nucleic acid  
CC encoding PCTAIRE protein kinase 2 and having a sequence comprising 20 bp.  
CC The antisense oligonucleotide is useful for preparing a composition for  
CC treating e.g., neurological disorders. This sequence represents a human  
CC PCTAIRE protein kinase 2 antisense oligonucleotide.  
XX  
SQ Sequence 20 BP; 1 A; 8 C; 2 G; 9 T; 0 U; 0 Other;  
Query Match 1.0%; Score 16; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.6e+02;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1583 CATGGGAAGAACAGAA 1598  
Db 17 CATGGGAAGAACAGAA 2  
|||||  
RESULT 195  
ADI19270  
ID ADI19270 standard; DNA; 20 BP.  
XX  
XX ADI19270;  
XX  
XX 22-APR-2004 (first entry)  
XX Human PCTAIRE protein kinase 2 antisense oligonucleotide #124.  
DE

XX gene therapy; antisense technology; PCTAIRE protein kinase 2;  
 KW neurological disorder; human; PCTAIRE protein kinase 2; ss.  
 XX Homo sapiens.  
 XX Key Location/Qualifiers  
 FH modified\_base 1..20  
 FT /\*tag= b  
 FT /mod\_base= OTHER  
 FT /note= "OTHER= Phosphorothioate backbone. All cytidines  
 FT modified\_base 1..5  
 FT /\*tag= a  
 FT /mod\_base= OTHER  
 FT /note= "OTHER= 2'-O-Methoxyethyl (2'-MOE) nucleotides"  
 FT modified\_base 15..20  
 FT /\*tag= c  
 FT /mod\_base= OTHER  
 FT /note= "OTHER= 2'-O-Methoxyethyl (2'-MOE) nucleotides"  
 FT US2003225256-A1.  
 PN 04-DEC-2003.  
 XX  
 XX 31-MAY-2002; 2002US-00160787.  
 XX  
 XX 31-MAY-2002; 2002US-00160787.  
 XX (ISIS-) ISIS PHARM INC.  
 PA Watt AT;  
 XX  
 XX WPI; 2004-022085/02.  
 XX  
 XX New antisense oligonucleotide, having a sequence targeted to a nucleic  
 PT acid encoding PCTAIRE protein kinase 2, useful for preparing a  
 PT composition for treating neurological disorders.  
 XX  
 XX Example 15; SEQ ID NO 137; 58pp; English.  
 PS  
 CC The invention describes a new antisense oligonucleotide, having a  
 CC sequence comprising 8-80 bp targeted to a nucleic acid encoding PCTAIRE  
 CC protein kinase 2, that specifically hybridises with the nucleic acid  
 CC encoding PCTAIRE protein kinase 2 and having a sequence comprising 20 bp.  
 CC The antisense oligonucleotide is useful for preparing a composition for  
 CC treating e.g., neurological disorders. This sequence represents a human  
 CC PCTAIRE protein kinase 2 antisense oligonucleotide.  
 XX  
 XX Sequence 20 BP; 9 A; 2 C; 8 G; 1 T; 0 U; 0 Other;  
 SQ  
 Query Match 1.0%; Score 16; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 1.6e+02;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1583 CATGGGAAGACAGAA 1598  
 Db 4 CATGGGAAGACAGAA 19  
 RESULT 196  
 ID ABN88070  
 XX ABN88070 standard; DNA; 19 BP.  
 XX  
 AC ABN88070;  
 XX  
 XX 12-AUG-2002 (first entry)  
 DT  
 XX  
 XX Caenorhabditis elegans related dsRNA2 upstream primer.  
 DE  
 KW Caenorhabditis elegans; C. elegans; reproduction; development;  
 KW antineurocyst; plant protectant; gene therapy; infection;  
 KW calabar swelling; lymphatic filariasis; elephantiasis; onchocerca;  
 KW

KW primer; ss.  
 XX Caenorhabditis elegans.  
 OS Synthetic.  
 XX WO200238600-A2.  
 XX 16-MAY-2002.  
 XX  
 XX 09-NOV-2001; 2001WO-BP013038.  
 PF  
 XX 09-NOV-2000; 2000US-0246721P.  
 PR  
 XX (CENI-) CENIX BIOSCIENCE GMBH.  
 PA  
 XX Echeverri C, Goenczy P, Hyman A, Coulson A, Jones S, Oegema K;  
 PI Kirkham M;  
 XX  
 XX WPI; 2002-471547/50.  
 DR  
 XX New Caenorhabditis elegans genes required for viability, growth or  
 PT reproduction of nematodes, useful for diagnosing or treating e.g.  
 PT onchocerca or elephantiasis in humans or animals, or plant diseases  
 PT caused by e.g. Heterodera.  
 XX  
 XX Example 2; Page 28; 35pp; English.  
 PS  
 CC The present invention describes an isolated nucleic acid molecule (I),  
 CC which encodes a polypeptide (II) required for the viability and/or growth  
 CC and/or reproduction of nematodes (Caenorhabditis elegans), or its  
 CC fragment. (I) and (II) have nematocite and plant protectant activities,  
 CC and can be used in gene therapy. (I) is useful for producing (II)  
 CC required for the viability, growth and/or reproduction of nematodes.  
 CC Nucleic acids, probes, polypeptides, fusion proteins and antibodies from  
 CC the present invention are also useful in a screening assay for  
 CC interacting drugs that inhibit, stimulate or affect worm growth,  
 CC viability or reproduction. They are useful for diagnosing or treating  
 CC human or animal diseases associated with the infection or presence of  
 CC nematode worms, e.g. Wuchereria bancrofti, Brugia malayi, Loa loa or  
 CC Onchocerca volvulus. These diseases include calabar swellings, lymphatic  
 CC filariasis (elephantiasis) or onchocercosis. The nucleic acids, probes,  
 CC polypeptides, fusion proteins and antibodies are also useful for  
 CC diagnosing or treating plant diseases associated with the infection or  
 CC presence of nematode worms. Furthermore, the nucleic acid and amino acid  
 CC sequences are useful for developing computational models, structural  
 CC models or other models for evaluating drug binding and efficacy. The  
 CC present sequence represents a primer which is used in an example from the  
 CC present invention in RNAi experiments  
 XX  
 XX Sequence 19 BP; 6 A; 3 C; 7 G; 3 T; 0 U; 0 Other;  
 SQ  
 Query Match 1.0%; Score 15.8; DB 1; Length 19;  
 Best Local Similarity 89.5%; Pred. No. 1.5e+02;  
 Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 551 GCAGACGCGCATGCTGGAT 569  
 Db 1 GCAGAGGCGAGATGCTGGAT 19  
 RESULT 197  
 ID ADD00110  
 XX ADD00110 standard; RNA; 19 BP.  
 XX  
 AC ADD00110;  
 XX  
 XX 01-JAN-2004 (first entry)  
 DT  
 XX  
 XX HCV coding region-derived 60% conserved RNA sequence 56.  
 DE  
 KW HCV infection; replication; pathogenesis; virucide; vaccine;  
 KW gene therapy; ds.  
 XX





PT virus.

XX Example 3; SEQ ID NO 305; 183pp; English.

XX

CC This invention relates to novel double-stranded short interfering nucleic

CC acids (siNA) that inhibits replication of hepatitis C virus (HCV), where

CC one strand is an antisense strand (AS) that is complementary to (part

CC of) an HCV RNA (portion) and a sense strand (SS) that is complementary to (part

CC AS), and where most of the pyrimidine nucleotides comprise a sugar

CC modification. The invention may allow development of compounds with

CC virucide, antiinflammatory, hepatotropic or cytostatic activities by

CC modulation (inhibition) of expression or activity of HCV RNA, by RNA

CC interference. The siNA's of the invention may be used to inhibit

CC replication of HCV, in cells, tissue explants or organisms, for treating

CC HCV infection and its consequences (liver failure; hepatocellular cancer

CC and cirrhosis), and also for drug screening, diagnosis, target

CC identification and validation, genetic engineering, pharmacogenomics,

CC studying gene function and gene mapping (for example of single-nucleotide

CC polymorphisms). The chemical modification improves stability, activity,

CC cellular uptake and/or binding affinity. The siNA can be directed to

CC conserved regions of HCV genes, so are active against many different

CC strains.

XX

XX Sequence 19 BP; 11 A; 5 C; 2 G; 0 T; 1 U; 0 Other;

XX

XX Query Match 1.0%; Score 15.8; DB 1; Length 19;

XX Best Local Similarity 84.2%; Pred. No. 1.5e+02;

XX Matches 16; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

XX

Qy 222 CTCATAGAAAAACCAACG 240

Db 1 CUCAAAGAAAAACCAACG 19

XX

XX ||| ||||| |||||

XX

XX ADF52411; AC AC

XX

XX 12-FEB-2004 (first entry)

XX

XX Hepatitis C virus siNA antisense strand SeqID1001.

XX

XX short interfering nucleic acid; siNA; virus replication inhibition;

XX hepatitis C virus; HCV; sugar modification; virucide; antiinflammatory;

XX hepatotropic; cytostatic; RNA interference; HCV infection; liver failure;

XX hepatocellular cancer; cirrhosis; ss.

XX

XX Hepatitis C virus.

XX

XX WO2003070750-A2.

XX

XX 28-AUG-2003.

XX

XX 20-FEB-2003; 2003WO-US005043.

XX

XX 20-FEB-2002; 2002US-0358580P.

XX

XX 11-MAR-2002; 2002US-0363124P.

XX

XX 26-MAR-2002; 2002WO-US0009187.

XX

XX 06-JUN-2002; 2002US-0386782P.

XX

XX 05-AUG-2002; 2002US-0401104P.

XX

XX 29-AUG-2002; 2002US-0406784P.

XX

XX 05-SEP-2002; 2002US-0408378P.

XX

XX 09-SEP-2002; 2002US-0409293P.

XX

XX 15-JAN-2003; 2003US-0440129P.

XX

XX (SIRN-) SIRNA THERAPEUTICS INC.

XX

XX Mcswiggen J, Beigelman L, Macejak D, Morrissey D;

XX

XX WPI; 2003-689778/65.

XX

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XX WPI; 2004-226852/21.
XX
XX New RNA molecule less than 49 bases and having a sequence effective to
XX mediate degradation or block translation of mRNA that is the
XX transcriptional product of a target gene, useful for treating Alzheimer's
XX disease or cancer.
XX
XX Claim 4; SEQ ID NO 7; 63pp; English.
XX
XX The present sequence is the sense strand of a short interfering RNA
XX (siRNA) targeted to human clusterin. The antisense strand is also
XX provided ADL70463. The siRNA can be used to interfere with the expression
XX of clusterin. Clusterin, also known as testosterone-repressed prostate
XX message-2 (TRPM-2) or sulfated glycoprotein-2 (SGP-2), is expressed in
XX increased amounts by prostate tumour cells following androgen withdrawal,
XX and has also been shown to be critical for neuritic toxicity in mouse
XX models of Alzheimer's disease. siRNAs of the invention can be used alone
XX or in combination with other chemotherapy or apoptosis inducing
XX treatments for the treatment of prostate cancer, sarcomas such as
XX osteosarcoma, renal cell carcinoma, breast cancer, bladder cancer, lung
XX cancer, colon cancer, ovarian cancer, anaplastic large cell lymphoma and
XX melanoma, and also for the treatment of Alzheimer's disease.
XX
XX Sequence 19 BP; 8 A; 3 C; 1 G; 2 T; 5 U; 0 Other;
XX
XX Query Match 1.0%; Score 15.8; DB 1; Length 19;
XX Best Local Similarity 63.2%; Pred. No. 1.5e+02;
XX Matches 12; Conservative 5; Mismatches 2; Indels 0; Gaps 0;
XX
QY 1616 TAATTCATATAAACTGCT 1634
DB 1 UAAUUCACACAAACUGUTT 19
:|||||:|||||:|:|
1 UAAUUCACACAAACUGUTT 19

RESULT 202
ADL70463/C
ID ADL70463 standard; RNA; 19 BP.
XX
XX AC ADL70463;
XX
XX 20-MAY-2004 (first entry)
XX
XX RNAi for human clusterin.
XX
XX RNA interference; RNAi; short interfering RNA; siRNA; human; clusterin;
XX cytosatic; neuroprotective; nootropic; gene silencing; DNA-RNA hybrid;
XX ss.
XX
XX Homo sapiens.
XX
XX Synthetic.
XX
XX Key Location/Qualifiers
XX modified_base 18..19
XX /*tag= a
XX /mod_base= OTHER
XX /note= "OTHER= dTdT"
XX
XX WO2004018676-A2.
XX
XX 04-MAR-2004.
XX
XX 21-AUG-2003; 2003WO-CA001277.
XX
XX 21-AUG-2003; 2002US-0405193P.
XX
XX 03-SEP-2002; 2002US-0408152P.
XX
XX 20-MAY-2003; 2003US-0472387P.
XX
XX (UYBR-) UNIV BRITISH COLUMBIA.
XX
XX Jansen B, Gleave ME, Signaevsky M, Beraldi E, Trougakos IP;
XX Gonos ES;
XX
```

```
DR WPI; 2004-226852/21.
XX
XX New RNA molecule less than 49 bases and having a sequence effective to
XX mediate degradation or block translation of mRNA that is the
XX transcriptional product of a target gene, useful for treating Alzheimer's
XX disease or cancer.
XX
XX Claim 4; SEQ ID NO 8; 63pp; English.
XX
XX The present sequence is the antisense strand of a short interfering RNA
XX (siRNA) targeted to human clusterin. The sense strand is also provided
XX ADL70462. The siRNA can be used to interfere with the expression of
XX clusterin. Clusterin, also known as testosterone-repressed prostate
XX message-2 (TRPM-2) or sulfated glycoprotein-2 (SGP-2), is expressed in
XX increased amounts by prostate tumour cells following androgen withdrawal,
XX and has also been shown to be critical for neuritic toxicity in mouse
XX models of Alzheimer's disease. siRNAs of the invention can be used alone
XX or in combination with other chemotherapy or apoptosis inducing
XX treatments for the treatment of prostate cancer, sarcomas such as
XX osteosarcoma, renal cell carcinoma, breast cancer, bladder cancer, lung
XX cancer, colon cancer, ovarian cancer, anaplastic large cell lymphoma and
XX melanoma, and also for the treatment of Alzheimer's disease.
XX
XX Sequence 19 BP; 5 A; 1 C; 3 G; 2 T; 8 U; 0 Other;
XX
XX Query Match 1.0%; Score 15.8; DB 1; Length 19;
XX Best Local Similarity 89.5%; Pred. No. 1.5e+02;
XX Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
QY 1614 ACTAATTCAATAAACTGT 1632
DB 19 AATAATTCAACAAACTGT 1
|||||:|||||:|:|
19 AATAATTCAACAAACTGT 1

RESULT 203
ADL70429/C
ID ADL70429 standard; RNA; 19 BP.
XX
XX AC ADL70429;
XX
XX 20-MAY-2004 (first entry)
XX
XX RNAi for human clusterin.
XX
XX Human; clusterin; RNAi; melanoma; cytostatic; gene silencing;
XX short interfering RNA; siRNA; DNA-RNA hybrid; ss.
XX
XX Homo sapiens.
XX
XX Synthetic.
XX
XX Key Location/Qualifiers
XX modified_base 18..19
XX /*tag= a
XX /mod_base= OTHER
XX /note= "OTHER= TT"
XX
XX WO2004018675-A1.
XX
XX 04-MAR-2004.
XX
XX 21-AUG-2003; 2003WO-CA001276.
XX
XX 21-AUG-2002; 2002US-0405193P.
XX
XX 03-SEP-2002; 2002US-0408152P.
XX
XX 02-DEC-2002; 2002US-0319748P.
XX
XX 20-MAY-2003; 2003US-0472387P.
XX
XX (UYBR-) UNIV BRITISH COLUMBIA.
XX
XX (GLEA/) GLEAVE M E.
XX
XX Jansen B;
XX
XX WPI; 2004-226851/21.
XX
```

XX Treating melanoma in a mammalian subject comprises administering to the  
PT subject a therapeutic agent effective to reduce the effective amount of  
PT clusterin in the melanoma cells.  
XX  
PS Claim 20; SEQ ID NO 27; 32pp; English.  
XX  
CC The present sequence is that of a short interfering RNA (siRNA) molecule  
CC targeted to human clusterin ADL70403. The invention relates to the  
CC treatment of melanoma through reduction in the effective amount of  
CC clusterin. The therapeutic agent may be an antisense oligonucleotide  
CC ADL70404-ADL70421 or short interfering RNA (siRNA) ADL70422-ADL70445  
CC targeted to clusterin. The siRNAs molecules direct cleavage of clusterin  
CC mRNA. A method for regulating expression of bcl-xL in a subject or cell  
CC line comprises administering an agent effective to modulate the amount of  
CC clusterin expression. In clusterin-expressing cells, expression of bcl-xL  
CC is down-regulated when the effective amount of clusterin is reduced. Such  
CC inhibition is significant because bcl-xL is known to act as an inhibitor  
CC of apoptosis.  
XX  
SQ Sequence 19 BP; 5 A; 1 C; 3 G; 2 T; 8 U; 0 Other;  
Query Match 1.0%; Score 15.8; DB 1; Length 19;  
Best Local Similarity 89.5%; Pred. No. 1.5e+02;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 1614 ACTAATTCAATAAACTGT 1632  
Db 19 AATAATTCAACAAAACCTGT 1  
RESULT 204  
ADL70426  
ID ADL70426 standard; RNA; 19 BP.  
XX  
AC ADL70426;  
XX  
DT 20-MAY-2004 (first entry)  
XX  
DE RNAi for human clusterin.  
XX  
KW Human; clusterin; RNAi; melanoma; cytostatic; gene silencing;  
KW short interfering RNA; siRNA; DNA-RNA hybrid; ss.  
XX  
OS Homo sapiens.  
OS Synthetic.  
XX  
FH Key Location/Qualifiers  
FT modified\_base 18..19  
FT /\*tag= a  
FT /mod\_base= OTHER  
FT /note= "OTHER= TT"  
XX  
PN WO2004018675-A1.  
XX  
PD 04-MAR-2004.  
XX  
PF 21-AUG-2003; 2003WO-CA001276.  
XX  
PR 21-AUG-2003; 2003WO-CA001276.  
XX  
PR 21-AUG-2002; 2002US-0405193P.  
PR 03-SEP-2002; 2002US-0408152P.  
PR 02-DEC-2002; 2002US-0319748P.  
PR 20-MAY-2003; 2003US-0472387P.  
XX  
PA (UYBR-) UNIV BRITISH COLUMBIA.  
PA (GLEA/) GLEAVE M E.  
XX  
PI Jansen B;  
XX  
DR WPI; 2004-226851/21.  
XX  
PT Treating melanoma in a mammalian subject comprises administering to the  
PT subject a therapeutic agent effective to reduce the effective amount of

PT clusterin in the melanoma cells.  
XX  
PS Claim 10; SEQ ID NO 24; 32pp; English.  
XX  
CC The present sequence is that of a short interfering RNA (siRNA) molecule  
CC targeted to human clusterin ADL70403. The invention relates to the  
CC treatment of melanoma through reduction in the effective amount of  
CC clusterin. The therapeutic agent may be an antisense oligonucleotide  
CC ADL70404-ADL70421 or short interfering RNA (siRNA) ADL70422-ADL70445  
CC targeted to clusterin. The siRNAs molecules direct cleavage of clusterin  
CC mRNA. A method for regulating expression of bcl-xL in a subject or cell  
CC line comprises administering an agent effective to modulate the amount of  
CC clusterin expression. In clusterin-expressing cells, expression of bcl-xL  
CC is down-regulated when the effective amount of clusterin is reduced. Such  
CC inhibition is significant because bcl-xL is known to act as an inhibitor  
CC of apoptosis.  
XX  
SQ Sequence 19 BP; 8 A; 3 C; 1 G; 2 T; 5 U; 0 Other;  
Query Match 1.0%; Score 15.8; DB 1; Length 19;  
Best Local Similarity 63.2%; Pred. No. 1.5e+02;  
Matches 12; Conservative 5; Mismatches 2; Indels 0; Gaps 0;  
QY 1616 TAATTCAATAAACTGTCT 1634  
Db 1 UAAUUCACAAACACUGUTT 19  
RESULT 205  
ADL70428  
ID ADL70428 standard; RNA; 19 BP.  
XX  
AC ADL70428;  
XX  
DT 20-MAY-2004 (first entry)  
XX  
DE RNAi for human clusterin.  
XX  
KW Human; clusterin; RNAi; melanoma; cytostatic; gene silencing;  
KW short interfering RNA; siRNA; DNA-RNA hybrid; ss.  
XX  
OS Homo sapiens.  
OS Synthetic.  
XX  
FH Key Location/Qualifiers  
FT modified\_base 18..19  
FT /\*tag= a  
FT /mod\_base= OTHER  
FT /note= "OTHER= TT"  
XX  
PN WO2004018675-A1.  
XX  
PD 04-MAR-2004.  
XX  
PF 21-AUG-2003; 2003WO-CA001276.  
XX  
PR 21-AUG-2002; 2002US-0405193P.  
PR 03-SEP-2002; 2002US-0408152P.  
PR 02-DEC-2002; 2002US-0319748P.  
PR 20-MAY-2003; 2003US-0472387P.  
XX  
PA (UYBR-) UNIV BRITISH COLUMBIA.  
PA (GLEA/) GLEAVE M E.  
XX  
PI Jansen B;  
XX  
DR WPI; 2004-226851/21.  
XX  
PT Treating melanoma in a mammalian subject comprises administering to the  
PT subject a therapeutic agent effective to reduce the effective amount of  
PT clusterin in the melanoma cells.  
XX  
PS Claim 20; SEQ ID NO 26; 32pp; English.



XX DT 20-JUL-1999 (first entry)  
XX DE Rabbit stromelysin hammerhead target SEQ ID NO:535.  
XX KW Arthritic condition; graft tolerance; immune response; target; cleavage;  
KW hammerhead ribozyme; hairpin ribozyme; human; rabbit; mouse; collagenase;  
KW stromelysin; synovial membrane; joint; arthritis; osteoarthritis;  
KW rheumatoid arthritis; autoimmune disease; allergy; inflammation;  
KW diagnosis; ss.  
XX XX  
OS Oryctolagus cuniculus.  
XX KW  
XX WO9618736-A2.  
XX XX  
XX 20-JUN-1996.  
XX XX  
XX 22-NOV-1995; 95WO-US015516.  
XX XX  
PR 13-DEC-1994; 94US-00354920.  
PR 23-DEC-1994; 94US-00363253.  
PR 23-DEC-1994; 94US-00363254.  
PR 17-FEB-1995; 95US-00390850.  
PR 20-APR-1995; 95US-00426124.  
PR 02-MAY-1995; 95US-00432874.  
PR 04-MAY-1995; 95US-00434509.  
PR 07-JUL-1995; 95US-0000951P.  
PR 07-JUL-1995; 95US-0000974P.  
PR 07-AUG-1995; 95US-00512861.  
PR 05-OCT-1995; 95US-00541365.  
XX XX  
PA (RIBO-) RIBOZYME PHARM INC.  
XX XX  
XX Beigelman L, Stinchcomb DT, Jarvis T, Draper K, Pavco P;  
PI Mcswiggen J, Gustofson J, Usman N, Wincott F, Matulic-Adamic J;  
PI Karpelesky A, Thompson JD, Modak A, Burgin A;  
XX WPI; 1996-300653/30.  
XX XX  
PT Enzymatic nucleic acid molecules having a hammer-head motif - used for  
PT the treatment of arthritis, induction of graft tolerance or treatment of  
PT auto-immune diseases.  
XX XX  
PS Example 1; Page 154; 307pp; English.  
XX XX  
CC The present invention describes a novel enzymatic nucleic acid (ENA)  
CC having a hammerhead motif (HM) comprising: (i) at least 5 ribose residues  
CC ; (ii) a 2'-C-allyl modification at position 4 of the ENA; (iii) at least  
CC ten 2'-O-methyl modifications; and (iv) a 3'-end modification. The ENA's  
CC can inhibit collagenase and stromelysin production in the synovial  
CC membrane of joints for the treatment or prevention of arthritis,  
CC particularly osteoarthritis or rheumatoid arthritis. The ENA's can also  
CC be used to treat antigen presenting cells of a donor to induce tolerance  
CC in a recipient to an alloantigen of a donor. They can also be used for  
CC enhancing graft tolerance or for treating autoimmune disease, and for  
CC treating allergies and other inflammatory conditions. The ENA's can also  
CC be used in diagnosis. Ribozyme therapy impacts on the expression of  
CC stromelysin without introducing the non-specific effects upon gene  
CC expression which accompany treatment with retinoids and dexamethasone.  
CC The concentration of ribozyme required to affect a therapeutic treatment  
CC is lower than that required of antisense molecules, and is highly  
CC specific. The present sequence is used in the exemplification of the  
CC present invention  
XX XX  
SQ Sequence 17 BP; 4 A; 2 C; 4 G; 0 T; 7 U; 0 Other;  
XX XX  
Query Match 0.9%; Score 15.4; DB 1; Length 17;  
Best Local Similarity 94.1%; Pred. No. 1.1e+02;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1589 AGAACAGAAATTCCTCC 1605  
DB 17 AAGAACAGAAATTCCTCC 1

RESULT 209  
ABK00170/c  
ID ABK00170 standard; RNA; 17 BP.  
XX AC ABK00170;  
XX DT 12-MAR-2002 (first entry)  
XX DE Human NOGO Hammerhead Ribozyme #170.  
XX XX  
KW Human; ss; antisense therapy; cytostatic; antiinflammatory; haemostatic;  
KW cerebroprotective; nootropic; neuroprotective; antiparkinsonian;  
KW muscular; CD20; neurite growth inhibitor gene; NOGO; hammerhead ribozyme;  
KW DNzyme; inozyme; G-cleaver; amberyzyme; zinzyme; lymphoma; leukaemia;  
KW B-cell lymphoma; non-Hodgkin's lymphoma; NHL; lymphocytic leukaemia;  
KW human immunodeficiency virus; HIV associated NHL; mantle-cell lymphoma;  
KW MCL; immunocytoma; IMC; immune thrombocytopenia; stroke; dementia;  
KW inflammatory arthropathy; central nervous system injury;  
KW cerebrovascular accident; CVA; Alzheimer's disease; multiple sclerosis;  
KW chemotherapy-induced neuropathy; amyotrophic lateral sclerosis; ALS;  
KW Parkinson's disease; ataxia; Huntington's disease;  
KW Creutzfeldt-Jakob disease; muscular dystrophy; neurodegenerative disease.  
XX XX  
OS Homo sapiens.  
OS Synthetic.  
XX WO200159103-A2.  
XX PN  
XX 16-AUG-2001.  
XX XX  
XX 09-FEB-2001; 2001WO-US004273.  
XX XX  
PR 11-FEB-2000; 2000US-0181797P.  
PR 28-FEB-2000; 2000US-0185516P.  
PR 06-MAR-2000; 2000US-0187128P.  
XX XX  
XX (RIBO-) RIBOZYME PHARM INC.  
PA (BLAT/) BLATT L.  
PA (MCSW/) MCSWIGGEN J.  
PA (CHOW/) CHOWRIRA B M.  
XX XX  
PI Blatt L, Mcswiggen J, Chowrira BM;  
XX WPI; 2001-607195/69.  
XX XX  
PT Nucleic acid molecules, e.g., enzymatic nucleic acids and antisense  
PT constructs, which down regulate expression of a CD20 gene or neurite  
PT growth inhibitor gene useful for treating, e.g., lymphoma, leukemia, and  
PT central nervous system injury.  
XX XX  
PS Claim 88; Page 68; 200pp; English.  
XX XX  
CC The invention relates to a nucleic acid molecule which down regulates  
CC expression of a CD20 gene and a nucleic acid molecule which down  
CC regulates expression of a neurite growth inhibitor gene (NOGO). The  
CC nucleic acids may be enzymatic nucleic acids (e.g. a ribozyme or a  
CC DNzyme) an Inozyme (an endolytic nucleic acid cleaving an RNA molecule  
CC possessing an NCH motif), a G-cleaver (cleaving RNA with a NYN motif) or  
CC an amberyzyme (cleaving RNA with an NGN triplet), a zinzyme (cleaving RNA  
CC with a YGY motif). The CD20-targeting nucleic acid is used to cleave RNA  
CC of CD20 in the presence of a divalent cation that is preferably Mg<sup>2+</sup>.  
CC Furthermore, it may be contacted with a cell to reduce CD20 activity of  
CC the cell and treat a patient having a condition associated with the level  
CC of CD20. The treatment may further comprise the use of one or more  
CC therapeutics. In particular, the CD20 targeting nucleic acid may be used to  
CC treat lymphoma, leukaemia, B-cell lymphoma, low-grade or follicular non-  
CC Hodgkin's lymphoma (NHL), bulky low-grade or follicular NHL, lymphocytic  
CC leukaemia, HIV (human immunodeficiency virus) associated NHL, mantle-cell  
CC lymphoma (MCL), immunocytoma (IMC), small B-cell lymphocytic lymphoma,  
CC immune thrombocytopenia, and inflammatory arthropathy. The NOGO-  
CC targeting nucleic acid is used to cleave RNA of the NOGO gene in the

CC presence of a divalent cation that is preferably Mg<sup>2+</sup>. Furthermore, the  
CC nucleic acid may be contacted with a cell to reduce NCOG activity of the  
CC cell and treat a patient having a condition associated with the level of  
CC NCOG. The treatment may further comprise the use of one or more  
CC therapies. In particular, the NCOG-targeting nucleic acid may be used to  
CC treat central nervous system (CNS) injury and cerebrovascular accident  
CC (CVA, stroke), Alzheimer's disease, dementia, multiple sclerosis (MS),  
CC chemotherapy-induced neuropathy, amyotrophic lateral sclerosis (ALS),  
CC Parkinson's disease, ataxia, Huntington's disease, Creutzfeldt-Jakob  
CC disease, muscular dystrophy, and/or other neurodegenerative disease  
CC states which respond to the modulation of NCOG expression. The present  
CC sequence is a hammerhead ribozyme of the invention  
XX  
SQ Sequence 17 BP; 8 A; 1 C; 3 G; 0 T; 5 U; 0 Other;

Query Match 0.9%; Score 15.4; DB 1; Length 17;  
Best Local Similarity 94.1%; Pred. No. 1.1e+02;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1619 TTCATTAACACGTCTT 1635  
Db 17 TTCATTAACACGTCTT 1

RESULT 210  
ABN08674  
ID ABN08674 standard; DNA; 17 BP.  
XX  
AC ABN08674;  
XX  
DT 29-MAY-2002 (first entry)  
XX  
DE Human GDMPL-1 17-mer scanning SEQ ID NO:5 sequence SEQ ID NO:8666.  
XX  
KW Human; genome-derived myosin-like protein 1; GDMPL-1; hGDMPL-1; heart;  
KW muscle; myosin; chromosome 22; gene therapy; vaccine; heart disease;  
KW skeletal muscle disorder; amplicon; screening; ss.  
XX  
OS Homo sapiens.  
XX  
FN WO200192524-A2.  
XX  
PD 06-DEC-2001.  
XX  
PF 25-MAY-2001; 2001WO-US016981.  
XX  
PR 26-MAY-2000; 2000US-0207456P.  
PR 21-SEP-2000; 2000US-0234687P.  
PR 27-SEP-2000; 2000US-0236359P.  
PR 04-OCT-2000; 2000GB-00024263.  
PR 30-JAN-2001; 2001WO-US000661.  
PR 30-JAN-2001; 2001WO-US000662.  
PR 30-JAN-2001; 2001WO-US000663.  
PR 30-JAN-2001; 2001WO-US000664.  
PR 30-JAN-2001; 2001WO-US000665.  
PR 30-JAN-2001; 2001WO-US000666.  
PR 30-JAN-2001; 2001WO-US000667.  
PR 30-JAN-2001; 2001WO-US000668.  
PR 30-JAN-2001; 2001WO-US000669.  
PR 30-JAN-2001; 2001WO-US000670.  
PR 05-FEB-2001; 2001US-0266860P.  
XX  
PA (AEOM-) AEOMICA INC.  
XX  
PI Gu Y, Ji Y, Penn SG, Hanzel DK, Rank DR, Chen W, Shannon ME;  
XX  
XX WPI; 2002-179446/23.  
XX  
DR New polypeptide, for raising antibodies that recognize hGDMPL-1 proteins,  
PT or as specific biomolecule capture probes for surface-enhanced laser  
PT desorption ionization, comprises human myosin-like protein hGDMPL-1.  
XX  
PS Disclosure; SEQ ID NO 8666; 214pp; English.

XX The present invention describes a human genome-derived myosin-like  
CC protein 1 (hGDMPL-1). The protein and polynucleotide sequences of hGDMPL-  
CC 1 can be used in gene therapy and vaccine production. The hGDMPL-1  
CC nucleic acids can be used as probes to detect, characterize and quantify  
CC hGDMPL-1 nucleic acids in samples, as amplification substrates, to  
CC provide initial substrates for the recombinant engineering of hGDMPL-1  
CC protein variants having desired phenotypic improvements, and for  
CC expressing the proteins. The hGDMPL-1 proteins or polypeptides may be  
CC used as immunogens to raise antibodies that specifically recognise hGDMPL  
CC -1 proteins, as standards in assays used to determine the concentration  
CC and/or amount specifically of hGDMPL proteins, as specific biomolecule  
CC capture probes for surface-enhanced laser desorption/ionisation, as  
CC therapeutic supplement in patients having specific deficiency in hGDMPL-1  
CC production, and in vaccines or for replacement therapy. The  
CC polynucleotide sequences encoding hGDMPL-1 may be used for diagnosing a  
CC disorder associated with the expression of hGDMPL-1, in particular heart  
CC and skeletal muscle disorders. hGDMPL-1 is localised to chromosome 22.  
CC The present sequence represents an oligomer used in the screening of the  
CC hGDMPL-1 sequence in the exemplification of the present invention. N.B.  
CC The sequence data for this patent did not form part of the printed  
CC specification, but was obtained in electronic format directly from WIPO  
CC at ftp.wipo.int/pub/published\_pct\_sequence  
XX  
SQ Sequence 17 BP; 9 A; 2 C; 6 G; 0 T; 0 U; 0 Other;  
Query Match 0.9%; Score 15.4; DB 1; Length 17;  
Best Local Similarity 94.1%; Pred. No. 1.1e+02;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 273 GAAGCCCAAGAGAGAA 289  
Db 1 GAAGCCCAAGAGAGAA 17  
RESULT 211  
ADB00465/c  
ID ADB00465 standard; DNA; 17 BP.  
XX  
AC ADB00465;  
XX  
DT 20-NOV-2003 (first entry)  
XX  
DE Human MDZ3 scanning oligonucleotide SEQ ID 1451.  
XX  
KW Cytostatic; immunostimulant; gene therapy; vaccine; human;  
KW zinc finger protein; MDZ3; MDZ4; MDZ7; MDZ12; chromosome 7q22.1;  
KW chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer;  
KW developmental disorder; ss.  
XX  
OS Homo sapiens.  
XX  
FN EP1281758-A2.  
XX  
PD 05-FEB-2003.  
XX  
PF 30-JUL-2002; 2002EP-00016874.  
XX  
PR 02-AUG-2001; 2001US-00922181.  
XX  
XX (AEOM-) AEOMICA INC.  
XX  
PI Shannon M, Gu Y, Nguyen C;  
XX  
XX WPI; 2003-423107/40.  
XX  
DR New zinc finger-containing proteins and nucleic acids, useful in  
PT manufacturing a medicament for treating or preventing a disorder  
PT associated with decreased or increased expression or activity of MDZ3,  
PT MDZ4, MDZ7 or MDZ12, e.g. cancer.  
XX  
PS Example 8; SEQ ID NO 1451; 103pp; English.  
XX

CC The present invention relates to novel human zinc finger-containing  
 CC proteins and their coding sequences: MD23, MD24, MD27, MD212. MD23 is  
 CC encoded at chromosome 7q22.1, MD24 is encoded at chromosome 6p21.3-22.2,  
 CC MD27 is encoded at chromosome 16p11.2 and MD212 is encoded at chromosome  
 CC 15q26.1. The MD23, MD24, MD27, and MD212 sequences are useful in therapy,  
 CC or in manufacturing a medicament for treating or preventing a disorder  
 CC associated with decreased or increased expression or activity of MD23,  
 CC MD24, MD27, or MD212, e.g. cancer or developmental disorders. The nucleic  
 CC acids and proteins are also useful for diagnosing or monitoring a disease  
 CC caused by altered expression of MD23, MD24, MD27, or MD212. The nucleic  
 CC acids can also be used as probes to detect and characterize gross  
 CC alterations in MD23, MD24, MD27, or MD212 genetic locus. The probes are  
 CC useful in constructing microarrays for measuring gene expression. The  
 CC proteins are useful as therapeutic agents for gene therapy or as  
 CC vaccines. The present sequence was used to illustrate the invention.  
 XX  
 SQ Sequence 17 BP; 3 A; 7 C; 5 G; 2 T; 0 U; 0 Other;

Query Match 0.9%; Score 15.4; DB 1; Length 17;  
 Best Local Similarity 94.1%; Pred. No. 1.1e+02;  
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 928 GCTGCTCGCGATGAG 944  
 |||||  
 DB 17 GCTGCTCGCGCTGAAG 1

RESULT 212  
 ACDS2817/C  
 ID ACDS2817 standard; RNA; 17 BP.  
 XX  
 AC ACDS2817;  
 XX  
 DT 24-SBP-2003 (first entry)  
 XX  
 DE HCV minus strand DNazyme substrate sequence #736.  
 XX  
 KW Nucleic acid molecule; Hepatitis C virus; HCV; Hepatitis B virus; HBV;  
 KW RNA stability; RNA expression; RNA synthesis; antisense;  
 KW enzymatic nucleic acid; hammerhead ribozyme; DNazyme; inozyme; zinzyme;  
 KW amberzyme; G-cleaver ribozyme; decoy molecule; aptamer;  
 KW HBV reverse transcriptase; Enhancer I region; viral replication;  
 KW degenerative; disease state; HBV infection; HCV infection; cirrhosis;  
 KW liver failure; hepatocellular carcinoma; hepatotropic; cytostatic;  
 KW virucide; antiinflammatory; substrate; ss.  
 XX  
 OS Hepatitis C virus.  
 XX  
 PN WO200281494-A1.  
 XX  
 PD 17-OCT-2002.  
 XX  
 PF 26-MAR-2002; 2002WO-US0009187.  
 XX  
 PR 26-MAR-2001; 2001US-00817879.  
 PR 08-JUN-2001; 2001US-00877478.  
 PR 08-JUN-2001; 2001US-0296876P.  
 PR 24-OCT-2001; 2001US-0335059P.  
 PR 05-DEC-2001; 2001US-0337055P.  
 XX  
 PA (RIBO-) RIBOZYME PHARM INC.  
 PA (BLAT/) BLATT L.  
 PA (MACE/) MACEJAK D.  
 PA (MCSW/) MCSWIGGEN J.  
 PA (MORR/) MORRISSEY D.  
 PA (PAVC/) PAVCO P.  
 PA (LEEP/) LEE P.  
 PA (DRAP/) DRAPER K.  
 PA (ROBE/) ROBERTS E.  
 XX  
 PI Blatt L, Macejak D, Mcswiggen J, Morrissey D, Pavco P, Lee P;  
 PI Draper K, Roberts E;  
 XX

DR WPI; 2003-229207/22.  
 XX Novel compound useful for treating cirrhosis, liver failure,  
 PT hepatocellular carcinoma, or condition associated with hepatitis C virus  
 PT infection.  
 XX  
 Claim 1; Page 288; 387pp; English.  
 PS  
 XX The present invention relates to nucleic acid molecules which modulate  
 CC the synthesis, expression and/or stability of Hepatitis C virus (HCV) or  
 CC Hepatitis B virus (HBV) RNA. The nucleic acid molecules include antisense  
 CC and enzymatic nucleic acids such as hammerhead ribozymes, DNazymes,  
 CC inozymes, zinzymes, amberzymes, and G-cleaver ribozymes. Also disclosed  
 CC are nucleic acid decoy molecules and aptamers that bind to HBV reverse  
 CC transcriptase and/or HBV reverse transcriptase primer sequences, as well  
 CC as oligonucleotides that specifically bind the Enhancer I region of HBV  
 CC DNA. The nucleic acids may be used to modulate the expression of HBV  
 CC genes and HBV viral replication. Also disclosed is a method for screening  
 CC compounds and/or potential therapies directed against HBV, and compounds  
 CC that modulate the expression and/or replication of HCV. The compounds and  
 CC methods of the invention are useful for the treatment of degenerative and  
 CC disease states related to HBV and HCV infection, replication and gene  
 CC expression such as cirrhosis, liver failure, and hepatocellular  
 CC carcinoma. The present sequence represents a substrate for one of the HCV  
 CC DNazyme or minus strand DNazyme sequences disclosed in the present  
 CC invention  
 XX  
 SQ Sequence 17 BP; 3 A; 4 C; 8 G; 0 T; 2 U; 0 Other;

Query Match 0.9%; Score 15.4; DB 1; Length 17;  
 Best Local Similarity 94.1%; Pred. No. 1.1e+02;  
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 767 CCACGCCATGTTCCGAC 783  
 |||||  
 DB 17 CCACGCCATGTTCCGAC 1

RESULT 213  
 ACDS9852  
 ID ACDS9852 standard; RNA; 17 BP.  
 XX  
 AC ACDS9852;  
 XX  
 DT 24-SBP-2003 (first entry)  
 XX  
 DE HCV DNazyme substrate sequence #1542.  
 XX  
 KW Nucleic acid molecule; Hepatitis C virus; HCV; Hepatitis B virus; HBV;  
 KW RNA stability; RNA expression; RNA synthesis; antisense;  
 KW enzymatic nucleic acid; hammerhead ribozyme; DNazyme; inozyme; zinzyme;  
 KW amberzyme; G-cleaver ribozyme; decoy molecule; aptamer;  
 KW HBV reverse transcriptase; Enhancer I region; viral replication;  
 KW degenerative; disease state; HBV infection; HCV infection; cirrhosis;  
 KW liver failure; hepatocellular carcinoma; hepatotropic; cytostatic;  
 KW virucide; antiinflammatory; substrate; ss.  
 XX  
 OS Hepatitis C virus.  
 XX  
 PN WO200281494-A1.  
 XX  
 PD 17-OCT-2002.  
 XX  
 PF 26-MAR-2002; 2002WO-US0009187.  
 XX  
 PR 26-MAR-2001; 2001US-00817879.  
 PR 08-JUN-2001; 2001US-00877478.  
 PR 08-JUN-2001; 2001US-0296876P.  
 PR 24-OCT-2001; 2001US-0335059P.  
 PR 05-DEC-2001; 2001US-0337055P.  
 XX  
 PA (RIBO-) RIBOZYME PHARM INC.  
 PA (BLAT/) BLATT L.  
 XX

PA (MACE/) MACEJAK D.  
PA (MCSW/) MCSWIGGEN J.  
PA (MORR/) MORRISSEY D.  
PA (PAVC/) PAVCO P.  
PA (LEEF/) LEE P.  
PA (DRAP/) DRAPER K.  
PA (ROBE/) ROBERTS E.  
XX  
PI Blatt L, Macejak D, Mcswiggen J, Morrissey D, Pavco P, Lee P;  
PI Draper K, Roberts E;  
XX  
XX WPI; 2003-229207/22.  
XX  
XX Novel compound useful for treating cirrhosis, liver failure,  
PT hepatocellular carcinoma, or condition associated with hepatitis C virus  
PT infection.  
XX  
XX Claim 1; Page 261; 387pp; English.  
XX  
XX The present invention relates to nucleic acid molecules which modulate  
CC the synthesis, expression and/or stability of Hepatitis C virus (HCV) or  
CC Hepatitis B virus (HBV) RNA. The nucleic acid molecules include antisense  
CC and enzymatic nucleic acids such as hammerhead ribozymes, DNazymes,  
CC inozymes, zinzymes, amberzymes, and G-cleaver ribozymes. Also disclosed  
CC are nucleic acid decoy molecules and aptamers that bind to HBV reverse  
CC transcriptase and/or HBV reverse transcriptase primer sequences, as well  
CC as oligonucleotides that specifically bind the Enhancer I region of HBV  
CC DNA. The nucleic acids may be used to modulate the expression of HBV  
CC genes and HBV viral replication. Also disclosed is a method for screening  
CC compounds and/or potential therapies directed against HBV, and compounds  
CC that modulate the expression and/or replication of HCV. The compounds and  
CC methods of the invention are useful for the treatment of degenerative and  
CC disease states related to HBV and HCV infection, replication and gene  
CC expression such as cirrhosis, liver failure, and hepatocellular  
CC carcinoma. The present sequence represents a substrate for one of the HCV  
CC DNazyme or minus strand DNazyme sequences disclosed in the present  
CC invention  
XX  
XX Sequence 17 BP; 2 A; 7 C; 4 G; 0 T; 4 U; 0 Other;  
SQ

Query Match 0.9%; Score 15.4; DB 1; Length 17;  
Best Local Similarity 70.6%; Pred. No. 1.1e+02;  
Matches 12; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 766 TCCACGCCATGTTCCAG 782  
:|||||:|:|:  
Db 1 UCCACGCCAUGUCCGG 17

RESULT 214  
ADB45503  
ID ADB45503 standard; DNA; 17 BP.  
XX  
XX ADB45503;  
XX  
XX 18-DEC-2003 (first entry)  
DT  
XX Tumour suppression/reversion associated nucleotide #5826.  
DE  
XX cytotstatic; antiviral; neuroprotective; nootropic; neuroleptic; ss;  
KW primer; probe; tumour suppression; tumour reversion; apoptosis;  
KW virus resistance; transgenic animals; Alzheimer's disease; schizophrenia;  
KW diagnosis.  
XX  
XX Homo sapiens.  
OS  
XX W02003040369-A2.  
XX  
XX 15-MAY-2003.  
PD  
XX 17-SEP-2002; 2002W0-IB004219.  
XX  
XX 17-SEP-2001; 2001FR-00011981.  
PR

(MOLE-) MOLECULAR ENGINES LAB.  
Telerman A, Amson R, Tuijnder M;  
WPI; 2003-441574/41.  
New nucleic acid encoding human prostate membrane-specific antigen,  
useful e.g. for treatment of tumors and viral infection, also related  
polypeptide and antibodies.  
Disclosure; Page 713; 771pp; French.  
The invention relates to the isolation of 6327 nucleotide sequences,  
fragments of at least 15 consecutive nucleotides of these nucleotides, a  
sequence having at least 80% identity, after optimal alignment, with the  
nucleotides, a sequence that hybridizes under stringent conditions with  
the nucleotides, or the complement, or corresponding RNA, of the  
nucleotides. The nucleotides are used as probes or primers for detecting,  
identifying, quantifying and/or amplifying nucleic acids, as in vitro  
sense and antisense sequences, of nucleotides involved in tumour  
suppression or reversion, apoptosis and or viral resistance, to produce  
recombinant polypeptides, and to prepare transgenic animals, as  
experimental models. The nucleotides (also vectors containing them and  
cells containing the vectors), the encoded polypeptides and antibodies  
(Ab) against the polypeptide are useful for prevention and/or treatment  
of viral infections or diseases characterized by development of tumours  
or cell degeneration (e.g. Alzheimer's disease or schizophrenia).  
Analysis of the expression of the nucleotides can be used for diagnosis  
and/or prognosis of these diseases. The nucleotides and polypeptides can  
also be used to screen for their specific interactive molecules,  
potentially useful for treating diseases associated with abnormal  
expression of the nucleotides.  
Sequence 17 BP; 4 A; 7 C; 2 G; 4 T; 0 U; 0 Other;  
SQ

Query Match 0.9%; Score 15.4; DB 1; Length 17;  
Best Local Similarity 94.1%; Pred. No. 1.1e+02;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1551 GATCCTGCACCTCTAACA 1567  
|||||:|:|:  
Db 1 GATCCTGCACCTCTACCA 17

RESULT 215  
ADI84296  
ID ADI84296 standard; RNA; 17 BP.  
XX  
XX ADI84296;  
XX  
XX 03-JUN-2004 (first entry)  
DT  
XX HCV DNazyme substrate sequence #1542.  
DE  
XX ss; enzymatic nucleic acid; RNA cleavage; hepatitis C virus; HCV;  
KW HCV infection; type I interferon; DNazyme.  
XX  
XX Hepatitis C virus.  
OS  
XX US2003125270-A1.  
PN  
XX 03-JUL-2003.  
PD  
XX 18-DEC-2000; 2000US-00740332.  
PF  
XX 18-DEC-2000; 2000US-00740332.  
PR  
XX (BLAT/) BLATT L.  
PA (MCSW/) MCSWIGGEN J.  
PA (ROBE/) ROBERTS E.  
PA (PAVC/) PAVCO P. A.  
PA (MACE/) MACEJACK D.





PT study and regulation of angiogenesis and for developing inhibitors.

XX Example 3; Page 55; 56pp; English.

XX PCR primers AAX85603-04 were used to amplify DNA encoding a human growth factor designated zapol. Zapol is an angiotensin homologue. The polypeptide is used to stimulate cell growth and tissue development. The polypeptides form multimeric proteins. Zapol has angiogenic or hematopoietic activity. The proteins can be used in assays for angiogenic activity. Zapol proteins may be used therapeutically to stimulate revascularization of tissue. Specific applications include treatment of full-thickness skin wounds, including venous stasis ulcers and other chronic, non-healing wounds, as well as fracture repair, skin grafting, reconstructive surgery, and establishment of vascular networks in transplanted cells and tissues. Zapol is also useful as a research agent, such as in the expansion of hematopoietic cells (including stem cells) and endothelial cells. The polypeptides are added to tissue culture media for these cell types

XX Sequence 18 BP; 1 A; 7 C; 4 G; 6 T; 0 U; 0 Other;

Query Match 0.9%; Score 15.4; DB 1; Length 18;  
Best Local Similarity 94.1%; Pred. No. 1.4e+02;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 284 GAAGAAGAGGATGCC 300  
|||||

Db 18 GAAGAAGAGGATGCC 2

RESULT 218

AD74784

ID AD74784 standard; DNA; 18 BP.

XX AC AD74784;

XX 16-DEC-2004 (first entry)

XX Allele specific primer A for human stenosis marker hCV25612495.

XX Human; ss; PCR; primer; Allele specific primer; coronary stenosis; angina; ischaemic chest pain; myocardial infarction;

XX sudden cardiac death; SNP; single nucleotide polymorphism.

XX Homo sapiens.

XX WO2004081186-A2.

XX 23-SEP-2004.

XX 10-MAR-2004; 2004WO-US007140.

XX 10-MAR-2003; 2003US-0453050P.

XX 30-APR-2003; 2003US-0466437P.

XX (APPL-) APPLERA CORP.

XX Cargill M, Devlin JJ, Luke WM;

XX WPI; 2004-668949/65.

XX Identifying an individual who has altered risk for developing stenosis comprises detecting single nucleotide polymorphism (SNP), in the individual's nucleic acids.

XX Claim 19; SEQ ID NO 68096; 146pp; English.

XX The invention relates to identifying an individual who has altered risk for developing coronary stenosis comprising detecting a single nucleotide polymorphism (SNP) in any one of the 67073 nucleotide sequences (not given in the specification), in the individual's nucleic acids, where the presence of the SNP is correlated with an altered risk for stenosis in the individual. Also included are an isolated nucleic acid molecule

CC (comprising at least 8 contiguous nucleotides where one of the nucleotides is an SNP as cited above, or their complement), an isolated polypeptide comprising an amino acid sequence selected from any of the 696 amino acid sequences (not defined in the specification), an antibody that specifically binds to the polypeptide (or its antigen-binding fragment), an amplified polynucleotide containing the SNP as cited (where the amplified polynucleotide is between about 16 and about 1,000 nucleotides in length), an isolated polynucleotide which specifically hybridises to a nucleic acid molecule containing the SNP, a kit for detecting a SNP in a nucleic acid, detecting a SNP in a nucleic acid molecule, detecting a variant polypeptide and identifying an agent useful in therapeutically or prophylactically treating stenosis. The detection step of the method is carried out by a process selected from allele-specific probe hybridisation, allele-specific primer extension, allele-specific amplification, sequencing, 5' nuclease digestion, molecular beacon assay, oligonucleotide ligation assay, size analysis, and single-stranded conformation polymorphism. The method is useful for identifying an individual who has altered risk for developing coronary stenosis, which can lead to angina (ischaemic chest pain), myocardial infarction and ultimately sudden cardiac death. The present sequence is an allele specific primer for amplifying a SNP-containing region of a human marker gene associated with stenosis. NOTE: SEQ ID 1-67771 are not shown in the specification but are provided on a CD-R named CL001510CDR which was not supplied with the specification.

XX Sequence 18 BP; 4 A; 3 C; 5 G; 5 T; 0 U; 1 Other;

Query Match 0.9%; Score 15.4; DB 1; Length 18;  
Best Local Similarity 88.9%; Pred. No. 1.4e+02;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 500 CTTCTGGATGAATGGTGA 517  
|||||

Db 1 CTTCTGGATGAATGGTGA 18

RESULT 219

AAV31968/C

ID AAV31968 standard; DNA; 15 BP.

XX AC AAV31968;

XX 21-AUG-1998 (first entry)

XX Peptide nucleic acid probe 111.

XX Peptide nucleic acid; PNA; probe; hybridisation; mycobacteria; ribosomal nucleic acid; rRNA; drug-resistant strain; mutation; ss.

XX Synthetic.

XX Mycobacterium sp.

XX Key Location/Qualifiers

FH modified\_base 1..15

FT /\*tag= a

FT /note= "This sequence contains a polyamide backbone

FT instead of a deoxyribose backbone"

XX WO9815648-A1.

XX 16-APR-1998.

XX 03-OCT-1997; 97WO-DK000425.

XX 04-OCT-1996; 96DK-00001096.

XX 18-OCT-1996; 96DK-00001156.

XX 05-MAY-1997; 97DK-00000512.

XX (DAKO-) DAKO AS.

XX Stender H, Lund K, Mollerup TA;

XX WPI; 1998-240831/21.

XX Peptide nucleic acid probes for detection of ribosomal nucleic acid of  
 PT mycobacteria - allow differentiation between species of tuberculosis  
 PT complex and others and can penetrate cell membranes without pretreatment.  
 XX  
 PS Claim 22; Page 67; 106pp; English.

XX This is the nucleotide sequence of the peptide nucleic acid (PNA) probe  
 CC used in the method of the invention, to detect ribosomal nucleic acid of  
 CC mycobacteria. The probes are used, in situ or in vitro, for detection of  
 CC the Mycobacterium tuberculosis complex (MTC), specifically M.  
 CC tuberculosis, and especially in sputum samples, but also in other body  
 CC fluids, biopsy specimens, foods, soil, air and water. Particularly, they  
 CC are used to diagnose, stage or monitor infection, or for identification  
 CC of drug-resistant strains (which generally have mutations in rRNA)  
 XX  
 SQ Sequence 15 BP; 3 A; 2 C; 1 G; 9 T; 0 U; 0 Other;

Query Match 0.9%; Score 15; DB 1; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 83;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 177 AAGGAAATTCAAAAT 191  
 DB 15 AAGGAAATTCAAAAT 1

RESULT 220

ACD62818/c  
 ID ACD62818 standard; RNA; 17 BP.

XX  
 AC ACD62818;

XX  
 DT 24-SEP-2003 (first entry)

XX HCV minus strand DNazyme substrate sequence #737.

XX Nucleic acid molecule; Hepatitis C virus; HCV; Hepatitis B virus; HBV;  
 KW RNA stability; RNA expression; RNA synthesis; antisense;  
 KW enzymatic nucleic acid; hammerhead ribozyme; DNazyme; inozyme; zinzyme;  
 KW ambarzyme; G-cleaver ribozyme; decoy molecule; aptamer;  
 KW HBV reverse transcriptase; Enhancer I region; viral replication;  
 KW degenerative; disease state; HBV infection; HCV infection; cirrhosis;  
 KW liver failure; hepatocellular carcinoma; hepatotropic; cytostatic;  
 KW viricide; antiinflammatory; substrate; ss.

XX Hepatitis C virus.

XX WO200281494-A1.

XX 17-OCT-2002.

XX 26-MAR-2002; 2002NO-US009187.

XX 26-MAR-2001; 2001US-00817879.

PR 08-JUN-2001; 2001US-00877478.

PR 08-JUN-2001; 2001US-0296876P.

PR 24-OCT-2001; 2001US-0335059P.

PR 05-DEC-2001; 2001US-0337055P.

XX (RIBO-) RIBOZYME PHARM INC.

PA (BLAT/) BLATT L.

PA (MACE/) MACEJAK D.

PA (MCSW/) MCSWIGGEN J.

PA (MORE/) MORRISSEY D.

PA (PAVC/) PAVCO P.

PA (LEEP/) LEE P.

PA (DRAP/) DRAPER K.

PA (ROBE/) ROBERTS E.

XX Blatt L, Macejak D, Mcswiggen J, Morrissey D, Pavco P, Lee P;

PI Draper K, Roberts E;

XX

DR WPI; 2003-229207/22.

XX Novel compound useful for treating cirrhosis, liver failure,  
 PT hepatocellular carcinoma, or condition associated with hepatitis C virus  
 PT infection.  
 XX

XX Claim 1; Page 288; 387pp; English.

XX The present invention relates to nucleic acid molecules which modulate  
 CC the synthesis, expression and/or stability of Hepatitis C virus (HCV) or  
 CC Hepatitis B virus (HBV) RNA. The nucleic acid molecules include antisense  
 CC and enzymatic nucleic acids such as hammerhead ribozymes, DNazymes,  
 CC inozymes, zinzymes, ambarzymes, and G-cleaver ribozymes. Also disclosed  
 CC are nucleic acid decoy molecules and aptamers that bind to HBV reverse  
 CC transcriptase and/or HBV reverse transcriptase primer sequences, as well  
 CC as oligonucleotides that specifically bind the Enhancer I region of HBV  
 CC DNA. The nucleic acids may be used to modulate the expression of HBV  
 CC genes and HBV viral replication. Also disclosed is a method for screening  
 CC compounds and/or potential therapies directed against HBV, and compounds  
 CC that modulate the expression and/or replication of HCV. The compounds and  
 CC methods of the invention are useful for the treatment of degenerative and  
 CC disease states related to HBV and HCV infection, replication and gene  
 CC expression such as cirrhosis, liver failure, and hepatocellular  
 CC carcinoma. The present sequence represents a substrate for one of the HCV  
 CC DNazyme or minus strand DNazyme sequences disclosed in the present  
 CC invention

XX Sequence 17 BP; 4 A; 3 C; 8 G; 0 T; 2 U; 0 Other;

Query Match 0.9%; Score 15; DB 1; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+02;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 766 TCCAGCGCCATGTTC 780

DB 15 TCCAGCGCCATGTTC 1

RESULT 221

ADI85768/c

ID ADI85768 standard; RNA; 17 BP.

XX  
 AC ADI85768;

XX 03-JUN-2004 (first entry)

XX HCV DNazyme substrate sequence #3014.

XX ss; enzymatic nucleic acid; RNA cleavage; hepatitis C virus; HCV;  
 KW HCV infection; type I interferon; DNazyme.

XX Hepatitis C virus.

XX US2003125270-A1.

XX 03-JUL-2003.

XX 18-DEC-2000; 2000US-00740332.

XX 18-DEC-2000; 2000US-00740332.

XX (BLAT/) BLATT L.

PA (MCSW/) MCSWIGGEN J.

PA (ROBE/) ROBERTS E.

PA (PAVC/) PAVCO P. A.

PA (MACE/) MACEJACK D.

XX Blatt L, Mcswiggen J, Roberts E, Pavco PA, Macejack D;

XX WPI; 2004-031273/03.

XX Enzymatic nucleic acid molecules which specifically cleave RNA derived  
 PT from hepatitis C virus (HCV), useful for the treatment of HCV infections,  
 PT

especially in combination with type I interferon therapy.

Claim 1; SEQ ID NO 3014; 198pp; English.

The invention relates to an enzymatic nucleic acid molecule which specifically cleaves RNA derived from hepatitis C virus (HCV), in which the binding arms of the enzymatic nucleic acid molecule comprises sequences complementary to any of the defined substrate sequences given in the specification. The nucleic acid molecule may be administered for the treatment of HCV infections, especially in combination with type I interferons. The present sequence represents a HCV DNase substrate sequence.

Sequence 17 BP; 4 A; 3 C; 8 G; 0 T; 2 U; 0 Other;

Query Match 0.9%; Score 15; DB 1; Length 17;  
Best Local Similarity 100.0%; Pred. No. 1.3e+02;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 766 TCCAGCCCATGTTCC 780

DB 15 TCCAGCCCATGTTCC 1

RESULT 222

ADO79635/c  
ID ADO79635 standard; DNA; 17 BP.

AC ADO79635;

DT 26-AUG-2004 (first entry)

DE KIAA0783 extend primer #27.

Cytostatic; Gene therapy; breast cancer; human; DLG1; KIAA0783; DPF3;  
CENPc1; SNF; single nucleotide polymorphism; PHF14;  
PHD finger protein 14; chromosome 7p21.3; zinc finger protein;  
transcription factor; extend; primer; ss.

OS Homo sapiens.

PN WO2004047514-A2.

PD 10-JUN-2004.

PF 25-NOV-2003; 2003WO-US037943.

PR 25-NOV-2002; 2002US-0429136P.

PR 24-JUL-2003; 2003US-0490234P.

XX (SEQU-) SEQUENOM INC.

XX Roth RB, Nelson MR, Braun A, Kammerer SM, Reneland R;

XX WPI; 2004-441037/41.

Identifying a subject at risk of breast cancer by detecting the presence of polymorphic variations in the DLG1, KIAA0783, DPF3 or CENPc1 regions which are associated with breast cancer in a nucleic acid sample from a subject.

Example 4; Page 78; 227pp; English.

The present invention relates to a method for identifying a subject at risk of breast cancer. The method comprising detecting the presence or absence of one or more polymorphic variations associated with breast cancer in a nucleic acid sample from a subject. The nucleic acid sample comprises the DLG1 region (ADO79402), KIAA0783 region (ADO79403), DPF3 region (ADO79404) or CENPc1 region (ADO79405). The gene DLG1 (discs. large homolog 1 (Drosophila)) is also known as synapse-associated protein 97, hdlg or SAP97. DLG1 has been mapped to chromosomal position 3q29. The gene KIAA0783 is also known as PHF14 and PHD finger protein 14. KIAA0783 has been mapped to chromosomal position 7p21.3. The KIAA0783 protein is a

novel gene with unknown function, however, being a zinc finger protein, it likely to be a transcription factor. The gene DPF3 (D4, zinc and double PHD fingers, family 3) is also known as CERD4, cer-d4, FLJ14079 and 2810403B03Rik. DPF3 is a Rho family guanine-nucleotide exchange factor. DPF3 has been mapped to chromosomal position 14q24.3-q31.1. The gene CENPc1 (centromere protein C1) is also known as Centromere autotantigen C1. CENPc1 has been mapped to chromosomal position 4q12-q13.3. CENPc1 is a centromere autotantigen and a component of the inner kinetochore plate. The CENPc1 protein is required for maintaining proper kinetochore size and a timely transition to anaphase. The method is useful for identifying a subject at risk of breast cancer, for early diagnosis, prevention and treatment of breast cancer, to analyze and predict a response to a breast cancer treatment, and in clinical drug trials. The present sequence was used in an example from the invention.

Sequence 17 BP; 3 A; 6 C; 5 G; 3 T; 0 U; 0 Other;

Query Match 0.9%; Score 15; DB 1; Length 17;  
Best Local Similarity 100.0%; Pred. No. 1.3e+02;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 438 AGTGGCTCAGGCCTG 452

DB 15 AGTGGCTCAGGCCTG 1

RESULT 223

AAQ35721/c  
ID AAQ35721 standard; DNA; 18 BP.

AC AAQ35721;

DT 25-MAR-2003 (revised)

DT 24-FEB-1993 (first entry)

DE EIV primer EIVAIP7A.

Expression cassette; equine influenza virus; EIV; hemagglutinin; HA;  
Al/Prague/56; NYVAC; ALVAC; recombinant vector; PCR; amplify; pCPV1;  
polymerase chain reaction; pRW764.2; H6 promoter; canarypox virus;  
Copenhagen vaccine; vaccinia virus; virulence factors; deletion loci;  
recipient loci; ss.

OS Synthetic.

PN WO9215672-A1.

PD 17-SEP-1992.

PF 09-MAR-1992; 92WO-US001906.

PR 07-MAR-1991; 91US-00666056.

PR 11-JUN-1991; 91US-00713967.

PR 06-MAR-1992; 92US-00847951.

XX (VIRO-) VIROGENETICS CORP.

XX Paoletti B, Perkus ME, Taylor J, Tartaglia J, Norton EK;

XX Riviere M, De Taine C, Limbach KJ, Johnson GP, Pincus SE, Cox WT;

XX Francis J, Gettig RR;

XX WPI; 1992-331718/40.

Vaccine comprises recombinant, attenuated pox-virus - use for vaccinating against viral infections such as rabies, hepatitis B, HIV, HSV, EBV, CMV, mumps etc.

Disclosure; Page 220; 456pp; English.

The sequences given in AAQ35720-23 were used to generate an expression cassette for the insertion of the equine influenza virus (EIV) hemagglutinin (HA) (Al/Prague/56) into NVVAC and ALVAC recombinant vectors. The HA gene sequence was isolated from an EIV cDNA library and

CC was amplified by polymerase chain reaction. The amplified sequence was  
 CC inserted into the linearised plasmid pRW764.2. The resultant plasmid was  
 CC designated pPCV1 and contains the vaccinia virus H6 promoter followed by  
 CC a polylinker region and flanked by canarypox virus homologous sequences.  
 CC NYVAC is derived from a Copenhagen vaccine strain of vaccinia virus and  
 CC ALVAC is derived from a canarypox virus which has been modified by  
 CC deletion of non-essential regions of the genome encoding known or  
 CC potential virulence factors. The deletion loci of both vectors were  
 CC engineered as recipient loci for the insertion of foreign genes. See also  
 CC AAQ35501-864. (Updated on 25-MAR-2003 to correct PN field.)  
 XX  
 SQ Sequence 18 BP; 2 A; 1 C; 4 G; 11 T; 0 U; 0 Other;

Query Match 0.9%; Score 14.8; DB 1; Length 18;

Best Local Similarity 88.9%; Pred. No. 1.7e+02;

Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 222 CTCATAGAAAAACAAC 239

DB 18 CTAATAGAAAAACAAC 1

RESULT 224

AAV95047/C

ID AAV95047 standard; RNA; 18 BP.

AC AAV95047;

XX 24-FEB-1999 (first entry)

XX Mouse IL-2 receptor g-chain substrate position 51.

XX Human; IL-2 receptor g-chain; interleukin 2 receptor gamma chain;  
 KW hammerhead ribozyme; hairpin ribozyme; substrate; expression; cancer;  
 KW autoimmune disease; psoriasis; allergy; inflammatory disease;  
 KW graft rejection; ss.

OS Mus sp.

XX WO9824913-A2.

XX 11-JUN-1998.

XX 02-DEC-1997; 97WO-US021748.

XX 03-DEC-1996; 96US-00758306.

XX (RIBO-) RIBOZYME PHARM INC.

XX Stinchcomb DT, Mcswiggen JA;

XX WPI; 1998-333332/29.

XX Ribozymes targetted to interleukin 2 - useful for treating e.g. cancer,  
 PT autoimmune disease and allergies.

XX Claim 4; Page 44; 61pp; English.

XX The present sequence invention describes ribozymes targeted to modulate  
 CC the synthesis and/or expression of interleukin (IL)-2R gamma encoded RNA.  
 CC AAV93889 to AAV94574 represent specifically claimed ribozymes, and  
 CC AAV94575 to AAV95260 represent specifically claimed substrate sequences  
 CC from the present invention. The ribozymes can be used for the treatment  
 CC of, e.g. graft rejection, autoimmune disease, cancer, psoriasis, allergy  
 CC and other inflammatory conditions. The ribozymes are also used to induce  
 CC tolerance in a recipient to alloantigen from a donor

XX Sequence 18 BP; 1 A; 8 C; 3 G; 0 T; 6 U; 0 Other;

Query Match

Best Local Similarity 0.9%; Score 14.8; DB 1; Length 18;

Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1121 GCTGAGCAGCTGAACGA 1138

DB 18 GCAGGAGCAGCTGAACGA 1

RESULT 225

AAH37505

ID AAH37505 standard; DNA; 18 BP.

XX AAH37505;

XX 14-AUG-2001 (first entry)

XX SNP specific upper PCR primer SEQ ID 301.

XX Single nucleotide polymorphism; SNP; single nucleotide primer extension;  
 KW SNPE; genotyping; agammaglobulinaemia; diabetes insipidus; cancer;  
 KW Lesch-Nyhan syndrome; muscular dystrophy; familial hypercholesterolaemia;  
 KW polycystic kidney disease; osteogenesis imperfecta; autoimmune disease;  
 KW acute intermittent porphyria; rheumatoid arthritis; multiple sclerosis;  
 KW inflammation; forensic investigation; paternity analysis; PCR primer; ss.

OS Homo sapiens.

XX WO200129262-A2.

XX 26-APR-2001.

XX 13-OCT-2000; 2000WO-US028436.

XX 15-OCT-1999; 99US-0160096P.

XX (ORCH-) ORCHID BIOSCIENCES INC.

XX Picoult-Newburg L, Pohl M;

XX WPI; 2001-290930/30.

XX New genotyping oligonucleotide, useful for detecting the presence,  
 PT absence or identity of single polynucleotide polymorphism in a nucleic  
 PT acid sample.

XX Claim 1; Page 51; 83pp; English.

XX Sequences AAH37205 - AAH40944 represent PCR primers, single nucleotide  
 CC primer extension (SNPE) primers, and the sequences of regions flanking  
 CC sites of single nucleotide polymorphisms SNPs. The present invention  
 CC includes kits for determining the presence or absence of a SNP, using the  
 CC oligonucleotides of the invention. The PCR primers are used to amplify a  
 CC SNP flanking sequence, the SNPE primer is used as a genotyping primer.  
 CC The oligonucleotides are useful for genotyping a nucleic acid sample by  
 CC performing a single-nucleotide primer extension reaction. The  
 CC oligonucleotides are useful for determining the presence, absence or  
 CC identity of a SNP and for genotyping nucleic acid samples, for e.g. to  
 CC assess by association analysis the genotype of an individual or group of  
 CC individuals, having a pathological phenotypic trait suspected of being  
 CC caused by one or more SNPs. Phenotypic traits include diseases e.g.  
 CC agammaglobulinaemia, diabetes insipidus, Lesch-Nyhan syndrome, muscular  
 CC dystrophy, familial hypercholesterolaemia, polycystic kidney disease,  
 CC osteogenesis imperfecta and acute intermittent porphyria. Phenotypic  
 CC traits also include symptoms of or susceptibility to multifactorial  
 CC disease of which a component is or may be genetic such as autoimmune  
 CC diseases, including, rheumatoid arthritis, multiple sclerosis,  
 CC inflammation, cancer, nervous system diseases and infection by pathogenic  
 CC microorganism. The method is also useful in forensic investigations and  
 CC paternity analysis. The present sequence represents a PCR primer specific  
 CC for a human SNP containing DNA sequence

XX Sequence 18 BP; 4 A; 8 C; 5 G; 1 T; 0 U; 0 Other;

Query Match

Best Local Similarity 0.9%; Score 14.8; DB 1; Length 18;

Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1492 CCAAGTACCAAGGCCCA 1509  
DB 1 CCAAGTGACCAAGGCCCA 18  
RESULT 226  
ACC79773  
ID ACC79773 standard; DNA; 18 BP.  
XX ACC79773;  
XX 02-SEP-2003 (first entry)  
XX Mouse PTPRB reverse PCR primer SEQ ID NO:11.  
XX Tec; protein tyrosine kinase; protein tyrosine phosphatase; PTP10D;  
KW egg derived tyrosine phosphatase; EDTP; antidiabetic; hypotensive;  
KW cardiant; antilipaeamic; osteopathic; cytosatic; anorectic; obesity;  
KW immunomodulator; gene therapy; metabolic disease; eating disorder;  
KW body weight regulation disorder; cachexia; diabetes mellitus; cancer;  
KW hypertension; coronary heart disease; hypercholesterolaemia; gallstone;  
KW dyslipidaemia; osteoarthritis; sleep apnea; mouse; PTPRB;  
KW protein tyrosine phosphatase receptor type B precursor; PCR primer; ss.  
XX Mus sp.  
OS Synthetic.  
XX WO2003047611-A2.  
PN 12-JUN-2003.  
XX 04-DEC-2002; 2002WO-EP013744.  
XX 04-DEC-2001; 2001EP-00128844.  
PR 07-DEC-2001; 2001EP-00129138.  
PR 02-JAN-2002; 2002EP-00000010.  
XX (DEVE-) DEVELOPEN ENTWICKLUNGSBIOLOGISCHE FORSCH.  
XX Meise M, Eulenber K, Fritsch R, Haeder T, Broenner G;  
PI Steuernagel A;  
XX WPI; 2003-532801/50.  
XX New compositions comprising tyrosine phosphatase PTP10D, protein tyrosine  
PT kinase Tec or egg-derived tyrosine phosphatase genes or proteins, useful  
PT for treating or preventing metabolic diseases, e.g. as obesity or  
PT cachexia.  
XX Example 4; Page 52; 83pp; English.  
PS The present invention describes a pharmaceutical composition comprising a  
XX nucleic acid (I) protein tyrosine phosphatase PTP10D, non-receptor  
CC protein tyrosine kinase Tec, egg derived tyrosine phosphatase (EDTP) gene  
CC family or encoded polypeptide, fragment or variant of nucleic acid  
CC molecule or polypeptide, an antibody, an aptamer or receptor recognising  
CC a nucleic acid molecule of PTP10D, Tec, or EDTP gene family or encoded  
CC polypeptide, and a carrier, diluent and/or adjuvant. The pharmaceutical  
CC composition can have antidiabetic, hypotensive, cardiant, antilipaeamic,  
CC osteopathic, cytosatic, anorectic and immunomodulator activities, and  
CC can be used in gene therapy. The composition is useful for the  
CC manufacture of an agent for detecting and/or verifying, for treating and  
CC alleviating and/or preventing a disorder, including metabolic diseases  
CC such as obesity and other body weight regulation disorders, as well as  
CC related disorders such as eating disorder, cachexia, diabetes mellitus,  
CC hypertension, coronary heart disease, hypercholesterolaemia,  
CC dyslipidaemia, osteoarthritis, gallstones, cancers (cancers of the  
CC reproductive organ), sleep apnea, and other diseases, in cells, cell  
CC masses, organs and/or subjects. The components of the composition may  
CC also be used in controlling the function of a gene and/or gene product  
CC which is influenced and/or modified by a PTP10D, Tec, or EDTP homologous  
CC polypeptide, and for identifying substances capable of interacting with a

CC PTP10D, Tec or EDTP homologous polypeptide. The nucleic acid molecule of  
CC PTP10D, Tec, or EDTP family or their fragments, may be used in the  
CC preparation of a non-human animal which over- or under-expresses the  
CC PTP10D, Tec, or EDTP gene product. The present sequence represents a PCR  
CC primer for mouse protein tyrosine phosphatase receptor type B precursor  
CC (PTPRB), which is used in an example from the present invention  
XX  
SQ Sequence 18 BP; 3 A; 10 C; 1 G; 4 T; 0 U; 0 Other;  
Query Match 0.9%; Score 14.8; DB 1; Length 18;  
Best Local Similarity 88.9%; Pred. No. 1.7e+02;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
Qy 764 CTTCCACGCCCATGTCCA 781  
DB 1 CTCCACGCCCATGTCCA 18  
RESULT 227  
ACF04428  
ID ACF04428 standard; DNA; 18 BP.  
XX ACF04428;  
XX 04-DEC-2003 (first entry)  
DT Hepatitis C virus RNA probe.  
DE Hepatitis C virus RNA probe.  
XX Silicon; silicon containing magnetic particle; superparamagnetic;  
KW silicon dioxide; nucleic acid isolation; probe; ss; HCV.  
XX Hepatitis C virus.  
OS  
FH Key Location/Qualifiers  
FT modified\_base 1 /\*tag= a  
FT /mod\_base= OTHER  
FT /note= "modified by FAM"  
FT modified\_base 18  
FT /\*tag= b  
FT /mod\_base= OTHER  
FT /note= "modified by TAMRA"  
XX WO2003058649-A1.  
XX 17-JUL-2003.  
XX 07-JAN-2003; 2003WO-EP0000054.  
XX 14-JAN-2002; 2002DE-01001084.  
XX (FARB ) BAYER AG.  
XX Hennig G, Hildenbrand K;  
PI WPI; 2003-542203/51.  
XX Silicon-coated magnetic particles, useful for purification of nucleic  
PT acid from body samples, do not need to be separated before quantification  
PT by polymerase chain reaction.  
XX Example 7; Page 23; 35pp; German.  
PS The present invention relates to silicon-coated magnetic particles in  
XX which the silicon content is less than 20wt.% of total. These can be used  
CC to isolate nucleic acids from body samples, especially serum,  
CC particularly for diagnostic detection of RNA from hepatitis C virus or  
CC HIV. The present sequence is a probe used to isolate RNA from hepatitis C  
CC virus from serum in the exemplification of the invention  
XX  
SQ Sequence 18 BP; 2 A; 11 C; 3 G; 1 T; 0 U; 1 Other;  
Query Match 0.9%; Score 14.6; DB 1; Length 18;  
Query Match

Best Local Similarity 93.3%; Pred. No. 1.8e+02; Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1509 AGCTCCAGGCCCCC 1523  
Db 1 AGCTCCAGGCCCCC 15

RESULT 228  
AA63904/c  
ID AAX63904 standard; RNA; 17 BP.  
XX AC AAX63904;  
XX DT 20-JUL-1999 (first entry)  
XX DE Rabbit stromelysin hammerhead target SEQ ID NO:536.  
XX KW Arthritic condition; graft tolerance; immune response; target; cleavage;  
KW hammerhead ribozyme; hairpin ribozyme; human; rabbit; mouse; collagenase;  
KW stromelysin; synovial membrane; joint; arthritis; osteoarthritis;  
KW rheumatoid arthritis; autoimmune disease; allergy; inflammation;  
KW diagnosis; ss.  
XX OS Oryctolagus cuniculus.  
XX PN WO9618736-A2.  
XX PD 20-JUN-1996.  
XX PF 22-NOV-1995; 95WO-US015516.  
XX PR 13-DEC-1994; 94US-00354920.  
XX PR 23-DEC-1994; 94US-00363253.  
XX PR 23-DEC-1994; 94US-00363254.  
XX PR 17-FEB-1995; 95US-00390850.  
XX PR 20-APR-1995; 95US-00426124.  
XX PR 02-MAY-1995; 95US-00432874.  
XX PR 04-MAY-1995; 95US-00434509.  
XX PR 07-JUL-1995; 95US-0000951P.  
XX PR 07-JUL-1995; 95US-0000974P.  
XX PR 07-AUG-1995; 95US-00512861.  
XX PR 05-OCT-1995; 95US-00541365.  
XX PA (RIBO-) RIBOZYME PHARM INC.  
XX PI Beigelman L, Stinchcomb DT, Jarvis T, Draper K, Pavco P;  
PI McSwiggen J, Gustofson J, Usman N, Wincott F, Matulic-Adamic J;  
PI Karpeisky A, Thompson JD, Modak A, Burgin A;  
XX WPI; 1996-300653/30.  
XX PT Enzymatic nucleic acid molecules having a hammer-head motif - used for  
PT the treatment of arthritis, induction of graft tolerance or treatment of  
PT auto-immune diseases.  
XX PS Example 1; Page 154; 307pp; English.  
XX CC The present invention describes a novel enzymatic nucleic acid (ENA)  
CC having a hammerhead motif (HM) comprising: (i) at least 5 ribose residues  
CC; (ii) a 2'-C-allyl modification at position 4 of the ENA; (iii) at least  
CC ten 2'-O-methyl modifications; and (iv) a 3'-end modification. The ENA's  
CC can inhibit collagenase and stromelysin production in the synovial  
CC membrane of joints for the treatment or prevention of arthritis.  
CC particularly osteoarthritis or rheumatoid arthritis. The ENA's can also  
CC be used to treat antigen presenting cells of a donor to induce tolerance  
CC in a recipient to an alloantigen of a donor. They can also be used for  
CC enhancing graft tolerance or for treating autoimmune disease, and for  
CC treating allergies and other inflammatory conditions. The ENA's can also  
CC be used in diagnosis. Ribozyme therapy impacts on the expression of  
CC stromelysin without introducing the non-specific effects upon gene  
CC expression which accompany treatment with retinoids and dexamethasone.  
CC The concentration of ribozyme required to affect a therapeutic treatment

CC is lower than that required of antisense molecules, and is highly  
CC specific. The present sequence is used in the exemplification of the  
CC present invention  
XX Sequence 17 BP; 4 A; 2 C; 3 G; 0 T; 8 U; 0 Other;  
SQ Query Match 0.9%; Score 14.4; DB 1; Length 17;  
Best Local Similarity 93.8%; Pred. No. 1.6e+02;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1589 AAGAACAGAAATGCTC 1604  
Db 16 AAGAACAGAAATGCTC 1

RESULT 229  
AAV93469  
ID AAV93469 standard; RNA; 17 BP.  
XX AC AAV93469;  
XX DT 18-FEB-1999 (first entry)  
XX DE Human B-raf substrate nucleotide position 1085.  
XX KW Human; c-raf; A-raf; B-raf; hammerhead ribozyme; hairpin ribozyme;  
KW target; substrate; catalyst; modulation; expression; Raf gene; delivery;  
KW screening; identification; synthesis; deprotection; purification; cancer;  
KW inflammation; psoriasis; non-hepatic ascites; infection; genetic drift;  
KW restenosis; rheumatoid arthritis; ss.  
XX OS Homo sapiens.  
XX PN WO9850530-A2.  
XX PD 12-NOV-1998.  
XX PF 05-MAY-1998; 98WO-US009249.  
XX PR 09-MAY-1997; 97US-0046059P.  
XX PR 09-JUN-1997; 97US-0049002P.  
XX PR 03-JUL-1997; 97US-0051718P.  
XX PR 22-AUG-1997; 97US-0056808P.  
XX PR 02-OCT-1997; 97US-0061321P.  
XX PR 02-OCT-1997; 97US-0061324P.  
XX PR 05-NOV-1997; 97US-0064866P.  
XX PR 19-DEC-1997; 97US-0068212P.  
XX PA (RIBO-) RIBOZYME PHARM INC.  
XX PI Jarvis T, Matulic-Adamic J, Reynolds M, Kisich K, Bellon L;  
PI Parry T, Beigelman L, McSwiggen JA, Karpeisky A, Burgin A;  
PI Thompson J, Workman CT, Beaudry A, Sweedler D;  
XX WPI; 1999-009494/01.  
XX PT Identifying new catalytic nucleic acid that modulates selected processes  
PT - especially ribozymes that cleave Raf RNA for treating cancer,  
PT restenosis, and also new ribozymes and modified nucleoside triphosphates  
PT used as antiviral agents and synthons.  
XX PS Claim 177; Page 168; 259pp; English.  
XX CC A method has been developed for the identification of a nucleic acid  
CC capable of modulating a process in a biological system. The method  
CC comprises: (a) introducing into the system a random library of nucleic  
CC acid catalysts (NAC) having a substrate binding domain (SBD), comprising  
CC a random sequence, and a catalytic domain (CD); and (b) identifying NAC  
CC in systems where modulation has occurred and/or determining the sequence  
CC of at least part of the SBDs in such systems. Nucleic acid molecules with  
CC endonuclease activity and catalytic activity, from the present invention,  
CC are used to modulate gene expression in plant and mammalian cells and to  
CC cleave target nucleic acid, particularly for treating systemic diseases





PR 30-JAN-2001; 2001WO-US000665.  
 PR 30-JAN-2001; 2001WO-US000666.  
 PR 30-JAN-2001; 2001WO-US000667.  
 PR 30-JAN-2001; 2001WO-US000668.  
 PR 30-JAN-2001; 2001WO-US000669.  
 PR 30-JAN-2001; 2001WO-US000670.  
 PR 05-FEB-2001; 2001US-0266860P.  
 XX (AEOM-) AEOMICA INC.  
 XX  
 XX Gu Y, Ji Y, Penn SG, Hanzel DK, Rank DR, Chen W, Shannon ME;  
 XX WPI; 2002-179446/23.  
 XX  
 XX New polypeptide, for raising antibodies that recognize hGDMPLP-1 proteins,  
 PT or as specific biomolecule capture probes for surface-enhanced laser  
 PT desorption ionization, comprises human myosin-like protein hGDMPLP-1.  
 XX  
 XX Disclosure; SEQ ID NO 8352; 214pp; English.  
 XX  
 XX The present invention describes a human genome-derived myosin-like  
 CC protein 1 (hGDMPLP-1). The protein and polynucleotide sequences of hGDMPLP-  
 CC 1 can be used in gene therapy and vaccine production. The hGDMPLP-1  
 CC nucleic acids can be used as probes to detect, characterise and quantify  
 CC hGDMPLP-1 nucleic acids in samples, as amplification substrates, to  
 CC provide initial substrates for the recombinant engineering of hGDMPLP-1  
 CC protein variants having desired phenotypic improvements, and for  
 CC expressing the proteins. The hGDMPLP-1 proteins or polypeptides may be  
 CC used as immunogens to raise antibodies that specifically recognise hGDMPLP  
 CC -1 proteins, as standards in assays used to determine the concentration  
 CC and/or amount specifically of hGDMPLP proteins, as specific biomolecule  
 CC capture probes for surface-enhanced laser desorption/ionisation, as  
 CC therapeutic supplement in patients having specific deficiency in hGDMPLP-1  
 CC production, and in vaccines or for replacement therapy. The  
 CC polynucleotide sequences encoding hGDMPLP-1 may be used for diagnosing a  
 CC disorder associated with the expression of hGDMPLP-1, in particular heart  
 CC and skeletal muscle disorders. hGDMPLP-1 is localised to chromosome 22.  
 CC The present sequence represents an oligomer used in the screening of the  
 CC hGDMPLP-1 sequence in the exemplification of the present invention. N.B.  
 CC The sequence data for this patent did not form part of the printed  
 CC specification, but was obtained in electronic format directly from WIPO  
 CC at ftp.wipo.int/pub/published\_pct\_sequence  
 XX  
 XX Sequence 17 BP; 5 A; 3 C; 7 G; 2 T; 0 U; 0 Other;  
 SQ  
 Query Match 0.9%; Score 14.4; DB 1; Length 17;  
 Best Local Similarity 93.8%; Pred. No. 1.6e+02;  
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 OY 1109 CACCTCTCTCTGCTG 1124  
 Db 17 CAGCTCTCTCTGCTG 2  
 RESULT 232  
 ABN08675  
 ID ABN08675 standard; DNA; 17 BP.  
 XX  
 AC ABN08675;  
 XX  
 XX 29-MAY-2002 (first entry)  
 XX  
 XX Human GDMPLP-1 17-mer scanning SEQ ID NO:5 sequence SEQ ID NO:8667.  
 DE  
 XX Human; genome-derived myosin-like protein 1; GDMPLP-1; hGDMPLP-1; heart;  
 KW muscle; myosin; chromosome 22; gene therapy; vaccine; heart disease;  
 KW skeletal muscle disorder; amplicon; screening; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 XX WO200192524-A2.  
 PN  
 XX 06-DEC-2001.  
 PD

XX 25-MAY-2001; 2001WO-US016981.  
 XX  
 XX 26-MAY-2000; 2000US-0207456P.  
 PR  
 PR 21-SEP-2000; 2000US-0234687P.  
 PR  
 PR 27-SEP-2000; 2000US-0236359P.  
 PR  
 PR 04-OCT-2000; 2000GB-00024263.  
 PR  
 PR 30-JAN-2001; 2001WO-US000661.  
 PR  
 PR 30-JAN-2001; 2001WO-US000662.  
 PR  
 PR 30-JAN-2001; 2001WO-US000663.  
 PR  
 PR 30-JAN-2001; 2001WO-US000664.  
 PR  
 PR 30-JAN-2001; 2001WO-US000665.  
 PR  
 PR 30-JAN-2001; 2001WO-US000666.  
 PR  
 PR 30-JAN-2001; 2001WO-US000667.  
 PR  
 PR 30-JAN-2001; 2001WO-US000668.  
 PR  
 PR 30-JAN-2001; 2001WO-US000669.  
 PR  
 PR 30-JAN-2001; 2001WO-US000670.  
 PR  
 PR 05-FEB-2001; 2001US-0266860P.  
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 PT desorption ionization, comprises human myosin-like protein hGDMPLP-1.  
 XX  
 XX Disclosure; SEQ ID NO 8667; 214pp; English.  
 XX  
 XX The present invention describes a human genome-derived myosin-like  
 CC protein 1 (hGDMPLP-1). The protein and polynucleotide sequences of hGDMPLP-  
 CC 1 can be used in gene therapy and vaccine production. The hGDMPLP-1  
 CC nucleic acids can be used as probes to detect, characterise and quantify  
 CC hGDMPLP-1 nucleic acids in samples, as amplification substrates, to  
 CC provide initial substrates for the recombinant engineering of hGDMPLP-1  
 CC protein variants having desired phenotypic improvements, and for  
 CC expressing the proteins. The hGDMPLP-1 proteins or polypeptides may be  
 CC used as immunogens to raise antibodies that specifically recognise hGDMPLP  
 CC -1 proteins, as standards in assays used to determine the concentration  
 CC and/or amount specifically of hGDMPLP proteins, as specific biomolecule  
 CC capture probes for surface-enhanced laser desorption/ionisation, as  
 CC therapeutic supplement in patients having specific deficiency in hGDMPLP-1  
 CC production, and in vaccines or for replacement therapy. The  
 CC polynucleotide sequences encoding hGDMPLP-1 may be used for diagnosing a  
 CC disorder associated with the expression of hGDMPLP-1, in particular heart  
 CC and skeletal muscle disorders. hGDMPLP-1 is localised to chromosome 22.  
 CC The present sequence represents an oligomer used in the screening of the  
 CC hGDMPLP-1 sequence in the exemplification of the present invention. N.B.  
 CC The sequence data for this patent did not form part of the printed  
 CC specification, but was obtained in electronic format directly from WIPO  
 CC at ftp.wipo.int/pub/published\_pct\_sequence  
 XX  
 XX Sequence 17 BP; 9 A; 2 C; 6 G; 0 T; 0 U; 0 Other;  
 SQ  
 Query Match 0.9%; Score 14.4; DB 1; Length 17;  
 Best Local Similarity 93.8%; Pred. No. 1.6e+02;  
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 OY 274 AAGCAAGAGAGAGAA 289  
 Db 1 AAGCAAGAGAGAGAA 16  
 RESULT 233  
 ABN08361/c  
 ID ABN08361 standard; DNA; 17 BP.  
 XX  
 AC ABN08361;  
 XX  
 XX 29-MAY-2002 (first entry)  
 XX  
 XX

DE	Human GDMLP-1 17-mer scanning SEQ ID NO:5 sequence SEQ ID NO:8353.	Db	16 CAGCTCCTCCTGCTG 1
XX	Human; genome-derived myosin-like protein 1; GDMLP-1; hGDMLP-1; heart;	RESULT 234	
KW	muscle; myosin; chromosome 22; gene therapy; vaccine; heart disease;	ABN10046/c	
KW	skeletal muscle disorder; amplicon; screening; ss.	ID	ABN10046 standard; DNA; 17 BP.
OS	Homo sapiens.	XX	ABN10046;
XX	WO200192524-A2.	XX	29-MAY-2002 (first entry)
PN	06-DEC-2001.	XX	Human GDMLP-1 17-mer scanning SEQ ID NO:5 sequence SEQ ID NO:10038.
PD		DE	
XX	25-MAY-2001; 2001WO-US016981.	XX	Human; genome-derived myosin-like protein 1; GDMLP-1; hGDMLP-1; heart;
XX	26-MAY-2000; 2000US-0207456P.	KW	muscle; myosin; chromosome 22; gene therapy; vaccine; heart disease;
XX	21-SEP-2000; 2000US-0234687P.	KW	skeletal muscle disorder; amplicon; screening; ss.
PR	27-SEP-2000; 2000US-0236359P.	XX	Homo sapiens.
PR	04-OCT-2000; 2000GB-00024263.	XX	WO200192524-A2.
PR	30-JAN-2001; 2001WO-US000661.	XX	06-DEC-2001.
PR	30-JAN-2001; 2001WO-US000662.	XX	25-MAY-2001; 2001WO-US016981.
PR	30-JAN-2001; 2001WO-US000663.	XX	26-MAY-2000; 2000US-0207456P.
PR	30-JAN-2001; 2001WO-US000664.	XX	21-SEP-2000; 2000US-0234687P.
PR	30-JAN-2001; 2001WO-US000665.	XX	27-SEP-2000; 2000US-0236359P.
PR	30-JAN-2001; 2001WO-US000666.	XX	04-OCT-2000; 2000GB-00024263.
PR	30-JAN-2001; 2001WO-US000667.	XX	30-JAN-2001; 2001WO-US000661.
PR	30-JAN-2001; 2001WO-US000668.	XX	30-JAN-2001; 2001WO-US000662.
PR	30-JAN-2001; 2001WO-US000669.	XX	30-JAN-2001; 2001WO-US000663.
PR	30-JAN-2001; 2001WO-US000670.	XX	30-JAN-2001; 2001WO-US000664.
PR	05-FEB-2001; 2001US-0266860P.	XX	30-JAN-2001; 2001WO-US000665.
XX	(AEOM-) AEOMICA INC.	XX	30-JAN-2001; 2001WO-US000666.
PA		XX	30-JAN-2001; 2001WO-US000667.
XX	Gu Y, Ji Y, Penn SG, Hanzel DK, Rank DR, Chen W, Shannon ME;	XX	30-JAN-2001; 2001WO-US000668.
PI	WPI; 2002-179446/23.	XX	30-JAN-2001; 2001WO-US000669.
XX	New polypeptide, for raising antibodies that recognize hGDMLP-1 proteins,	XX	30-JAN-2001; 2001WO-US000670.
XX	or as specific biomolecule capture probes for surface-enhanced laser	XX	05-FEB-2001; 2001US-0266860P.
PT	desorption ionization, comprises human myosin-like protein hGDMLP-1.	XX	(AEOM-) AEOMICA INC.
PT	Disclosure; SEQ ID NO 8353; 214pp; English.	XX	Gu Y, Ji Y, Penn SG, Hanzel DK, Rank DR, Chen W, Shannon ME;
PS		XX	WPI; 2002-179446/23.
XX	The present invention describes a human genome-derived myosin-like	XX	New polypeptide, for raising antibodies that recognize hGDMLP-1 proteins,
XX	protein 1 (hGDMLP-1). The protein and polynucleotide sequences of hGDMLP-	XX	or as specific biomolecule capture probes for surface-enhanced laser
CC	1 can be used in gene therapy and vaccine production. The hGDMLP-1	XX	desorption ionization, comprises human myosin-like protein hGDMLP-1.
CC	nucleic acids can be used as probes to detect, characterise and quantify	XX	Disclosure; SEQ ID NO 10038; 214pp; English.
CC	hGDMLP-1 nucleic acids in samples, as amplification substrates, to	XX	The present invention describes a human genome-derived myosin-like
CC	provide initial substrates for the recombinant engineering of hGDMLP-1	XX	protein 1 (hGDMLP-1). The protein and polynucleotide sequences of hGDMLP-
CC	protein variants having desired phenotypic improvements, and for	XX	1 can be used in gene therapy and vaccine production. The hGDMLP-1
CC	expressing the proteins. The hGDMLP-1 proteins or polypeptides may be	XX	nucleic acids can be used as probes to detect, characterise and quantify
CC	used as immunogens to raise antibodies that specifically recognise hGDMLP	XX	hGDMLP-1 nucleic acids in samples, as amplification substrates, to
CC	-1 proteins, as standards in assays used to determine the concentration	XX	provide initial substrates for the recombinant engineering of hGDMLP-1
CC	and/or amount specifically of hGDMLP proteins, as specific biomolecule	XX	protein variants having desired phenotypic improvements, and for
CC	capture probes for surface-enhanced laser desorption ionisation, as	XX	expressing the proteins. The hGDMLP-1 proteins or polypeptides may be
CC	therapeutic supplement in patients having specific deficiency in hGDMLP-1	XX	used as immunogens to raise antibodies that specifically recognise hGDMLP
CC	production, and in vaccines or for replacement therapy. The	XX	-1 proteins, as standards in assays used to determine the concentration
CC	polynucleotide sequences encoding hGDMLP-1 may be used for diagnosing a	XX	and/or amount specifically of hGDMLP proteins, as specific biomolecule
CC	disorder associated with the expression of hGDMLP-1, in particular heart	XX	capture probes for surface-enhanced laser desorption ionisation, as
CC	and skeletal muscle disorders. hGDMLP-1 is localised to chromosome 22.	XX	therapeutic supplement in patients having specific deficiency in hGDMLP-1
CC	The present sequence represents an oligomer used in the screening of the	XX	production, and in vaccines or for replacement therapy. The
CC	hGDMLP-1 sequence in the exemplification of the present invention. N.B.	XX	polynucleotide sequences encoding hGDMLP-1 may be used for diagnosing a
CC	The sequence data for this patent did not form part of the printed	XX	disorder associated with the expression of hGDMLP-1, in particular heart
CC	specification, but was obtained in electronic format directly from WIPO	XX	and skeletal muscle disorders. hGDMLP-1 is localised to chromosome 22.
CC	at ftp.wipo.int/pub/published_pct_sequence	XX	The present sequence represents an oligomer used in the screening of the
XX	Sequence 17 BP; 5 A; 3 C; 8 G; 1 T; 0 U; 0 Other;	XX	hGDMLP-1 sequence in the exemplification of the present invention. N.B.
XX		XX	The sequence data for this patent did not form part of the printed
XX		XX	specification, but was obtained in electronic format directly from WIPO
XX		XX	at ftp.wipo.int/pub/published_pct_sequence
XX		XX	Sequence 17 BP; 5 A; 3 C; 8 G; 1 T; 0 U; 0 Other;
XX		XX	
XX	Query Match 0.98; Score 14.4; DB 1; Length 17;	XX	
XX	Best Local Similarity 93.88; Pred. No. 1.6e+02;	XX	
XX	Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;	XX	
XX	1109 CACCTCCTCCTGCTG 1124	XX	
XX		XX	

CC specification, but was obtained in electronic format directly from WIPO  
CC at ftp.wipo.int/pub/published\_pct\_sequence  
XX  
SQ Sequence 17 BP; 2 A; 4 C; 8 G; 3 T; 0 U; 0 Other;  
  
Query Match 0.9%; Score 14.4; DB 1; Length 17;  
Best Local Similarity 93.8%; Pred. No. 1.6e+02;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 715 CCGCATCGTCGCAG 730  
Db 16 CCGCATCGTCGCAG 1  
  
RESULT 235  
ABN08673  
ID ABN08673 standard; DNA; 17 BP.  
XX  
AC ABN08673;  
XX  
DT 29-MAY-2002 (first entry)  
XX  
DE Human GDMPLP-1 17-mer scanning SEQ ID NO:5 sequence SEQ ID NO:8665.  
XX  
KW Human; genome-derived myosin-like protein 1; GDMPLP-1; hGDMPLP-1; heart;  
KW muscle; myosin; chromosome 22; gene therapy; vaccine; heart disease;  
KW skeletal muscle disorder; amplicon; screening; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO200192524-A2.  
XX  
PD 06-DEC-2001.  
XX  
PF 25-MAY-2001; 2001WO-US016981.  
XX  
PR 26-MAY-2000; 2000US-0207456P.  
PR 21-SEP-2000; 2000US-0234687P.  
PR 27-SEP-2000; 2000US-0236359P.  
PR 04-OCT-2000; 2000GB-00024263.  
PR 30-JAN-2001; 2001WO-US000661.  
PR 30-JAN-2001; 2001WO-US000662.  
PR 30-JAN-2001; 2001WO-US000663.  
PR 30-JAN-2001; 2001WO-US000664.  
PR 30-JAN-2001; 2001WO-US000665.  
PR 30-JAN-2001; 2001WO-US000666.  
PR 30-JAN-2001; 2001WO-US000667.  
PR 30-JAN-2001; 2001WO-US000668.  
PR 30-JAN-2001; 2001WO-US000669.  
PR 30-JAN-2001; 2001WO-US000670.  
PR 05-FEB-2001; 2001US-0266860P.  
XX  
PA (AEOM-) AEOMICA INC.  
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PI Gu Y, Ji Y, Penn SG, Hanzel DK, Rank DR, Chen W, Shannon ME;  
XX  
XX WPI; 2002-179446/23.  
XX  
DR  
XX  
PT New polypeptide, for raising antibodies that recognize hGDMPLP-1 proteins,  
PT or as specific biomolecule capture probes for surface-enhanced laser  
PT desorption ionization, comprises human myosin-like protein hGDMPLP-1.  
XX  
PS Disclosure; SEQ ID NO 8665; 214pp; English.  
XX  
XX  
CC The present invention describes a human genome-derived myosin-like  
CC protein 1 (hGDMPLP-1). The protein and polynucleotide sequences of hGDMPLP-  
CC 1 can be used in gene therapy and vaccine production. The hGDMPLP-1  
CC nucleic acids can be used as probes to detect, characterise and quantify  
CC hGDMPLP-1 nucleic acids in samples, as amplification substrates, to  
CC provide initial substrates for the recombinant engineering of hGDMPLP-1  
CC protein variants having desired phenotypic improvements, and for  
CC expressing the proteins. The hGDMPLP-1 proteins or polypeptides may be  
CC used as immunogens to raise antibodies that specifically recognise hGDMPLP-1

CC -1 proteins, as standards in assays used to determine the concentration  
CC and/or amount specifically of hGDMPLP proteins, as specific biomolecule  
CC capture probes for surface-enhanced laser desorption ionisation, as  
CC therapeutic supplement in patients having specific deficiency in hGDMPLP-1  
CC production, and in vaccines or for replacement therapy. The  
CC polynucleotide sequences encoding hGDMPLP-1 may be used for diagnosing a  
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CC and skeletal muscle disorders. hGDMPLP-1 is localised to chromosome 22.  
CC The present sequence represents an oligomer used in the screening of the  
CC hGDMPLP-1 sequence in the exemplification of the present invention. N.B.  
CC The sequence data for this patent did not form part of the printed  
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CC at ftp.wipo.int/pub/published\_pct\_sequence  
XX  
SQ Sequence 17 BP; 8 A; 2 C; 7 G; 0 T; 0 U; 0 Other;  
  
Query Match 0.9%; Score 14.4; DB 1; Length 17;  
Best Local Similarity 93.8%; Pred. No. 1.6e+02;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 273 GAAGCCCAAGAGAGA 288  
Db 2 GAAGCCCAAGAGAGA 17  
  
RESULT 236  
ABN10045/c  
ID ABN10045 standard; DNA; 17 BP.  
XX  
AC ABN10045;  
XX  
DT 29-MAY-2002 (first entry)  
XX  
DE Human GDMPLP-1 17-mer scanning SEQ ID NO:5 sequence SEQ ID NO:10037.  
XX  
KW Human; genome-derived myosin-like protein 1; GDMPLP-1; hGDMPLP-1; heart;  
KW muscle; myosin; chromosome 22; gene therapy; vaccine; heart disease;  
KW skeletal muscle disorder; amplicon; screening; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO200192524-A2.  
XX  
PD 06-DEC-2001.  
XX  
PF 25-MAY-2001; 2001WO-US016981.  
XX  
PR 26-MAY-2000; 2000US-0207456P.  
PR 21-SEP-2000; 2000US-0234687P.  
PR 27-SEP-2000; 2000US-0236359P.  
PR 04-OCT-2000; 2000GB-00024263.  
PR 30-JAN-2001; 2001WO-US000661.  
PR 30-JAN-2001; 2001WO-US000662.  
PR 30-JAN-2001; 2001WO-US000663.  
PR 30-JAN-2001; 2001WO-US000664.  
PR 30-JAN-2001; 2001WO-US000665.  
PR 30-JAN-2001; 2001WO-US000666.  
PR 30-JAN-2001; 2001WO-US000667.  
PR 30-JAN-2001; 2001WO-US000668.  
PR 30-JAN-2001; 2001WO-US000669.  
PR 30-JAN-2001; 2001WO-US000670.  
PR 05-FEB-2001; 2001US-0266860P.  
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PA (AEOM-) AEOMICA INC.  
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PI Gu Y, Ji Y, Penn SG, Hanzel DK, Rank DR, Chen W, Shannon ME;  
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PT New polypeptide, for raising antibodies that recognize hGDMPLP-1 proteins,  
PT or as specific biomolecule capture probes for surface-enhanced laser  
PT desorption ionization, comprises human myosin-like protein hGDMPLP-1.  
XX

PS Disclosure; SEQ ID NO 10037; 214pp; English.

XX The present invention describes a human genome-derived myosin-like

CC protein 1 (hGDMLP-1). The protein and polynucleotide sequences of hGDMLP-

CC 1 can be used in gene therapy and vaccine production. The hGDMLP-1

CC nucleic acids can be used as probes to detect, characterise and quantify

CC hGDMLP-1 nucleic acids in samples, as amplification substrates, to

CC provide initial substrates for the recombinant engineering of hGDMLP-1

CC protein variants having desired phenotypic improvements, and for

CC expressing the proteins. The hGDMLP-1 proteins or polypeptides may be

CC used as immunogens to raise antibodies that specifically recognise hGDMLP

CC -1 proteins, as standards in assays used to determine the concentration

CC and/or amount specifically of hGDMLP proteins, as specific biomolecule

CC capture probes for surface-enhanced laser desorption/ionisation, as

CC therapeutic supplement in patients having specific deficiency in hGDMLP-1

CC production, and in vaccines or for replacement therapy. The

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CC disorder associated with the expression of hGDMLP-1, in particular heart

CC and skeletal muscle disorders. hGDMLP-1 is localised to chromosome 22.

CC The present sequence represents an oligomer used in the screening of the

CC hGDMLP-1 sequence in the exemplification of the present invention. N.B.

CC The sequence data for this patent did not form part of the printed

CC specification, but was obtained in electronic format directly from WIPO

CC at ftp.wipo.int/pub/published\_pct\_sequence

XX

XX Sequence 17 BP; 2 A; 3 C; 8 G; 4 T; 0 U; 0 Other;

SQ

Query Match 0.9%; Score 14.4; DB 1; Length 17;

Best Local Similarity 93.8%; Pred. No. 1.6e+02;

Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 715 CCCGATCGTCGCGAG 730

DB 17 CCCGATCGTCACAG 2

RESULT 237

ACN07604

ID ACN07604 standard; RNA; 17 BP.

XX

XX ACN07604;

XX

XX 22-APR-2004 (first entry)

XX

XX WNV minus strand Hammerhead Ribozyme substrate SEQ ID NO 7607.

DE

XX WNV; West Nile Virus; antiinflammatory; cytostatic; hepatotropic;

XX virucide; neuroprotective; antibacterial; replication; pancreatitis;

XX encephalitis; myocarditis; meningitis; infection; hepatitis;

XX liver failure; cancer; cirrhosis; Hammerhead; Inozyme; DNazyme;

XX Amberzyme; Zinzyne; ss.

XX

XX West Nile Virus.

OS

XX WO200268637-A2.

XX

XX 06-SEP-2002.

XX

XX 19-OCT-2001; 2001WO-US048350.

XX

XX 20-OCT-2000; 2000US-0242411P.

XX

XX (RIBO-) RIBOZYME PHARM INC.

XX (BLAT/) BLATT L.

XX (MCSW/) MCSWIGGEN J A.

XX

XX Blatt L, Mcswiggen JA;

XX

XX WPI; 2002-706994/76.

XX

XX New nucleic acid molecule that modulates replication of West Nile Virus

XX (WNV), useful for treating a condition related to WNV infection e.g.

XX pancreatitis, meningitis, hepatocellular carcinoma or cirrhosis.

PT

PS Claim 23; SEQ ID NO 7607; 495pp; English.

XX

XX The invention relates to nucleic acid molecules that modulate replication

CC of the West Nile Virus (WNV). The nucleic acid molecules are useful for

CC treating a condition related to WNV infection e.g. pancreatitis,

CC encephalitis, myocarditis, meningitis, neurologic infection, hepatitis,

CC liver failure, hepatocellular carcinoma or cirrhosis. The nucleic acid

CC molecule is selected from the group of ribozymes consisting of

CC Hammerhead, Inozyme, G-cleaver, DNazyme, Amberzyme and Zinzyne. The

CC nucleic acid molecules further comprise at least five ribose residues, at

CC least ten 2'-O-methyl modifications, phosphorothioate linkages on at

CC least three of the 5' terminal nucleotides and a 3' end modification of a

CC 3'-3' inverted abasic moiety. Nucleic acid molecules SEQ ID NO 1 to 37080

CC are claimed; however, SEQ ID NO 2194-2206 and 17502-17514 are not given

CC in the specification. The present sequence is that of a nucleic acid

CC molecule of the invention

XX

XX Sequence 17 BP; 2 A; 7 C; 5 G; 0 T; 3 U; 0 Other;

SQ

Query Match 0.9%; Score 14.4; DB 1; Length 17;

Best Local Similarity 75.0%; Pred. No. 1.6e+02;

Matches 12; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1234 CGGACGTTCTTCGCG 1249

DB 1 CGGACGUUCCAUCCGG 16

RESULT 238

ACN09975

ID ACN09975 standard; RNA; 17 BP.

XX

XX ACN09975;

XX

XX 22-APR-2004 (first entry)

XX

XX WNV minus strand Inozyme substrate SEQ ID NO 9978.

DE

XX WNV; West Nile Virus; antiinflammatory; cytostatic; hepatotropic;

XX virucide; neuroprotective; antibacterial; replication; pancreatitis;

XX encephalitis; myocarditis; meningitis; infection; hepatitis;

XX liver failure; cancer; cirrhosis; Hammerhead; Inozyme; DNazyme;

XX Amberzyme; Zinzyne; ss.

XX

XX West Nile Virus.

OS

XX WO200268637-A2.

XX

XX 06-SEP-2002.

XX

XX 19-OCT-2001; 2001WO-US048350.

XX

XX 20-OCT-2000; 2000US-0242411P.

XX

XX (RIBO-) RIBOZYME PHARM INC.

XX (BLAT/) BLATT L.

XX (MCSW/) MCSWIGGEN J A.

XX

XX Blatt L, Mcswiggen JA;

XX

XX WPI; 2002-706994/76.

XX

XX New nucleic acid molecule that modulates replication of West Nile Virus

XX (WNV), useful for treating a condition related to WNV infection e.g.

XX pancreatitis, meningitis, hepatocellular carcinoma or cirrhosis.

PT

CC liver failure, hepatocellular carcinoma or cirrhosis. The nucleic acid molecule is selected from the group of ribozymes consisting of Hammerhead, Inozyme, G-cleaver, DNazyme, Amberzyme and Zinzyne. The nucleic acid molecules further comprise at least five ribose residues, at least ten 2'-O-methyl modifications, phosphorothioate linkages on at least three of the 5' terminal nucleotides and a 3' end modification of a 3'-3' inverted abasic moiety. Nucleic acid molecules SEQ ID NO 1 to 37080 are claimed; however, SEQ ID NO 2194-2206 and 17502-17514 are not given in the specification. The present sequence is that of a nucleic acid molecule of the invention

XX  
SQ Sequence 17 BP; 2 A; 9 C; 2 G; 0 T; 4 U; 0 Other;  
Query Match 0.9%; Score 14.4; DB 1; Length 17;  
Best Local Similarity 68.8%; Pred. NO. 1.6e+02;  
Matches 11; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1104 CTCACACCTCTCTCT 1119  
DB 1 CUCGACACCUCCUCCU 16

RESULT 239  
ACN07053/C  
ID ACN07053 standard; RNA; 17 BP.  
XX AC ACN07053;  
XX  
DT 22-APR-2004 (first entry)  
XX  
DE WNV Amberzyme substrate SEQ ID NO 7056.  
XX  
KW WNV; West Nile Virus; antiinflammatory; cytostatic; hepatotropic; virucide; neuroprotective; antibacterial; replication; pancreatitis; encephalitis; myocarditis; meningitis; infection; hepatitis;  
KW liver failure; cancer; cirrhosis; Hammerhead; Inozyme; DNazyme; Amberzyme; Zinzyne; ss.  
XX  
OS West Nile Virus.  
XX  
PN WO200268637-A2.  
XX  
PD 06-SEP-2002.  
XX  
PF 19-OCT-2001; 2001WO-US048350.  
XX  
PR 20-OCT-2000; 2000US-0242411P.  
XX  
PA (RIBO-) RIBOZYME PHARM INC.  
PA (BLAT/) BLATT L.  
PA (MCSW/) MCSWIGGEN J A.  
XX  
PI Blatt L, Mcswiggen JA;  
XX  
DR WPI; 2002-706994/76.  
XX  
PT New nucleic acid molecule that modulates replication of West Nile Virus (WNV), useful for treating a condition related to WNV infection e.g. pancreatitis, meningitis, hepatocellular carcinoma or cirrhosis.  
XX  
PS Claim 23; SEQ ID NO 7056; 495pp; English.  
XX  
CC The invention relates to nucleic acid molecules that modulate replication of the West Nile Virus (WNV). The nucleic acid molecules are useful for treating a condition related to WNV infection e.g. pancreatitis, encephalitis, myocarditis, meningitis, neurologic infection, hepatitis, liver failure, hepatocellular carcinoma or cirrhosis. The nucleic acid molecule is selected from the group of ribozymes consisting of Hammerhead, Inozyme, G-cleaver, DNazyme, Amberzyme and Zinzyne. The nucleic acid molecules further comprise at least five ribose residues, at least ten 2'-O-methyl modifications, phosphorothioate linkages on at least three of the 5' terminal nucleotides and a 3' end modification of a 3'-3' inverted abasic moiety. Nucleic acid molecules SEQ ID NO 1 to 37080 are claimed; however, SEQ ID NO 2194-2206 and 17502-17514 are not given in the specification. The present sequence is that of a nucleic acid molecule of the invention

CC are claimed; however, SEQ ID NO 2194-2206 and 17502-17514 are not given in the specification. The present sequence is that of a nucleic acid molecule of the invention

XX  
SQ Sequence 17 BP; 4 A; 2 C; 9 G; 0 T; 2 U; 0 Other;  
Query Match 0.9%; Score 14.4; DB 1; Length 17;  
Best Local Similarity 93.8%; Pred. NO. 1.6e+02;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1104 CTCACACCTCTCTCT 1119  
DB 17 CTCGACACCTCTCTCT 2

RESULT 240  
ACN07193/C  
ID ACN07193 standard; RNA; 17 BP.  
XX AC ACN07193;  
XX  
DT 22-APR-2004 (first entry)  
XX  
DE WNV Amberzyme substrate SEQ ID NO 7196.  
XX  
KW WNV; West Nile Virus; antiinflammatory; cytostatic; hepatotropic; virucide; neuroprotective; antibacterial; replication; pancreatitis; encephalitis; myocarditis; meningitis; infection; hepatitis;  
KW liver failure; cancer; cirrhosis; Hammerhead; Inozyme; DNazyme; Amberzyme; Zinzyne; ss.  
XX  
OS West Nile Virus.  
XX  
PN WO200268637-A2.  
XX  
PD 06-SEP-2002.  
XX  
PF 19-OCT-2001; 2001WO-US048350.  
XX  
PR 20-OCT-2000; 2000US-0242411P.  
XX  
PA (RIBO-) RIBOZYME PHARM INC.  
PA (BLAT/) BLATT L.  
PA (MCSW/) MCSWIGGEN J A.  
XX  
PI Blatt L, Mcswiggen JA;  
XX  
DR WPI; 2002-706994/76.  
XX  
PT New nucleic acid molecule that modulates replication of West Nile Virus (WNV), useful for treating a condition related to WNV infection e.g. pancreatitis, meningitis, hepatocellular carcinoma or cirrhosis.  
XX  
PS Claim 23; SEQ ID NO 7196; 495pp; English.  
XX  
CC The invention relates to nucleic acid molecules that modulate replication of the West Nile Virus (WNV). The nucleic acid molecules are useful for treating a condition related to WNV infection e.g. pancreatitis, encephalitis, myocarditis, meningitis, neurologic infection, hepatitis, liver failure, hepatocellular carcinoma or cirrhosis. The nucleic acid molecule is selected from the group of ribozymes consisting of Hammerhead, Inozyme, G-cleaver, DNazyme, Amberzyme and Zinzyne. The nucleic acid molecules further comprise at least five ribose residues, at least ten 2'-O-methyl modifications, phosphorothioate linkages on at least three of the 5' terminal nucleotides and a 3' end modification of a 3'-3' inverted abasic moiety. Nucleic acid molecules SEQ ID NO 1 to 37080 are claimed; however, SEQ ID NO 2194-2206 and 17502-17514 are not given in the specification. The present sequence is that of a nucleic acid molecule of the invention

XX  
SQ Sequence 17 BP; 3 A; 5 C; 7 G; 0 T; 2 U; 0 Other;  
Query Match 0.9%; Score 14.4; DB 1; Length 17;

Best Local Similarity 93.8%; Pred. No. 1.6e+02;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1234 CGGACGTTCTTCGG 1249  
Db 17 CGGACGTTCTTCGG 2

## RESULT 241

ACN04500/C

ID ACN04500 standard; RNA; 17 BP.

XX AC ACN04500;

XX DT 22-APR-2004 (first entry)

XX WNV Zinzyne substrate SEQ ID NO 4503.

XX WNV; West Nile Virus; antiinflammatory; cytostatic; hepatotropic;  
KW virucide; neuroprotective; antibacterial; replication; pancreatitis;  
KW encephalitis; myocarditis; meningitis; infection; hepatitis;  
KW liver failure; cancer; cirrhosis; Hammerhead; Inozyme; DNAzyme;  
KW Amberzyme; Zinzyne; ss.  
XX OS West Nile Virus.

XX PN WO200268637-A2.

XX PD 06-SEP-2002.

XX PF 19-OCT-2001; 2001WO-US048350.

XX PR 20-OCT-2000; 2000US-0242411P.

XX PA (RIBO-) RIBOZYME PHARM INC.

XX PA (BLAT/) BLATT L.

XX PA (MCSW/) MCSWIGGEN J A.

XX PI Blatt L, Mcswiggen JA;

XX WPI; 2002-706994/76.

XX New nucleic acid molecule that modulates replication of West Nile Virus  
(WNV), useful for treating a condition related to WNV infection e.g.  
PT pancreatitis, meningitis, hepatocellular carcinoma or cirrhosis.  
PS Claim 23; SEQ ID NO 4503; 495pp; English.

XX The invention relates to nucleic acid molecules that modulate replication  
of the West Nile Virus (WNV). The nucleic acid molecules are useful for  
treating a condition related to WNV infection e.g. pancreatitis,  
encephalitis, myocarditis, meningitis, neurologic infection, hepatitis,  
liver failure, hepatocellular carcinoma or cirrhosis. The nucleic acid  
molecule is selected from the group of ribozymes consisting of  
Hammerhead, Inozyme, G-cleaver, DNAzyme, Amberzyme and Zinzyne. The  
nucleic acid molecules further comprise at least five ribose residues, at  
least ten 2'-O-methyl modifications, phosphorothioate linkages on at  
least three of the 5' terminal nucleotides and a 3' end modification of a  
3'-3' inverted abasic moiety. Nucleic acid molecules SEQ ID NO 1 to 37080  
are claimed; however, SEQ ID NO 2194-2206 and 17502-17514 are not given  
in the specification. The present sequence is that of a nucleic acid  
molecule of the invention

Sequence 17 BP; 4 A; 1 C; 10 G; 0 T; 2 U; 0 Other;

Query Match 0.9%; Score 14.4; DB 1; Length 17;

Best Local Similarity 93.8%; Pred. No. 1.6e+02;

Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1104 CTCGACACCTCTCTCT 1119

Db 16 CTCGACACCTCTCTCT 1

## RESULT 242

ACN07603

ID ACN07603 standard; RNA; 17 BP.

XX AC ACN07603;

XX DT 22-APR-2004 (first entry)

XX WNV minus strand Hammerhead Ribozyme substrate SEQ ID NO 7606.

XX WNV; West Nile Virus; antiinflammatory; cytostatic; hepatotropic;  
KW virucide; neuroprotective; antibacterial; replication; pancreatitis;  
KW encephalitis; myocarditis; meningitis; infection; hepatitis;  
KW liver failure; cancer; cirrhosis; Hammerhead; Inozyme; DNAzyme;  
KW Amberzyme; Zinzyne; ss.  
XX OS West Nile Virus.

XX PN WO200268637-A2.

XX PD 06-SEP-2002.

XX PF 19-OCT-2001; 2001WO-US048350.

XX PR 20-OCT-2000; 2000US-0242411P.

XX PA (RIBO-) RIBOZYME PHARM INC.

XX PA (BLAT/) BLATT L.

XX PA (MCSW/) MCSWIGGEN J A.

XX PI Blatt L, Mcswiggen JA;

XX WPI; 2002-706994/76.

XX New nucleic acid molecule that modulates replication of West Nile Virus  
(WNV), useful for treating a condition related to WNV infection e.g.  
PT pancreatitis, meningitis, hepatocellular carcinoma or cirrhosis.  
PS Claim 23; SEQ ID NO 7606; 495pp; English.

XX The invention relates to nucleic acid molecules that modulate replication  
of the West Nile Virus (WNV). The nucleic acid molecules are useful for  
treating a condition related to WNV infection e.g. pancreatitis,  
encephalitis, myocarditis, meningitis, neurologic infection, hepatitis,  
liver failure, hepatocellular carcinoma or cirrhosis. The nucleic acid  
molecule is selected from the group of ribozymes consisting of  
Hammerhead, Inozyme, G-cleaver, DNAzyme, Amberzyme and Zinzyne. The  
nucleic acid molecules further comprise at least five ribose residues, at  
least ten 2'-O-methyl modifications, phosphorothioate linkages on at  
least three of the 5' terminal nucleotides and a 3' end modification of a  
3'-3' inverted abasic moiety. Nucleic acid molecules SEQ ID NO 1 to 37080  
are claimed; however, SEQ ID NO 2194-2206 and 17502-17514 are not given  
in the specification. The present sequence is that of a nucleic acid  
molecule of the invention

Sequence 17 BP; 2 A; 6 C; 6 G; 0 T; 3 U; 0 Other;

Query Match

Best Local Similarity 0.9%; Score 14.4; DB 1; Length 17;

Matches 12; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1234 CGGACGTTCTTCGG 1249

Db 2 CGGACGUUCCAUCCGG 17

## RESULT 243

ABT3885/C

ID ABT3885 standard; DNA; 17 BP.

XX AC ABT3885;

XX

DT 12-JUN-2003 (first entry)  
XX Tumour suppression related human fukutin oligo SEQ ID No 4522.  
DE Cytostatic; virucide; neuroprotective; nootropic; neuroleptic; gene chip;  
XX antisense; sense; tumour; cell degeneration; cancer; Alzheimer's disease;  
KW schizophrenia; protein chip; gene therapy; tumour suppression;  
KW human fukutin; ds.  
XX Homo sapiens.  
OS  
XX  
XX  
PN WO2003025175-A2.  
XX  
XX 27-MAR-2003.  
XX  
XX 17-SEP-2002; 2002WO-IB004208.  
XX  
XX 17-SEP-2001; 2001FR-00011978.  
XX  
XX (MOLE-) MOLECULAR ENGINES LAB.  
XX  
XX Telerman A, Amson R, Tuijnder M;  
XX  
XX WPI; 2003-313353/30.  
XX  
XX New isolated nucleic acid, useful for treating viral diseases associated  
PT with tumors and cell degeneration, also related polypeptides, antibodies  
PT and transfected cells.  
XX  
XX Disclosure; Page 562; 720pp; French.  
XX  
XX The invention relates to a novel isolated 17 mer nucleic acid sequence,  
CC given in the specification, a sequence containing at least 15 consecutive  
CC nucleotides from the 17 mer sequence, a sequence with, after optimal  
CC alignment, at least 80 % identity to the 17 mer sequence, a sequence that  
CC hybridizes to them under highly stringent conditions, or the complement  
CC of any of them, or the corresponding RNA. The novel isolated nucleic  
CC acids of the invention are useful as probes and primers for detecting,  
CC identifying, quantifying and/or amplifying a nucleic acid, e.g. as one  
CC component of a gene chip, in vitro as (anti)sense reagents, and for  
CC production of recombinant polypeptides. Any of the nucleic acids,  
CC polypeptides, vectors containing the nucleic acids, cells containing the  
CC vector or antibodies directed against the polypeptides are useful for  
CC preparation of pharmaceuticals for prevention and/or treatment of viral  
CC diseases that are characterised by development of tumours or cell  
CC degeneration, specifically cancer but also Alzheimer's disease and  
CC schizophrenia. Analysis of the expression of the 17 mer nucleic acids in  
CC patient samples is useful for diagnosis and/or prognosis of these  
CC diseases. The polypeptides can also be used to generate antibodies, and  
CC both the polypeptide and antibodies are useful as components of protein  
CC chips. The nucleic acid sequences of the invention can be used in gene  
CC therapy. This polynucleotide sequence represents a tumour suppression  
CC related human fukutin oligonucleotide of the invention  
XX  
SQ Sequence 17 BP; 2 A; 6 C; 2 G; 7 T; 0 U; 0 Other;  
Query Match 0.9%; Score 14.4; DB 1; Length 17;  
Best Local Similarity 93.8%; Pred. No. 1.6e+02;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 326 AAAGCTGAAGGAGCTC 341  
Db 16 AAAGCTGAAGGAGATC 1  
RESULT 244  
ADB00466/c  
ID ADB00466 standard; DNA; 17 BP.  
XX  
XX ADB00466;  
XX  
XX 20-NOV-2003 (first entry)  
XX  
XX

DE Human MD23 scanning oligonucleotide SEQ ID 1452.  
XX  
XX Cytostatic; immunostimulant; gene therapy; vaccine; human;  
KW zinc finger protein; MD23; MD24; MD27; MD212; chromosome 7q22.1;  
KW chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer;  
KW developmental disorder; ss.  
XX  
OS Homo sapiens.  
XX  
XX EP1281758-A2.  
XX  
XX 05-FEB-2003.  
XX  
XX 30-JUL-2002; 2002EP-00016874.  
XX  
XX 02-AUG-2001; 2001US-00922181.  
XX  
XX (AEOM-) AEOMICA INC.  
XX  
XX Shannon M, Gu Y, Nguyen C;  
XX WPI; 2003-423107/40.  
XX  
XX New zinc finger-containing proteins and nucleic acids, useful in  
PT manufacturing a medicament for treating or preventing a disorder  
PT associated with decreased or increased expression or activity of MD23,  
PT MD24, MD27 or MD212, e.g. cancer.  
XX  
XX Example 8; SEQ ID NO 1452; 103pp; English.  
XX  
XX The present invention relates to novel human zinc finger-containing  
CC proteins and their coding sequences: MD23, MD24, MD27, MD212. MD23 is  
CC encoded at chromosome 7q22.1, MD24 is encoded at chromosome 6p21.3-22.2,  
CC MD27 is encoded at chromosome 16p11.2 and MD212 is encoded at chromosome  
CC 15q26.1. The MD23, MD24, MD27, and MD212 sequences are useful in therapy,  
CC or in manufacturing a medicament for treating or preventing a disorder  
CC associated with decreased or increased expression or activity of MD23,  
CC MD24, MD27, or MD212, e.g. cancer or developmental disorders. The nucleic  
CC acids and proteins are also useful for diagnosing or monitoring a disease  
CC caused by altered expression of MD23, MD24, MD27, or MD212. The nucleic  
CC acids can also be used as probes to detect and characterize gross  
CC alterations in MD23, MD24, MD27, or MD212 genetic locus. The probes are  
CC useful in constructing microarrays for measuring gene expression. The  
CC proteins are useful as therapeutic agents for gene therapy or as  
CC vaccines. The present sequence was used to illustrate the invention.  
XX  
SQ Sequence 17 BP; 4 A; 6 C; 5 G; 2 T; 0 U; 0 Other;  
Query Match 0.9%; Score 14.4; DB 1; Length 17;  
Best Local Similarity 93.8%; Pred. No. 1.6e+02;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 928 GCTGCTGCGGATGAA 943  
Db 16 GCTGCTGCGGCTGAA 1  
RESULT 245  
ADB00464/c  
ID ADB00464 standard; DNA; 17 BP.  
XX  
XX ADB00464;  
XX  
XX 20-NOV-2003 (first entry)  
XX  
XX Human MD23 scanning oligonucleotide SEQ ID 1450.  
DE  
XX  
XX Cytostatic; immunostimulant; gene therapy; vaccine; human;  
KW zinc finger protein; MD23; MD24; MD27; MD212; chromosome 7q22.1;  
KW chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer;  
KW developmental disorder; ss.  
XX  
OS Homo sapiens.  
XX

XX EP1281758-A2.  
XX 05-FEB-2003.  
XX 30-JUL-2002; 2002EP-00016874.  
XX 02-AUG-2001; 2001US-00922181.  
XX (ABOM-) ABOMICA INC.  
XX Shannon M, Gu Y, Nguyen C;  
XX WPI; 2003-423107/40.  
XX New zinc finger-containing proteins and nucleic acids, useful in  
XX manufacturing a medicament for treating or preventing a disorder  
XX associated with decreased or increased expression or activity of MDZ3,  
XX MDZ4, MDZ7 or MDZ12, e.g. cancer.  
XX Example 8; SEQ ID NO 1450; 103pp; English.  
XX The present invention relates to novel human zinc finger-containing  
XX proteins and their coding sequences: MDZ3, MDZ4, MDZ7, MDZ12. MDZ3 is  
XX encoded at chromosome 7q22.1, MDZ4 is encoded at chromosome 6p21.3-22.2,  
XX MDZ7 is encoded at chromosome 16p11.2 and MDZ12 is encoded at chromosome  
XX 15q26.1. The MDZ3, MDZ4, MDZ7, and MDZ12 sequences are useful in therapy,  
XX or in manufacturing a medicament for treating or preventing a disorder  
XX associated with decreased or increased expression or activity of MDZ3,  
XX MDZ4, MDZ7, or MDZ12, e.g. cancer or developmental disorders. The nucleic  
XX acids and proteins are also useful for diagnosing or monitoring a disease  
XX caused by altered expression of MDZ3, MDZ4, MDZ7, or MDZ12. The nucleic  
XX acids can also be used as probes to detect and characterize gross  
XX alterations in MDZ3, MDZ4, MDZ7, or MDZ12 genetic locus. The probes are  
XX useful in constructing microarrays for measuring gene expression. The  
XX proteins are useful as therapeutic agents for gene therapy or as  
XX vaccines. The present sequence was used to illustrate the invention.  
XX  
XX Sequence 17 BP; 3 A; 6 C; 6 G; 2 T; 0 U; 0 Other;  
SQ  
Query Match 0.9%; Score 14.4; DB 1; Length 17;  
Best Local Similarity 93.8%; Pred. No. 1.6e+02;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 929 CTGCTGCGGATGAAG 944  
DB 17 CTGCTGCGGCTGAAG 2  
RESULT 246  
ABZ61479/c  
ID ABZ61479 standard; RNA; 17 BP.  
XX ABZ61479;  
XX  
XX 21-MAR-2003 (first entry)  
XX  
XX Human H-Ras DNase target #270.  
XX  
XX Human; ribozyme; short interfering RNA; siRNA; HER2; K-Ras;  
XX enzymatic nucleic acid; H-Ras; N-Ras; HIV; cytostatic; anti-HIV;  
XX anti-rheumatic; cancer; AIDS; ss.  
XX Homo sapiens.  
XX OS  
XX WO200297114-A2.  
XX  
XX 05-DEC-2002.  
XX  
XX 29-MAY-2002; 2002WO-US016840.  
XX  
XX 29-MAY-2001; 2001US-0294140P.  
XX  
XX 06-JUN-2001; 2001US-0296249P.  
XX

PR 10-SEP-2001; 2001US-0318471P.  
XX (RIBO-) RIBOZYME PHARM INC.  
XX Mcswiggen J;  
XX WPI; 2003-140484/13.  
XX  
XX Novel short interfering RNA and enzymatic nucleic acid useful for  
XX treating cancer, modulates the expression of a nucleic acid encoding  
XX HER2, K-Ras, H-Ras, N-Ras, and human deficiency virus sequences.  
XX  
XX Claim 58; Page 116; 185pp; English.  
XX  
XX The invention relates to a novel short interfering RNA (siRNA) nucleic  
XX acid molecule or an enzymatic nucleic acid molecule, that modulates  
XX expression of a nucleic acid molecule encoding HER2, K-Ras, H-Ras, N-Ras,  
XX human immunodeficiency virus (HIV) or a component of HIV. The nucleic  
XX acid molecule of the invention has cytostatic, anti-HIV, and anti-  
XX rheumatic activity. The nucleic acid molecules are useful for reducing  
XX HER2, K-Ras, H-Ras, and HIV activity in a cell. The nucleic acids are  
XX also useful for treating breast, ovarian, colorectal, lung, prostate,  
XX bladder, or pancreatic cancer, and HIV infection, and AIDS. The sequences  
XX shown in ABZ59989 - ABZ62216, ABZ64544 - ABZ65531, ABZ65520 - ABZ66524,  
XX ABZ66530 - ABZ66585 represent substrate/target sequences for the human  
XX ribozymes of the invention  
SQ Sequence 17 BP; 1 A; 5 C; 9 G; 0 T; 2 U; 0 Other;  
Query Match 0.9%; Score 14.4; DB 1; Length 17;  
Best Local Similarity 93.8%; Pred. No. 1.6e+02;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1507 CCAGCTTCGAGCCCC 1522  
DB 17 CCAGCTTCGAGCCCC 2  
RESULT 247  
ACD59853  
ID ACD59853 standard; RNA; 17 BP.  
XX  
XX ACD59853;  
XX  
XX 24-SEP-2003 (first entry)  
XX  
XX HCV DNase substrate sequence #1543.  
XX  
XX Nucleic acid molecule; Hepatitis C virus; HCV; Hepatitis B virus; HBV;  
XX RNA stability; RNA expression; RNA synthesis; antisense;  
XX enzymatic nucleic acid; hammerhead ribozyme; DNase; zinzyme; zinzyme;  
XX amberyse; G-cleaver ribozyme; decoy molecule; aptamer;  
XX HBV reverse transcriptase; Enhancer I region; viral replication;  
XX degenerative; disease state; HBV infection; HCV infection; cirrhosis;  
XX liver failure; hepatocellular carcinoma; hepatotropic; cytostatic;  
XX virucide; antiinflammatory; substrate; ss.  
XX  
XX Hepatitis C virus.  
XX OS  
XX WO200281494-A1.  
XX  
XX 17-OCT-2002.  
XX  
XX 26-MAR-2002; 2002WO-US009187.  
XX  
XX 26-MAR-2001; 2001US-00817879.  
XX  
XX 08-JUN-2001; 2001US-00877478.  
XX  
XX 08-JUN-2001; 2001US-0296876P.  
XX  
XX 24-OCT-2001; 2001US-0335059P.  
XX  
XX 05-DEC-2001; 2001US-0337055P.  
XX  
XX (RIBO-) RIBOZYME PHARM INC.  
XX (BLAT/) BLATT L.  
XX



PA (MACE/) MACEJAK D.  
PA (MCSW/) MCSWIGGEN J.  
PA (MORR/) MORRISSEY D.  
PA (PAVC/) PAVCO P.  
PA (LESP/) LEE P.  
PA (DRAP/) DRAPER K.  
PA (ROBE/) ROBERTS E.  
XX  
PI Blatt L, Macejak D, Mcswiggen J, Morrissey D, Pavco P, Lee P;  
PI Draper K, Roberts E;  
XX  
XX WPI; 2003-229207/22.  
XX  
PT Novel compound useful for treating cirrhosis, liver failure,  
PT hepatocellular carcinoma, or condition associated with hepatitis C virus  
PT infection.  
XX  
XX Claim 1; Page 261; 387pp; English.  
XX  
CC The present invention relates to nucleic acid molecules which modulate  
CC the synthesis, expression and/or stability of Hepatitis C virus (HCV) or  
CC Hepatitis B virus (HBV) RNA. The nucleic acid molecules include antisense  
CC and enzymatic nucleic acids such as hammerhead ribozymes, DNazymes,  
CC inozymes, zinzymes, amberzymes, and G-cleaver ribozymes. Also disclosed  
CC are nucleic acid decoy molecules and aptamers that bind to HBV reverse  
CC transcriptase and/or HBV reverse transcriptase primer sequences, as well  
CC as oligonucleotides that specifically bind the Enhancer I region of HBV  
CC DNA. The nucleic acids may be used to modulate the expression of HBV  
CC genes and HBV viral replication. Also disclosed is a method for screening  
CC compounds and/or potential therapies directed against HBV, and compounds  
CC that modulate the expression and/or replication of HCV. The compounds and  
CC methods of the invention are useful for the treatment of degenerative and  
CC disease states related to HBV and HCV infection, replication and gene  
CC expression such as cirrhosis, liver failure, and hepatocellular  
CC carcinoma. The present sequence represents a substrate for one of the HCV  
CC DNzyme or minus strand DNzyme sequences disclosed in the present  
CC invention  
XX  
SQ Sequence 17 BP; 2 A; 7 C; 4 G; 0 T; 4 U; 0 Other;  
  
Query Match 0.9%; Score 14.4; DB 1; Length 17;  
Best Local Similarity 75.0%; Pred. No. 1.6e+02;  
Matches 12; Conservative 3; Mismatches 1; Indels 0; Gaps 0;  
  
QY 768 CACGCCATGTCAGC 783  
|||||:|:|:|  
DB 1 CACGCCAUGUUCGCG 16  
  
RESULT 248  
ACDS3920/c  
ID ACDS3920 standard; RNA; 17 BP.  
XX  
AC ACDS3920;  
XX  
XX  
DT 24-SEP-2003 (first entry)  
XX  
DB HBV zinzyme substrate sequence #90.  
XX  
XX Nucleic acid molecule; Hepatitis C virus; HCV; Hepatitis B virus; HBV;  
KW RNA stability; RNA expression; RNA synthesis; antisense;  
KW enzymatic nucleic acid; hammerhead ribozyme; DNzyme; inozyme; zinzyme;  
KW amzyme; G-cleaver ribozyme; decoy molecule; aptamer;  
KW HBV reverse transcriptase; Enhancer I region; viral replication;  
KW degenerative; disease state; HBV infection; HCV infection; cirrhosis;  
KW liver failure; hepatocellular carcinoma; hepatotropic; cytostatic;  
KW viricide; antiinflammatory; substrate; ss.  
XX  
OS Hepatitis B virus.  
XX  
XX WO200281494-A1.  
PN  
XX  
PD 17-OCT-2002.

XX  
PF 26-MAR-2002; 2002WO-US009187.  
XX  
PR 26-MAR-2001; 2001US-00817879.  
PR 08-JUN-2001; 2001US-00877478.  
PR 08-JUN-2001; 2001US-0296876P.  
PR 24-OCT-2001; 2001US-0335059P.  
PR 05-DEC-2001; 2001US-0337055P.  
XX  
XX (RIBO-) RIBOZYME PHARM INC.  
PA (BLAT/) BLATT L.  
PA (MACE/) MACEJAK D.  
PA (MCSW/) MCSWIGGEN J.  
PA (MORR/) MORRISSEY D.  
PA (PAVC/) PAVCO P.  
PA (LESP/) LEE P.  
PA (DRAP/) DRAPER K.  
PA (ROBE/) ROBERTS E.  
XX  
PI Blatt L, Macejak D, Mcswiggen J, Morrissey D, Pavco P, Lee P;  
PI Draper K, Roberts E;  
XX  
XX WPI; 2003-229207/22.  
XX  
PT Novel compound useful for treating cirrhosis, liver failure,  
PT hepatocellular carcinoma, or condition associated with hepatitis C virus  
PT infection.  
XX  
XX Example 1; Page 175; 387pp; English.  
XX  
CC The present invention relates to nucleic acid molecules which modulate  
CC the synthesis, expression and/or stability of Hepatitis C virus (HCV) or  
CC Hepatitis B virus (HBV) RNA. The nucleic acid molecules include antisense  
CC and enzymatic nucleic acids such as hammerhead ribozymes, DNazymes,  
CC inozymes, zinzymes, amberzymes, and G-cleaver ribozymes. Also disclosed  
CC are nucleic acid decoy molecules and aptamers that bind to HBV reverse  
CC transcriptase and/or HBV reverse transcriptase primer sequences, as well  
CC as oligonucleotides that specifically bind the Enhancer I region of HBV  
CC DNA. The nucleic acids may be used to modulate the expression of HBV  
CC genes and HBV viral replication. Also disclosed is a method for screening  
CC compounds and/or potential therapies directed against HBV, and compounds  
CC that modulate the expression and/or replication of HCV. The compounds and  
CC methods of the invention are useful for the treatment of degenerative and  
CC disease states related to HBV and HCV infection, replication and gene  
CC expression such as cirrhosis, liver failure, and hepatocellular  
CC carcinoma. The present sequence represents a substrate for one of the HBV  
CC ribozyme, inozyme, G-cleaver, zinzyme, DNzyme or amberzyme sequences  
CC disclosed in the present invention  
XX  
SQ Sequence 17 BP; 3 A; 0 C; 11 G; 0 T; 3 U; 0 Other;  
  
Query Match 0.9%; Score 14.4; DB 1; Length 17;  
Best Local Similarity 93.8%; Pred. No. 1.6e+02;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 1519 CCCCCAACTCCGCCA 1534  
|||||:|:|:|  
DB 16 CCCCCAACTCCTCCCA 1  
  
RESULT 249  
ADB43621  
ID ADB43621 standard; DNA; 17 BP.  
XX  
AC ADB43621;  
XX  
DT 18-DEC-2003 (revised)  
DT 04-DEC-2003 (first entry)  
XX  
XX Tumour suppression/reversion associated nucleotide #3944.  
XX  
XX cytostatic; antiviral; neuroprotective; neurotropic; neuroleptic; ss;  
KW primer; probe; tumour suppression; tumour reversion; apoptosis;

KW virus resistance; transgenic animals; Alzheimer's disease; schizophrenia;  
KW diagnosis.  
XX Homo sapiens.  
XX WO2003040369-A2.  
XX 15-MAY-2003.  
XX 17-SEP-2002; 2002WO-IB004219.  
XX 17-SEP-2001; 2001FR-00011981.  
XX (MOLE-) MOLECULAR ENGINES LAB.  
XX Telerman A, Amson R, Tuijinder M;  
XX WPI; 2003-441574/41.  
XX New nucleic acid encoding human prostate membrane-specific antigen,  
XX useful e.g. for treatment of tumors and viral infection, also related  
XX polypeptide and antibodies.  
XX Disclosure; Page 493; 771pp; French.  
XX The invention relates to the isolation of 6327 nucleotide sequences,  
XX fragments of at least 15 consecutive nucleotides of these nucleotides, a  
XX sequence having at least 80% identity, after optimal alignment, with the  
XX nucleotides, a sequence that hybridizes under stringent conditions with  
XX the nucleotides, or the complement, or corresponding RNA, of the  
XX nucleotides. The nucleotides are used as probes or primers for detecting,  
XX identifying, quantifying and/or amplifying nucleic acids, as in vitro  
XX sense and antisense sequences, of nucleotides involved in tumour  
XX suppression or reversion, apoptosis and or viral resistance, to produce  
XX recombinant polypeptides, and to prepare transgenic animals, as  
XX experimental models. The nucleotides (also vectors containing them and  
XX cells containing the vectors), the encoded polypeptides and antibodies  
XX (Ab) against the polypeptide are useful for prevention and/or treatment  
XX of viral infections or diseases characterized by development of tumours  
XX or cell degeneration (e.g. Alzheimer's disease or schizophrenia).  
XX Analysis of the expression of the nucleotides can be used for diagnosis  
XX and/or prognosis of these diseases. The nucleotides and polypeptides can  
XX also be used to screen for their specific interactive molecules,  
XX potentially useful for treating diseases associated with abnormal  
XX expression of the nucleotides.  
XX Sequence 17 BP; 7 A; 2 C; 5 G; 3 T; 0 U; 0 Other;  
SQ Query Match 0.9%; Score 14.4; DB 1; Length 17;  
Best Local Similarity 93.8%; Pred. No. 1.6e+02;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 154 ATCAGGGGAAGTAAGTA 169  
Db |||||||  
2 ATCAGGGGAAGTAAGTA 17  
RESULT 250  
ADE30979  
ID ADE30979 standard; DNA; 17 BP.  
XX ADE30979;  
XX 29-JAN-2004 (first entry)  
XX Cholesterol homeostasis/adipogenesis related DNA seq id 366.  
XX expression vector; anorectic; antiarteriosclerotic; cardiant;  
XX antiadipetic; elevated cholesterol; elevated lipid; adipogenesis;  
KW obesity; atherosclerosis; diabetes mellitus; cardiant;  
KW coronary artery heart disease; cholesterol homeostasis; ss;  
XX differential expression.  
XX

OS Homo sapiens.  
XX US2003180764-A1.  
XX 25-SEP-2003.  
XX 08-JAN-2003; 2003US-00339793.  
XX 09-JAN-2002; 2002US-0347286P.  
XX (LYNX-) LYNX THERAPEUTICS INC.  
XX Shang J, Bowen B;  
XX WPI; 2003-830986/77.  
XX Polynucleotides differentially regulated in response to cholesterol and  
XX adipogenesis are useful to detect and treat associated conditions such as  
XX obesity, atherosclerosis, diabetes mellitus and coronary artery heart  
XX disease.  
XX Claim 8; SEQ ID NO 366; 59pp; English.  
XX The invention describes a composition comprising at least one expression  
XX vector comprising a polynucleotide of the invention. The composition has  
XX anorectic, antiarteriosclerotic, cardiant and antiadipetic properties.  
XX The invention is used to detect and treat conditions associated with  
XX elevated cholesterol and lipid or during adipogenesis, particularly  
XX obesity, atherosclerosis, diabetes mellitus or coronary artery heart  
XX disease. This sequence represents a polynucleotide differentially  
XX expressed during cholesterol homeostasis and adipogenesis.  
XX Sequence 17 BP; 5 A; 9 C; 1 G; 2 T; 0 U; 0 Other;  
SQ Query Match 0.9%; Score 14.4; DB 1; Length 17;  
Best Local Similarity 93.8%; Pred. No. 1.6e+02;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 990 ACCAAGACCCCTCCC 1005  
Db |||||||  
2 ATCAACACCCCTCCC 17  
RESULT 251  
ABX95832  
ID ABX95832 standard; DNA; 17 BP.  
XX ABX95832;  
XX 24-JUL-2003 (first entry)  
XX Human Phe311Ileu mutant Abl kinase, allele specific PCR primer F311T.  
XX Human; Abl kinase domain; tyrosine kinase activity; leukaemia;  
KW N-(4-methyl-3-(4-pyridin-3-yl-pyrimidin-2-ylamino)-phenyl)-4-;  
KW (4-methyl-piperazin-1-ylmethyl)-benzamide; PCR; primer; ss.  
XX Homo sapiens.  
XX Synthetic.  
XX WO2003031608-A2.  
XX 17-APR-2003.  
XX 04-OCT-2002; 2002WO-EP011144.  
XX 05-OCT-2001; 2001US-0327389P.  
PR 12-OCT-2001; 2001US-0328740P.  
PR 11-JAN-2002; 2002US-0347351P.  
XX (NOVS) NOVARTIS AG.  
PA (UYBO-) UNIV BORDEAUX 2 SEGALLEN VICTOR.  
PA (UYMU-) UNIV TECH MUEENCHEN.

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PA (UYOR-) UNIV OREGON HEALTH SCI.
PA (UYHE-) UNIV HEIDELBERG.
PA (CHRU-) CHRU LILLE.
PA (MEDV-) MEDVET SCI PTY LTD.
XX
PI Barthe C, Branford S, Corbin A, Druker BJ, Duyster J, Hochhaus A;
PI Hughes T, Kreil S, Leguay T, Mahon F, Marit G, Mueller M;
PI Peschel C, Preudhomme C, Roche Lestienne C, Rudzki Z;
XX
XX WPI; 2003-363366/34.
XX
XX New isolated polypeptide having mutated native human Abl kinase domains,
XX useful for screening compounds that inhibit tyrosine kinase activity and
XX for diagnosing leukemias.
XX
XX Example 6; Page 34; 57pp; English.
XX
XX The present invention relates to mutated human Abl kinase domains that
XX are functional and resistant to inhibition of their tyrosine kinase
XX activity by N-(4-methyl-3-(4-pyridin-3-yl-pyrimidin-2-ylamino)-phenyl)-4
XX -(4-methyl-piperazin-1-ylmethyl)-benzamide, or its salt. The mutant Abl
XX polypeptides are useful in screening for compounds that inhibit the
XX tyrosine kinase activity of such polypeptides. Polynucleotide sequences
XX encoding the mutant polypeptides are useful for the production of the
XX mutant polypeptides. The mutant polypeptides are also useful in the
XX diagnosis of leukaemias. The present sequence represents a PCR primer
XX used in the examples of the present invention
XX
XX Sequence 17 BP; 2 A; 9 C; 5 G; 1 T; 0 U; 0 Other;
XX
XX Query Match 0.9%; Score 14.4; DB 1; Length 17;
XX Best Local Similarity 93.8%; Pred. No. 1.6e+02;
XX Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
QY 635 CACCCGGGAGCCCCAG 650
Db 1 CACCCGGGAGCCCCCG 16
XX
RESULT 252
ABX95833
ID ABX95833 standard; DNA; 17 BP.
AC
AC ABX95833;
XX
XX 24-JUL-2003 (first entry)
XX
XX Human Phe311Leu mutant Abl kinase, allele specific PCR primer F311C.
XX
XX Human; Abl kinase domain; tyrosine kinase activity; leukaemia;
XX N-(4-methyl-3-(4-pyridin-3-yl-pyrimidin-2-ylamino)-phenyl)-4-;
XX (4-methyl-piperazin-1-ylmethyl)-benzamide; PCR; primer; ss.
XX
XX Homo sapiens.
XX Synthetic.
XX
XX WO2003031608-A2.
XX
XX 17-APR-2003.
XX
XX 04-OCT-2002; 2002WO-EP011144.
XX
XX 05-OCT-2001; 2001US-0327389P.
XX
XX 12-OCT-2001; 2001US-0328740P.
XX
XX 11-JAN-2002; 2002US-0347351P.
XX
XX (NOVS ) NOVARTIS AG.
XX (UYBO-) UNIV BORDEAUX 2 SEGALEN VICTOR.
XX (UYMU-) UNIV TECH MUENCHEN.
XX (UYOR-) UNIV OREGON HEALTH SCI.
XX (UYHE-) UNIV HEIDELBERG.
XX (CHRU-) CHRU LILLE.
XX (MEDV-) MEDVET SCI PTY LTD.

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XX
XX Barthe C, Branford S, Corbin A, Druker BJ, Duyster J, Hochhaus A;
XX Hughes T, Kreil S, Leguay T, Mahon F, Marit G, Mueller M;
XX Peschel C, Preudhomme C, Roche Lestienne C, Rudzki Z;
XX
XX WPI; 2003-363366/34.
XX
XX New isolated polypeptide having mutated native human Abl kinase domains,
XX useful for screening compounds that inhibit tyrosine kinase activity and
XX for diagnosing leukemias.
XX
XX Example 6; Page 34; 57pp; English.
XX
XX The present invention relates to mutated human Abl kinase domains that
XX are functional and resistant to inhibition of their tyrosine kinase
XX activity by N-(4-methyl-3-(4-pyridin-3-yl-pyrimidin-2-ylamino)-phenyl)-4
XX -(4-methyl-piperazin-1-ylmethyl)-benzamide, or its salt. The mutant Abl
XX polypeptides are useful in screening for compounds that inhibit the
XX tyrosine kinase activity of such polypeptides. Polynucleotide sequences
XX encoding the mutant polypeptides are useful for the production of the
XX mutant polypeptides. The mutant polypeptides are also useful in the
XX diagnosis of leukaemias. The present sequence represents a PCR primer
XX used in the examples of the present invention
XX
XX Sequence 17 BP; 2 A; 10 C; 5 G; 0 T; 0 U; 0 Other;
XX
XX Query Match 0.9%; Score 14.4; DB 1; Length 17;
XX Best Local Similarity 93.8%; Pred. No. 1.6e+02;
XX Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
QY 635 CACCCGGGAGCCCCAG 650
Db 1 CACCCGGGAGCCCCCG 16
XX
RESULT 253
ADL18587
ID ADL18587 standard; DNA; 17 BP.
XX
XX AC ADL18587;
XX
XX 06-MAY-2004 (first entry)
XX
XX RT-PCR primer HP6.
XX
XX DNA storage; DNA analysis; virus identification; bacteria identification;
XX reverse transcriptase; RT-PCR; primer; ss; HP6.
XX
XX Synthetic.
XX
XX US2003134312-A1.
XX
XX 17-JUL-2003.
XX
XX 15-NOV-2002; 2002US-00298255.
XX
XX 15-NOV-2001; 2001US-0336005P.
XX
XX (WEAT-) WHATMAN INC.
XX
XX Burgoyne LA;
XX
XX WPI; 2003-843261/78.
XX
XX New device comprising a filter layer comprising a dry solid medium
XX comprising a hydrophilic solid matrix, and an isolation layer, useful for
XX storing and analyzing a nucleic acid containing moiety.
XX
XX Example 1; SEQ ID NO 4; 14pp; English.
XX
XX The invention relates to a device for storage and analysis of a nucleic
XX acid containing a moiety in a biological sample, comprising a filter
XX layer comprising a dry solid medium comprising a hydrophilic solid

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CC matrix, and an isolation layer comprising a dry solid medium comprising a  
 CC neutral solid matrix attached to a composition comprising a detergent.  
 CC Storing and analysing a nucleic acid containing a moiety in a biological  
 CC sample comprises applying a biological sample to the filter layer,  
 CC filtering the components of the biological sample through the filter  
 CC layer to the isolation layer, retaining the nucleic acid components in  
 CC the isolation layer while removing the non-nucleic acid components,  
 CC drying the isolation layer, providing a primer and analysing the nucleic  
 CC acid components using at least one primer. The device and method are  
 CC useful for storing and analysing a nucleic acid containing a moiety in a  
 CC biological sample. They are also useful for identifying known or unknown  
 CC viruses or bacteria contained in a fluid. This sequence represents a  
 CC reverse transcriptase PCR (RT-PCR) primer used in the scope of the  
 CC invention.

XX SQ Sequence 17 BP; 3 A; 10 C; 3 G; 1 T; 0 U; 0 Other;  
 Query Match 0.9%; Score 14.4; DB 1; Length 17;  
 Best Local Similarity 93.8%; Pred. No. 1.6e+02;  
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1508 CAGCCTCAGGCCCC 1523  
 |||||  
 Db 1 CAGCCTCAGGACCC 16

RESULT 254  
 ADM59611/c  
 ID ADM59611 standard; RNA; 17 BP.  
 XX  
 AC ADM59611;  
 XX  
 DT 03-JUN-2004 (first entry)  
 XX  
 DE Hepatitis B virus (HBV) RNA target sequence #1745.  
 XX  
 KW Hepatitis B virus; HBV; ss; enzymatic nucleic acid; RNA cleavage;  
 KW Hepatitis B virus infection; hepatitis; hepatocellular carcinoma;  
 KW cirrhosis; liver failure; lamivudine; interferon; genetic drift;  
 KW virucide; hepatotropic; antiinflammatory; cytostatic.  
 XX  
 OS Hepatitis B virus.  
 XX  
 PN US2004054156-A1.  
 XX  
 PD 18-MAR-2004.  
 XX  
 PF 15-JAN-2003; 2003US-00342902.  
 XX  
 PR 14-MAY-1992; 92US-00882712.  
 PR 07-FEB-1994; 94US-00193627.  
 PR 08-NOV-1999; 99US-00436430.  
 PR 20-MAR-2000; 2000US-00531025.  
 PR 09-AUG-2000; 2000US-00636385.  
 PR 24-OCT-2000; 2000US-00696347.  
 PR 08-JUN-2001; 2001US-00877478.  
 XX  
 (DRAP/) DRAPER K.  
 PA (BLAT/) BLATT L.  
 PA (MCSW/) MCSWIGGEN J A.  
 PA (MORR/) MORRISSEY D.  
 XX  
 PI Draper K, Blatt L, Mcswiggen JA, Morrissey D;  
 XX  
 WPI; 2004-247781/23.  
 XX  
 XX Novel enzymatic nucleic acid molecule such as DNazymes and inozymes  
 PT specifically cleaving RNA derived from hepatitis B virus and comprising  
 PT one or more binding arms, useful for treating hepatitis and cirrhosis.  
 XX  
 PS Disclosure; SEQ ID NO 1745; 122pp; English.  
 XX  
 CC The invention relates to an enzymatic nucleic acid molecule that

CC specifically cleaves RNA derived from hepatitis B virus (HBV) and  
 CC comprising one or more binding arms, without requiring the presence of a  
 CC 2'-OH group within the molecule for activity. The nucleic acids are  
 CC useful for treating hepatitis B virus infection, hepatitis,  
 CC hepatocellular carcinoma, cirrhosis and liver failure, either alone or in  
 CC combination with other therapies such as lamivudine and interferons. The  
 CC nucleic acids are useful as diagnostic tools to examine genetic drift and  
 CC mutations within diseased cells, for detecting the presence of HBV RNA in  
 CC a cell, for the study of RNA and for down-regulating gene expression of  
 CC target genes in bacterial, fungal, viral, plant or mammalian cells. This  
 CC sequence represents an HBV RNA target sequence, used in the scope of the  
 CC invention. Note: The sequence data for this patent is also available in  
 CC electronic format from USPTO at seqdata.uspto.gov/sequence.html.

XX SQ Sequence 17 BP; 3 A; 0 C; 11 G; 0 T; 3 U; 0 Other;  
 Query Match 0.9%; Score 14.4; DB 1; Length 17;  
 Best Local Similarity 93.8%; Pred. No. 1.6e+02;  
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1519 CCCCCCACTCCGCCA 1534  
 |||||  
 Db 16 CCCCCCACTCCTCCA 1

RESULT 255  
 ADI84297  
 ID ADI84297 standard; RNA; 17 BP.  
 XX  
 AC ADI84297;  
 XX  
 DT 03-JUN-2004 (first entry)  
 XX  
 DE HCV DNazyme substrate sequence #1543.  
 XX  
 KW ss; enzymatic nucleic acid; RNA cleavage; hepatitis C virus; HCV;  
 KW HCV infection; type I interferon; DNazyme.  
 XX  
 OS Hepatitis C virus.  
 XX  
 PN US2003125270-A1.  
 XX  
 PD 03-JUL-2003.  
 XX  
 PF 18-DEC-2000; 2000US-00740332.  
 XX  
 PR 18-DEC-2000; 2000US-00740332.  
 XX  
 (BLAT/) BLATT L.  
 PA (MCSW/) MCSWIGGEN J.  
 PA (ROBE/) ROBERTS E.  
 PA (PAVC/) PAVCO P A.  
 PA (MACE/) MACEJACK D.  
 XX  
 PI Blatt L, Mcswiggen J, Roberts E, Pavco PA, Macejack D;  
 XX  
 WPI; 2004-031273/03.  
 XX  
 XX Enzymatic nucleic acid molecules which specifically cleave RNA derived  
 PT from hepatitis C virus (HCV), useful for the treatment of HCV infections,  
 PT especially in combination with type I interferon therapy.  
 XX  
 PS Claim 1; SEQ ID NO 1543; 198pp; English.  
 XX  
 CC The invention relates to an enzymatic nucleic acid molecule which  
 CC specifically cleaves RNA derived from hepatitis C virus (HCV), in which  
 CC the binding arms of the enzymatic nucleic acid molecule comprises  
 CC sequences complementary to any of the defined substrate sequences given  
 CC in the specification. The nucleic acid molecule may be administered for  
 CC the treatment of HCV infections, especially in combination with type I  
 CC interferons. The present sequence represents a HCV DNazyme substrate  
 CC sequence.

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SQ Sequence 17 BP; 2 A; 7 C; 4 G; 0 T; 4 U; 0 Other;
  Query Match      0.9%; Score 14.4; DB 1; Length 17;
  Best Local Similarity 75.0%; Pred. No. 1.6e+02;
  Matches 12; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 768 CAGCCCATGTTCCAGC 783
Db 1 CAGCCCAUGUCCGCC 16

RESULT 256
ADI85767/c
ID ADI85767 standard; RNA; 17 BP.
XX AC ADI85767;
XX DT 03-JUN-2004 (first entry)
XX DE HCV DNAzyme substrate sequence #3013.
XX KW ss; enzymatic nucleic acid; RNA cleavage; hepatitis C virus; HCV;
XX KW HCV infection; type I interferon; DNAzyme.
XX OS Hepatitis C virus.
XX PN US2003125270-A1.
XX PD 03-JUL-2003.
XX PF 18-DEC-2000; 2000US-00740332.
XX PR 18-DEC-2000; 2000US-00740332.
XX PA (BLAT/) BLATT L.
XX PA (MCSW/) MCSWIGGEN J.
XX PA (ROBE/) ROBERTS E.
XX PA (PVC/) PAVCO P A.
XX PA (MACE/) MACEJACK D.
XX PI Blatt L, Mcswiggen J, Roberts E, Pavco PA, Macejack D;
XX WPI; 2004-031273/03.
XX Enzymatic nucleic acid molecules which specifically cleave RNA derived
PT from hepatitis C virus (HCV), useful for the treatment of HCV infections,
PT especially in combination with type I interferon therapy.
XX PS Claim 1; SEQ ID NO 3013; 198pp; English.
XX CC The invention relates to an enzymatic nucleic acid molecule which
CC specifically cleaves RNA derived from hepatitis C virus (HCV), in which
CC the binding arms of the enzymatic nucleic acid molecule comprises
CC sequences complementary to any of the defined substrate sequences given
CC in the specification. The nucleic acid molecule may be administered for
CC the treatment of HCV infections, especially in combination with type I
CC interferons. The present sequence represents a HCV DNAzyme substrate
CC sequence.
XX Sequence 17 BP; 3 A; 5 C; 7 G; 0 T; 2 U; 0 Other;
  Query Match      0.9%; Score 14.4; DB 1; Length 17;
  Best Local Similarity 93.8%; Pred. No. 1.6e+02;
  Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 768 CAGCCCATGTTCCAGC 783
Db 16 CAGCCCATGTTCCGCC 1

RESULT 257
ACN71763
ID ACN71763 standard; DNA; 17 BP.
XX AC ACN71763;
XX DT 02-DEC-2004 (first entry)
XX DE Human GDMPLP-1 probe SEQ ID NO:8665.
XX KW Human; ss; probe; myosin-like protein-1; hGDMPLP-1;
XX KW hGDMPLP-1 agonist hGDMPLP antagonist; hGDMPLP inhibitor; heart disorder;
XX KW skeletal muscle function.
XX OS Homo sapiens.
XX PN US2004137589-A1.
XX PD 15-JUL-2004.
XX PF 26-NOV-2003; 2003US-00723361.
XX PR 26-MAY-2000; 2000US-0207456P.
XX PR 21-SEP-2000; 2000US-0234687P.
XX PR 27-SEP-2000; 2000US-0236359P.
XX PR 04-OCT-2000; 2000GB-00024263.
XX PR 30-JAN-2001; 2001WO-US000661.
XX PR 30-JAN-2001; 2001WO-US000662.
XX PR 30-JAN-2001; 2001WO-US000663.
XX PR 30-JAN-2001; 2001WO-US000664.
XX PR 30-JAN-2001; 2001WO-US000665.
XX PR 30-JAN-2001; 2001WO-US000666.
XX PR 30-JAN-2001; 2001WO-US000667.
XX PR 30-JAN-2001; 2001WO-US000668.
XX PR 30-JAN-2001; 2001WO-US000669.
XX PR 30-JAN-2001; 2001WO-US000670.
XX PR 05-FEB-2001; 2001US-0266860P.
XX PR 25-MAY-2001; 2001US-00866108.
XX PA (GUY/) GU Y.
XX PA (JIY/) JI Y.
XX PA (PENN/) PENN S G.
XX PA (HANZ/) HANZEL D K.
XX PA (RANK/) RANK D.
XX PA (CHEN/) CHEN W.
XX PA (SHAN/) SHANNON M E.
XX PI Gu Y, Ji Y, Penn SG, Hanzel DK, Rank D, Chen W, Shannon ME;
XX WPI; 2004-533378/51.
XX Novel myosin-like protein-1, useful for treating or preventing disorder
PT associated with decreased expression or activity of human genome-derived
PT myosin-like protein-1 such as disorder of heart and/or skeletal muscle
PT function.
XX PS Disclosure; SEQ ID NO 8665; 0pp; English.
XX CC The invention relates to a novel polypeptide (I) comprising a sequence
CC (S1) of myosin-like protein-1 (hGDMPLP-1) having 2568 amino acids fully
CC defined in the specification, a fragment of at least 8 amino acids of
CC (S1), 95% deviation from (S1) which are conservative substitutions, and
CC 65% identity to (S1). A polypeptide of the invention acts as a agonist or
CC antagonist of hGDMPLP-1, or as an inhibitor of hGDMPLP-1 activity. A
CC pharmaceutical composition of the invention is useful for treating or
CC preventing a disorder associated with decreased expression or activity of
CC hGDMPLP-1, such as a disorder of heart and/or skeletal muscle function.
CC The present sequence represents a 17-mer nucleotide, used in the
CC invention for scanning the sequence represented in ACN63103
XX Sequence 17 BP; 8 A; 2 C; 7 G; 0 T; 0 U; 0 Other;
  Query Match      0.9%; Score 14.4; DB 1; Length 17;
  Best Local Similarity 93.8%; Pred. No. 1.6e+02;
  Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 273 GAAGCCAAGAGAAGA 288  
DB 2 GAAGCCAAGAGAAGA 17

RESULT 258  
ACN73136/c

ID ACN73136 standard; DNA; 17 BP.

XX ACN73136;  
XX 02-DEC-2004 (first entry)  
XX Human GDMPLP-1 probe SEQ ID NO:10038.  
XX Human; ss; probe; myosin-like protein-1; hGDMPLP-1;  
KW hGDMPLP-1 agonist hGDMPLP antagonist; hGDMPLP inhibitor; heart disorder;  
KW skeletal muscle function.  
XX Homo sapiens.  
XX US2004137589-A1.  
XX 15-JUL-2004.  
XX 26-NOV-2003; 2003US-00723361.  
XX 26-MAY-2000; 2000US-0207456P.  
XX 21-SEP-2000; 2000US-0234687P.  
XX 27-SEP-2000; 2000US-0236359P.  
XX 04-OCT-2000; 2000GB-00024283.  
XX 30-JAN-2001; 2001WO-US000661.  
XX 30-JAN-2001; 2001WO-US000662.  
XX 30-JAN-2001; 2001WO-US000663.  
XX 30-JAN-2001; 2001WO-US000664.  
XX 30-JAN-2001; 2001WO-US000665.  
XX 30-JAN-2001; 2001WO-US000666.  
XX 30-JAN-2001; 2001WO-US000667.  
XX 30-JAN-2001; 2001WO-US000668.  
XX 30-JAN-2001; 2001WO-US000669.  
XX 30-JAN-2001; 2001WO-US000670.  
XX 05-FEB-2001; 2001US-0266860P.  
XX 25-MAY-2001; 2001US-00866108.

XX (GUY/) GU Y.  
XX (JIY/) JI Y.  
XX (PENN/) PENN S G.  
XX (HANZ/) HANZEL D K.  
XX (RANK/) RANK D.  
XX (CHEN/) CHEN W.  
XX (SHAN/) SHANNON M E.

Gu Y, Ji Y, Penn SG, Hanzel DK, Rank D, Chen W, Shannon ME;  
WPI; 2004-533378/51.

XX Novel myosin-like protein-1, useful for treating or preventing disorder  
PT associated with decreased expression or activity of human genome-derived  
PT myosin-like protein-1 such as disorder of heart and/or skeletal muscle  
PT function.  
XX Disclosure; SEQ ID NO 10038; Opp; English.

XX The invention relates to a novel polypeptide (I) comprising a sequence  
CC (S1) of myosin-like protein-1 (hGDMPLP-1) having 2568 amino acids fully  
CC defined in the specification, a fragment of at least 8 amino acids of  
CC (S1), 95% deviation from (S1) which are conservative substitutions, and  
CC 65% identity to (S1). A polypeptide of the invention acts as an agonist or  
CC antagonist of hGDMPLP-1, or as an inhibitor of hGDMPLP-1 activity. A  
CC pharmaceutical composition of the invention is useful for treating or  
CC preventing a disorder associated with decreased expression or activity of  
CC hGDMPLP-1, such as a disorder of heart and/or skeletal muscle function.  
CC The present sequence represents a 17-mer nucleotide, used in the

CC invention for scanning the sequence represented in ACN63103  
XX Sequence 17 BP; 2 A; 4 C; 8 G; 3 T; 0 U; 0 Other;  
SQ Query Match 0.9%; Score 14.4; DB 1; Length 17;  
Best Local Similarity 93.8%; Pred. No. 1.6e+02;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 715 CCGCATCGTCGCGAG 730  
DB 16 CCGCATCGTCGCGAG 1

RESULT 259  
ACN73135/c

ID ACN73135 standard; DNA; 17 BP.  
XX ACN73135;  
XX 02-DEC-2004 (first entry)  
XX Human GDMPLP-1 probe SEQ ID NO:10037.  
XX Human; ss; probe; myosin-like protein-1; hGDMPLP-1;  
KW hGDMPLP-1 agonist hGDMPLP antagonist; hGDMPLP inhibitor; heart disorder;  
KW skeletal muscle function.  
XX Homo sapiens.  
XX US2004137589-A1.  
XX 15-JUL-2004.  
XX 26-NOV-2003; 2003US-00723361.  
XX 26-MAY-2000; 2000US-0207456P.  
XX 21-SEP-2000; 2000US-0234687P.  
XX 27-SEP-2000; 2000US-0236359P.  
XX 04-OCT-2000; 2000GB-00024263.  
XX 30-JAN-2001; 2001WO-US000661.  
XX 30-JAN-2001; 2001WO-US000662.  
XX 30-JAN-2001; 2001WO-US000663.  
XX 30-JAN-2001; 2001WO-US000664.  
XX 30-JAN-2001; 2001WO-US000665.  
XX 30-JAN-2001; 2001WO-US000666.  
XX 30-JAN-2001; 2001WO-US000667.  
XX 30-JAN-2001; 2001WO-US000668.  
XX 30-JAN-2001; 2001WO-US000669.  
XX 05-FEB-2001; 2001US-0266860P.  
XX 25-MAY-2001; 2001US-00866108.

XX (GUY/) GU Y.  
XX (JIY/) JI Y.  
XX (PENN/) PENN S G.  
XX (HANZ/) HANZEL D K.  
XX (RANK/) RANK D.  
XX (CHEN/) CHEN W.  
XX (SHAN/) SHANNON M E.

Gu Y, Ji Y, Penn SG, Hanzel DK, Rank D, Chen W, Shannon ME;  
WPI; 2004-533378/51.

XX Novel myosin-like protein-1, useful for treating or preventing disorder  
PT associated with decreased expression or activity of human genome-derived  
PT myosin-like protein-1 such as disorder of heart and/or skeletal muscle  
PT function.  
XX Disclosure; SEQ ID NO 10037; Opp; English.

XX The invention relates to a novel polypeptide (I) comprising a sequence  
CC (S1) of myosin-like protein-1 (hGDMPLP-1) having 2568 amino acids fully  
CC defined in the specification, a fragment of at least 8 amino acids of  
CC (S1), 95% deviation from (S1) which are conservative substitutions, and  
CC 65% identity to (S1). A polypeptide of the invention acts as an agonist or  
CC antagonist of hGDMPLP-1, or as an inhibitor of hGDMPLP-1 activity. A  
CC pharmaceutical composition of the invention is useful for treating or  
CC preventing a disorder associated with decreased expression or activity of  
CC hGDMPLP-1, such as a disorder of heart and/or skeletal muscle function.  
CC The present sequence represents a 17-mer nucleotide, used in the

CC defined in the specification, a fragment of at least 8 amino acids of  
CC (S1), 95% deviation from (S1) which are conservative substitutions, and  
CC 65% identity to (S1). A polypeptide of the invention acts as an agonist or  
CC antagonist of hGDMLP-1, or as an inhibitor of hGDMLP-1 activity. A  
CC pharmaceutical composition of the invention is useful for treating or  
CC preventing a disorder associated with decreased expression or activity of  
CC hGDMLP-1, such as a disorder of heart and/or skeletal muscle function.  
CC The present sequence represents a 17-mer nucleotide, used in the  
CC invention for scanning the sequence represented in ACN63103  
XX  
SQ Sequence 17 BP; 2 A; 3 C; 8 G; 4 T; 0 U; 0 Other;

Query Match 0.9%; Score 14.4; DB 1; Length 17;  
Best Local Similarity 93.8%; Pred. No. 1.6e+02;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 715 CCCGATCGTCGCAG 730  
Db |||||  
17 CCCGATCGTCGCAG 2

RESULT 260  
ACN71450/c  
ID ACN71450 standard; DNA; 17 BP.

XX ACN71450;

XX 02-DEC-2004 (first entry)

DE Human GDMLP-1 probe SEQ ID NO:8352.

XX Human; ss; probe; myosin-like protein-1; hGDMLP-1;  
KW hGDMLP-1 agonist hGDMLP antagonist; hGDMLP inhibitor; heart disorder;  
KW skeletal muscle function.

XX Homo sapiens.

XX US2004137589-A1.

XX 15-JUL-2004.

XX 26-NOV-2003; 2003US-00723361.

XX 26-MAY-2000; 2000US-0207456P.

PR 21-SEP-2000; 2000US-0234687P.

PR 27-SEP-2000; 2000US-0236359P.

PR 04-OCT-2000; 2000GB-00024263.

PR 30-JAN-2001; 2001WO-US000661.

PR 30-JAN-2001; 2001WO-US000662.

PR 30-JAN-2001; 2001WO-US000663.

PR 30-JAN-2001; 2001WO-US000664.

PR 30-JAN-2001; 2001WO-US000665.

PR 30-JAN-2001; 2001WO-US000666.

PR 30-JAN-2001; 2001WO-US000667.

PR 30-JAN-2001; 2001WO-US000668.

PR 30-JAN-2001; 2001WO-US000669.

PR 05-FEB-2001; 2001US-0266860P.

PR 25-MAY-2001; 2001US-00866108.

XX (GUY/) GU Y.

PA (JIY/) JI Y.

PA (PENN/) PENN S G.

PA (HANZ/) HANZEL D K.

PA (RANK/) RANK D.

PA (CHEN/) CHEN W.

PA (SHAN/) SHANNON M E.

XX Gu Y, Ji Y, Penn SG, Hanzel DK, Rank D, Chen W, Shannon ME;

XX WPI; 2004-533378/51.

DR Novel myosin-like protein-1, useful for treating or preventing disorder

PT

PT associated with decreased expression or activity of human genome-derived  
PT myosin-like protein-1 such as disorder of heart and/or skeletal muscle  
PT function.

XX Disclosure; SEQ ID NO 8352; Opp; English.

CC The invention relates to a novel polypeptide (I) comprising a sequence  
CC (S1) of myosin-like protein-1 (hGDMLP-1) having 2568 amino acids fully  
CC defined in the specification, a fragment of at least 8 amino acids of  
CC (S1), 95% deviation from (S1) which are conservative substitutions, and  
CC 65% identity to (S1). A polypeptide of the invention acts as an agonist or  
CC antagonist of hGDMLP-1, or as an inhibitor of hGDMLP-1 activity. A  
CC pharmaceutical composition of the invention is useful for treating or  
CC preventing a disorder associated with decreased expression or activity of  
CC hGDMLP-1, such as a disorder of heart and/or skeletal muscle function.  
CC The present sequence represents a 17-mer nucleotide, used in the  
CC invention for scanning the sequence represented in ACN63103  
XX

SQ Sequence 17 BP; 5 A; 3 C; 7 G; 2 T; 0 U; 0 Other;

Query Match 0.9%; Score 14.4; DB 1; Length 17;  
Best Local Similarity 93.8%; Pred. No. 1.6e+02;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1109 CACCTCTCTCTGCTG 1124  
Db |||||  
17 CAGCTCTCTCTGCTG 2

RESULT 261

ACN71451/c

ID ACN71451 standard; DNA; 17 BP.

XX ACN71451;

XX 02-DEC-2004 (first entry)

XX Human GDMLP-1 probe SEQ ID NO:8353.

XX Human; ss; probe; myosin-like protein-1; hGDMLP-1;  
KW hGDMLP-1 agonist hGDMLP antagonist; hGDMLP inhibitor; heart disorder;  
KW skeletal muscle function.

XX Homo sapiens.

XX US2004137589-A1.

XX 15-JUL-2004.

XX 26-NOV-2003; 2003US-00723361.

XX 26-MAY-2000; 2000US-0207456P.

PR 21-SEP-2000; 2000US-0234687P.

PR 27-SEP-2000; 2000US-0236359P.

PR 04-OCT-2000; 2000GB-00024263.

PR 30-JAN-2001; 2001WO-US000661.

PR 30-JAN-2001; 2001WO-US000662.

PR 30-JAN-2001; 2001WO-US000663.

PR 30-JAN-2001; 2001WO-US000664.

PR 30-JAN-2001; 2001WO-US000665.

PR 30-JAN-2001; 2001WO-US000666.

PR 30-JAN-2001; 2001WO-US000667.

PR 30-JAN-2001; 2001WO-US000668.

PR 30-JAN-2001; 2001WO-US000669.

PR 05-FEB-2001; 2001US-0266860P.

PR 25-MAY-2001; 2001US-00866108.

XX (GUY/) GU Y.

PA (JIY/) JI Y.

PA (PENN/) PENN S G.

PA (HANZ/) HANZEL D K.

PA (RANK/) RANK D.





XX WPI; 1995-036508/05.  
XX Sequencing complex genomes, present as fragments in a cosmid library - by  
PT sequencing end-specific nucleotides of each clone then correlating with  
PT spatial relationship of cosmid, esp. for mammalian chromosomes.  
XX  
XX Example 3; Page 44; 128pp; English.  
XX In a sequence-sample mapping procedure using a Giardia lamblia 20-genome  
CC equivalent cosmid library, each end of the genomic insert in a cosmid was  
CC detected as a vector/genomic chimera by hybridisation with probes  
CC flanking the T3 and T7 promoter sites of sCos-1. The 1046 bp T3 probe was  
CC amplified from sCos-1 with the primers AAQ80946 and AAQ80947 and the 1004  
CC bp T7 probe was amplified with primers AAQ80948 and AAQ80949. The T7  
CC probe was labelled with 35S- dATP and the T3 probe with 33P-dATP for dual  
CC -label hybridisations. Maps were constructed by determining an order of  
CC fragments with no gaps using a computer program. (Updated on 25-MAR-2003  
CC to correct PN field.)  
XX  
SQ Sequence 18 BP; 4 A; 2 C; 9 G; 3 T; 0 U; 0 Other;  
  
Query Match 0.9%; Score 14.4; DB 1; Length 18;  
Best Local Similarity 93.8%; Pred. No. 1.9e+02;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
Qy 1520 CCCCAACTCCGCCAG 1535  
Db 18 CCTTAACTCCGCCAG 3  
  
RESULT 264  
ADM06417  
ID ADM06417 standard; DNA; 18 BP.  
XX  
XX ADM06417;  
XX  
XX 20-MAY-2004 (first entry)  
XX Human PCR primer SEQ ID NO:5102.  
XX  
XX human; gene therapy; diagnostic marker; pharmaceutical; ss; PCR; primer.  
XX  
XX Homo sapiens.  
XX  
XX EP1347046-A1.  
XX  
XX 24-SEP-2003.  
XX  
XX 12-APR-2002; 2002EP-00008400.  
XX  
XX 22-MAR-2002; 2002JP-00137785.  
XX  
XX (REAS-) RES ASSOC BIOTECHNOLOGY.  
XX  
XX Isogai T, Sugiyama T, Otsuki T, Wakamatsu A, Sato H, Ishii S;  
PI Yamamoto J, Isono Y, Hio Y, Otsuka K, Nagai K, Irie R, Tamechika I;  
PI Seki N, Yoshikawa T, Otsuka M, Nagahari K, Masuho Y;  
XX WPI; 2003-723558/69.  
XX  
XX New polynucleotides and polypeptides are useful in gene therapy, for  
PT developing a diagnostic marker or medicines for regulating their  
PT expression and activity, or as a target of gene therapy.  
XX  
XX Example 8; SEQ ID NO 5102; 305pp; English.  
XX  
XX The invention relates to a novel human polynucleotide and the encoded  
CC polypeptide. A polynucleotide of the invention may have a use in gene  
CC therapy. An oligonucleotide of the invention ADM06202-ADM06773 is useful  
CC as a primer for synthesizing the polynucleotide or as a probe for  
CC detecting the polynucleotide. The polynucleotides ADM01316-ADM03758 are  
CC useful in gene therapy, for developing a diagnostic marker or medicines

CC for regulating their expression and activity, or as a target of gene  
CC therapy. The proteins ADM03759-ADM06201 encoded by the polynucleotides  
CC are useful as pharmaceutical agents. The present sequence represents an  
CC oligonucleotide used in the invention.  
XX  
SQ Sequence 18 BP; 4 A; 3 C; 7 G; 4 T; 0 U; 0 Other;  
  
Query Match 0.9%; Score 14.4; DB 1; Length 18;  
Best Local Similarity 93.8%; Pred. No. 1.9e+02;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
Qy 1094 GTGGAAGATGCTCAAC 1109  
Db 1 GTGGAAGATGCTCGAC 16  
  
RESULT 265  
ADM92954  
ID ADM92954 standard; DNA; 18 BP.  
XX  
XX AC ADM92954;  
XX  
XX 03-JUN-2004 (first entry)  
XX  
XX SNP-containing cardiovascular associated gene primer #285.  
XX  
XX SNP; single nucleotide polymorphism; cardiovascular associated gene;  
KW allelic variation; atherosclerosis; ischemia; reperfusion; hypertension;  
KW restenosis; arterial inflammation; myocardial infarction; stroke; primer;  
KW ss.  
XX  
XX Homo sapiens.  
XX  
XX WO2003057911-A2.  
XX  
XX 17-JUL-2003.  
XX  
XX 07-JAN-2003; 2003WO-EP0000060.  
XX  
XX 08-JAN-2002; 2002EP-00000153.  
XX  
XX (FARB ) BAYER AG.  
XX  
XX Stropp U, Schwes S, Kallabis H;  
XX  
XX WPI; 2003-577532/54.  
XX  
XX New isolated polynucleotides comprising single nucleotide polymorphisms  
PT of the cardiovascular gene, useful for assessing predisposition or  
PT susceptibility to a cardiovascular disease, e.g. atherosclerosis,  
PT restenosis or stroke.  
XX  
XX Disclosure; Page 78; 187pp; English.  
XX  
XX The invention relates an isolated polynucleotide (I) encoded by a  
CC cardiovascular associated (CA) gene, having allelic variation contained  
CC in a functional surrounding like full length cDNA for CA gene  
CC polypeptide, and with or without the CA gene promoter sequence. (I) is a  
CC polynucleotide comprising single nucleotide polymorphisms predicting  
CC cardiovascular disease. The polynucleotides are useful for assessing  
CC predisposition or susceptibility to a cardiovascular disease, e.g.  
CC atherosclerosis, ischemia/reperfusion, hypertension, restenosis, arterial  
CC inflammation, myocardial infarction, and stroke. These may also be used  
CC to predict personal medication schemes omitting adverse drug reactions,  
CC or as probes for detecting genetic polymorphisms and as templates for the  
CC recombinant production of normal or variant peptides/polypeptides encoded  
CC by the genes. This sequence corresponds to a PCR primer to amplify one of  
CC the genes of the invention.  
XX  
SQ Sequence 18 BP; 8 A; 5 C; 2 G; 3 T; 0 U; 0 Other;  
  
Query Match 0.9%; Score 14.4; DB 1; Length 18;  
Best Local Similarity 93.8%; Pred. No. 1.9e+02;

Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;		
QY	1488 GTACCAAGTAACGAG 1503	
Db	1 GTACCAATTAAACGAG 16	
RESULT 266		
ID	ADH71057/c	
XX	ADH71057 standard; DNA; 18 BP.	
AC	ADH71057;	
XX		
DT	25-MAR-2004 (first entry)	
XX		
DE	Human Vbeta point mutation PCR primer #10.	
XX	human; T-cell associated disease; Vbeta; autoimmune disease;	
KW	degenerative nervous system disease; graft versus host disease;	
KW	hypersensitivity disease; infectious disease; neoplastic disease;	
KW	Addison's disease; atrophic gastritis;	
KW	degenerative nervous system disease; multiple sclerosis;	
KW	Alzheimer's disease; hypersensitivity disease; type I hypersensitivity;	
KW	allergy; type II hypersensitivity; Goodpasture's syndrome;	
KW	type IV hypersensitivity; leprosy; infectious disease; viral infection;	
KW	HIV; fungal infection; Candida; parasitic infection; schistosoma;	
KW	filaria; bacterial infection; Mycobacterium; neoplastic disease;	
KW	lymphoproliferative disease; leukaemia; lymphoma; cancer; brain cancer;	
KW	breast cancer; ss; PCR; primer.	
XX		
OS	Homo sapiens.	
XX		
FN	US2002150891-A1.	
XX		
PD	17-OCT-2002.	
XX		
PF	05-MAR-1999; 99US-00263959.	
XX		
PR	19-SEP-1994; 94US-00309335.	
PR	19-SEP-1995; 95US-00531241.	
XX		
PA	(HOOD/) HOOD L E.	
PA	(ROWE/) ROWEN L.	
XX		
PI	Hood LE, Rowen L;	
XX		
DR	WPI; 2004-059052/06.	
XX		
PT	Kit for diagnosing and treating T-cell associated diseases e.g.	
PT	autoimmune, degenerative nervous system and infectious disease, comprises	
PT	nucleic acid primers specifically priming and allowing amplification of a	
PT	Vbeta gene.	
XX		
PS	Disclosure; SEQ ID NO 1251; 164pp; English.	
XX		
CC	The invention relates to a kit for diagnosing and treating T-cell	
CC	associated diseases which comprises a panel of nucleic acid primers	
CC	specifically priming and allowing amplification of each Vbeta gene,	
CC	VbetaRNA or cDNA. The kit is useful for diagnosing organ transplant	
CC	rejection and diagnosing and treating T-cell associated diseases	
CC	including autoimmune diseases, degenerative nervous system diseases,	
CC	graft versus host disease, hypersensitivity diseases, infectious diseases	
CC	and neoplastic diseases. Autoimmune diseases include Addison's disease,	
CC	atrophic gastritis. Degenerative nervous system diseases include multiple	
CC	sclerosis and Alzheimer's disease. Hypersensitivity diseases include Type	
CC	I hypersensitivities such as contact with allergens that lead to	
CC	allergies, Type II hypersensitivities such as those present in	
CC	Goodpasture's syndrome and Type IV hypersensitivities such as those	
CC	manifested in leprosy. Infectious diseases include viral infections	
CC	caused by viruses such as HIV, fungal infections such as those caused by	
CC	the yeast genus Candida, parasitic infections such as those caused by	
CC	schistosomes, filaria and bacterial infections such as those caused by	
CC	Mycobacterium. Neoplastic diseases include lymphoproliferative diseases	

CC	such as leukaemias, lymphomas and cancers such as cancer of the brain,
CC	breast. The present sequence represents a Vbeta point mutation PCR
CC	primer.
XX	
SQ	Sequence 18 BP; 1 A; 4 C; 9 G; 4 T; 0 U; 0 Other;
Query Match	
Best Local Similarity 0.9%; Score 14.4; DB 1; Length 18;	
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;	
QY	634 TCACCGGGGAGCCCCA 649
Db	17 TCACCGGGGAGCCCCA 2
RESULT 267	
ID	AAF47085
XX	AAF47085 standard; DNA; 15 BP.
AC	AAF47085;
XX	
DT	30-MAR-2001 (first entry)
XX	
DE	IGFBP3 oligonucleotide #505.
XX	
KW	Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;
KW	cytostatic; dermatological; cardiac; virucide; ophthalmological; keloid;
KW	skin disorder; insulin-like Growth Factor 1 receptor; IGF-1; pitriasis;
KW	IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;
KW	growth factor mediated cell proliferation; ichthyosis; serborrhea; ruba;
KW	keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;
KW	hyperneovascular condition; hyperplasia; kidney disease;
KW	neovascular condition of the retina; ss.
XX	
OS	Homo sapiens.
XX	
FN	WO200078341-A1.
XX	
PD	28-DEC-2000.
XX	
PF	21-JUN-2000; 2000WO-AU000693.
XX	
PR	21-JUN-1999; 99US-0140345P.
XX	
PA	(MURD-) MURDOCH CHILDRENS RES INST.
XX	
FI	Wraight CJ, Werther GA, Edmondson SR;
XX	
DR	WPI; 2001-041421/05.
XX	
PT	Ameliorating the effects of a disorder, e.g. psoriasis, by administering
PT	UV (ultra-violet) treatment (optional) and an antisense nucleic acid that
PT	inhibits or reduces growth factor mediated cell proliferation and/or
PT	inflammation.
XX	
PS	Example 7; Page 47; 201pp; English.
XX	
CC	The present invention relates to a method for ameliorating the effects of
CC	skin disorders. The method comprises contacting the skin with an
CC	antisense oligonucleotide, (for Insulin-like Growth Factor [IGF]-1
CC	receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of
CC	inhibiting or reducing growth factor mediated cell proliferation,
CC	inflammation and/or other disorders. The present sequence is an
CC	oligonucleotide which can be used to design the antisense
CC	oligonucleotides of the present invention (see AAF45151 and AAF45153-
CC	F45161). The method is useful for ameliorating the effects of psoriasis,
CC	ichthyosis, pitriasis, ruba, pilaris, serborrhea, keloids, keratosis,
CC	neoplasias, scleroderma, warts, benign growths, cancers of the skin, a
CC	hyperneovascular condition such as a neovascular condition of the retina,
CC	brain or skin, growth factor-mediated malignancies, other sclerotic
CC	disease, kidney disease, hyperproliferation of the inside of blood
CC	vessels or any other hyperplasia

SQ	Sequence 15 BP; 5 A; 4 C; 4 G; 2 T; 0 U; 0 Other;	Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Query Match		
Best Local Similarity 100.0%; Pred. No. 1.2e+02;		
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
QY	136 AGCTCCAGGAATG 149	
DB	1 AGCTCCAGGAATG 14	
RESULT 268		
AAAF47084		
ID	AAAF47084 standard; DNA; 15 BP.	
XX	AC	AAAF47084;
XX	DT	30-MAR-2001 (first entry)
XX	DE	IGFBP3 oligonucleotide #504.
KW	Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;	
KW	cytostatic; dermatological; cardiant; virucide; ophthalmological; keloid;	
KW	skin disorder; insulin-like Growth Factor 1 receptor; IGF-1; ptyriasis;	
KW	IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;	
KW	growth factor mediated cell proliferation; ichthyosis; serborrhea; ruba;	
KW	keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;	
KW	hyperneovascular condition; hyperplasia; kidney disease;	
KW	neovascular condition of the retina; ss.	
XX	OS	Homo sapiens.
XX	OS	WO200078341-A1.
XX	PN	28-DEC-2000.
XX	PD	
XX	PF	21-JUN-2000; 2000WO-AU000693.
XX	PP	21-JUN-1999; 99US-0140345P.
XX	PR	(MURD-) MURDOCH CHILDRENS RES INST.
XX	PA	
PI	Wright CJ, Werther GA, Edmondson SR;	
XX	WPI; 2001-041421/05.	
XX	DR	
XX	PI	Kmiec EB, Gamper HB, Rice MC, Kim J;
XX	WPI; 2002-106307/14.	
XX	DR	
PT	Ameliorating the effects of a disorder, e.g. psoriasis, by administering	
PT	UV (ultra-violet) treatment (optional) and an antisense nucleic acid that	
PT	inhibits or reduces growth factor mediated cell proliferation and/or	
PT	inflammation.	
XX	Example 7; Page 47; 201pp; English.	
XX	The present invention relates to a method for ameliorating the effects of	
XX	skin disorders. The method comprises contacting the skin with an	
CC	antisense oligonucleotide, (for Insulin-like Growth Factor [IGF]-1	
CC	receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of	
CC	inhibiting or reducing growth factor mediated cell proliferation,	
CC	inflammation and/or other disorders. The present sequence is an	
CC	oligonucleotide which can be used to design the antisense	
CC	oligonucleotides of the present invention (see AAF45151 and AAF45153-	
CC	F45161). The method is useful for ameliorating the effects of psoriasis,	
CC	ichthyosis, pityriasis, ruba, pilaris, serborrhea, keloids, keratosis,	
CC	neoplasias, scleroderma, warts, benign growths, cancers of the skin, a	
CC	hyperneovascular condition such as a neovascular condition of the retina,	
CC	brain or skin, growth factor-mediated malignancies, other sclerotic	
CC	disease, kidney disease, hyperproliferation of the inside of blood	
CC	vessels or any other hyperplasia	
XX	Sequence 15 BP; 5 A; 4 C; 4 G; 2 T; 0 U; 0 Other;	
Query Match		
Best Local Similarity 100.0%; Pred. No. 1.2e+02;		
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
QY	136 AGCTCCAGGAATG 149	
DB	1 AGCTCCAGGAATG 15	
RESULT 269		
ABK25595/c		
ID	ABK25595 standard; DNA; 17 BP.	
XX	AC	ABK25595;
XX	DT	09-APR-2002 (first entry)
XX	DE	Stress tolerance conferring genome altering oligonucleotide #63.
XX	KW	Chromosomal genomic alteration; genome altering oligonucleotide; PCR; ss;
KW	o-methyl modification; LNA modification; phosphorothioate linkage;	
KW	DNA repair; DNA alteration; environmental tolerance; hygromycin-B;	
KW	abiotic stress tolerance; improved nutritional value; hygromycin; primer;	
KW	amino acid over production; herbicide resistance; glyphosate resistance;	
KW	imidazolinone herbicide resistance; sulphonylurea herbicide resistance;	
KW	porphyric herbicide resistance; triazine resistance; disease resistance;	
KW	modified oil production; modified starch production; waxy starch;	
KW	altered floral morphology; male-sterile plant; albino mutant;	
KW	modified fatty acid content; reduced palmitate production; albino plant;	
KW	increased stearate production; reduced linolenic acid production;	
KW	photosynthetic process.	
XX	OS	Eucalyptus camaldulensis.
OS	OS	Synthetic.
XX	PN	WO200192512-A2.
XX	PD	06-DEC-2001.
XX	PF	01-JUN-2001; 2001WO-US017672.
XX	PR	01-JUN-2000; 2000US-0208538P.
PR	30-OCT-2000; 2000US-0244989P.	
PR	27-MAR-2001; 2001US-00818875.	
XX	XX	(UYDE ) UNIV DELAWARE.
XX	PI	Kmiec EB, Gamper HB, Rice MC, Kim J;
XX	WPI; 2002-106307/14.	
XX	DR	
PT	New oligonucleotides with modified nuclease-resistant termini, useful for	
PT	creating plants with desired phenotypes, e.g. stress tolerance, improved	
PT	nutritional value, herbicide or disease resistance, or modified oil	
PT	production.	
XX	Claim 7; Page 100; 220pp; English.	
XX	The invention relates to an oligonucleotide for targeted alteration of a	
XX	genetic sequence, which comprises a single-stranded oligonucleotide	
CC	having a DNA domain. The DNA domain has at least one mismatch with	
CC	respect to the genetic sequence to be altered and further comprises	
CC	chemical modifications of the oligonucleotide. The chemical modifications	
CC	consist of o-methyl modification, an LNA modification, two or more	
CC	phosphorothioate linkages on a terminus, or a combination of any two or	
CC	more of these modifications. The oligonucleotides are useful for	
CC	directing repair or alteration of plant genetic information. The	
CC	oligonucleotides are particularly useful for creating plants with desired	
CC	phenotypes, e.g. environmental or abiotic stress tolerance, improved	
CC	nutritional value (e.g. altering amino acid content of plants or	
CC	conferring amino acid over production), herbicide resistance (e.g.	
CC	glyphosate resistance, imidazolinone and sulphonylurea herbicide	
CC	resistance, porphyric herbicide resistance or triazine resistance).	
CC	disease resistance, modified oil production, modified starch production	
CC	(e.g. increased starch or production of waxy starch), altered floral	

CC morphology (e.g. male-sterile plants) or modified fatty acid content  
 CC (e.g. reduced palmitate, increased stearate or reduced linolenic acid).  
 CC The oligonucleotides are also useful for producing albino mutants for the  
 CC analysis of photosynthetic processes. This sequence represents a genome  
 CC altering oligonucleotide of the invention  
 XX  
 SQ Sequence 17 BP; 2 A; 6 C; 4 G; 5 T; 0 U; 0 Other;  
 Query Match 0.9%; Score 14; DB 1; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 1.8e+02;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1202 GGTACACACGGTGG 1215  
 DB 14 GGTACACACGGTGG 1  
 RESULT 270  
 ABK25596  
 ID ABK25596 standard; DNA; 17 BP.  
 XX  
 AC ABK25596;  
 XX  
 DT 09-APR-2002 (first entry)  
 XX  
 DE Stress tolerance conferring genome altering oligonucleotide #64.  
 XX  
 KW Chromosomal genomic alteration; genome altering oligonucleotide; PCR; ss;  
 KW o-methyl modification; LNA modification; phosphorothioate linkage;  
 KW DNA repair; DNA alteration; improved nutritional tolerance; hygromycin-B;  
 KW abiotic stress tolerance; environmental tolerance; hygromycin; primer;  
 KW amino acid over production; herbicide resistance; glyphosate resistance;  
 KW imidazolinone herbicide resistance; sulphonylurea herbicide resistance;  
 KW porphyrin herbicide resistance; triazine resistance; disease resistance;  
 KW modified oil production; modified starch production; waxy starch;  
 KW altered floral morphology; male-sterile plant; albino mutant;  
 KW modified fatty acid content; reduced palmitate production; albino plant;  
 KW increased stearate production; reduced linolenic acid production;  
 KW photosynthetic process.  
 XX  
 OS Eucalyptus camaldulensis.  
 OS Synthetic.  
 XX  
 PN WO200192512-A2.  
 XX  
 PD 06-DEC-2001.  
 XX  
 PF 01-JUN-2001; 2001WO-US017672.  
 XX  
 PR 01-JUN-2000; 2000US-0208538P.  
 PR 30-OCT-2000; 2000US-0244989P.  
 PR 27-MAR-2001; 2001US-00818875.  
 XX  
 PA (UYDE ) UNIV DELAWARE.  
 XX  
 XX Kmiec EB, Gamber HB, Rice MC, Kim J;  
 XX  
 XX WPI; 2002-106307/14.  
 XX  
 PT New oligonucleotides with modified nuclease-resistant termini, useful for  
 PT creating plants with desired phenotypes, e.g. stress tolerance, improved  
 PT nutritional value, herbicide or disease resistance, or modified oil  
 PT production.  
 XX  
 PS Claim 7; Page 100; 220pp; English.  
 XX  
 CC The invention relates to an oligonucleotide for targeted alteration of a  
 CC genetic sequence, which comprises a single-stranded oligonucleotide  
 CC having a DNA domain. The DNA domain has at least one mismatch with  
 CC respect to the genetic sequence to be altered and further comprises  
 CC chemical modifications of the oligonucleotide. The chemical modifications  
 CC consist of o-methyl modification, an LNA modification, two or more  
 CC phosphorothioate linkages on a terminus, or a combination of any two or

CC more of these modifications. The oligonucleotides are useful for  
 CC directing repair or alteration of plant genetic information. The  
 CC oligonucleotides are particularly useful for creating plants with desired  
 CC phenotypes, e.g. environmental or abiotic stress tolerance, improved  
 CC nutritional value (e.g. altering amino acid content of plants or  
 CC conferring amino acid over production), herbicide resistance (e.g.  
 CC glyphosate resistance, imidazolinone and sulphonylurea herbicide  
 CC resistance, porphyrin herbicide resistance or triazine resistance),  
 CC disease resistance, modified oil production, modified starch production  
 CC (e.g. increased starch or production of waxy starch), altered floral  
 CC morphology (e.g. male-sterile plants) or modified fatty acid content  
 CC (e.g. reduced palmitate, increased stearate or reduced linolenic acid).  
 CC The oligonucleotides are also useful for producing albino mutants for the  
 CC analysis of photosynthetic processes. This sequence represents a genome  
 CC altering oligonucleotide of the invention  
 XX  
 SQ Sequence 17 BP; 5 A; 4 C; 6 G; 2 T; 0 U; 0 Other;

Query Match 0.9%; Score 14; DB 1; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 1.8e+02;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1202 GGTACACACGGTGG 1215  
 DB 4 GGTACACACGGTGG 17

RESULT 271  
 ACDS9851  
 ID ACDS9851 standard; RNA; 17 BP.  
 XX  
 AC ACDS9851;  
 XX  
 DT 24-SEP-2003 (first entry)  
 XX  
 DE HCV DNAzyme substrate sequence #1541.  
 XX  
 KW Nucleic acid molecule; Hepatitis C virus; HCV; Hepatitis B virus; HBV;  
 KW RNA stability; RNA expression; RNA synthesis; antisense;  
 KW enzymatic nucleic acid; hammerhead ribozyme; DNAzyme; inozyme; zinzyme;  
 KW amberzyme; G-cleaver ribozyme; decoy molecule; aptamer;  
 KW HBV reverse transcriptase; Enhancer I region; viral replication;  
 KW degenerative; disease state; HBV infection; HCV infection; cirrhosis;  
 KW liver failure; hepatocellular carcinoma; hepatotropic; cytostatic;  
 KW virucide; antiinflammatory; substrate; ss.  
 XX  
 OS Hepatitis C virus.  
 XX  
 PN WO200281494-A1.  
 XX  
 PD 17-OCT-2002.  
 XX  
 PF 26-MAR-2002; 2002WO-US009187.  
 XX  
 PR 26-MAR-2001; 2001US-00817879.  
 PR 08-JUN-2001; 2001US-00877478.  
 PR 08-JUN-2001; 2001US-0296876P.  
 PR 24-OCT-2001; 2001US-0335059P.  
 PR 05-DEC-2001; 2001US-0337055P.  
 XX  
 XX (RIBO-) RIBOZYME PHARM INC.  
 PA (BLAT/) BLATT L.  
 PA (MACE/) MACEJAK D.  
 PA (MCSW/) MCSWISGEN J.  
 PA (MORR/) MORRISSEY D.  
 PA (PAVC/) PAVCO P.  
 PA (LEEP/) LEE P.  
 PA (DRAP/) DRAPER K.  
 PA (ROBE/) ROBERTS B.  
 XX  
 PI Blatt L, Macejak D, Mcswisgen J, Morrissey J, Pavco P, Lee P;  
 PI Draper K, Roberts B;  
 XX

DR WPI; 2003-229207/22.  
 XX Novel compound useful for treating cirrhosis, liver failure,  
 PT hepatocellular carcinoma, or condition associated with hepatitis C virus  
 PT infection.  
 XX  
 XX Claim 1; Page 261; 387pp; English.  
 XX The present invention relates to nucleic acid molecules which modulate  
 CC the synthesis, expression and/or stability of Hepatitis C virus (HCV) or  
 CC Hepatitis B virus (HBV) RNA. The nucleic acid molecules include antisense  
 CC and enzymatic nucleic acids such as hammerhead ribozymes, DNazymes,  
 CC inozymes, zinzymes, amberzymes, and G-cleaver ribozymes. Also disclosed  
 CC are nucleic acid decoy molecules and aptamers that bind to HBV reverse  
 CC transcriptase and/or HBV reverse transcriptase primer sequences, as well  
 CC as oligonucleotides that specifically bind the Enhancer I region of HBV  
 CC DNA. The nucleic acids may be used to modulate the expression of HBV  
 CC genes and HBV viral replication. Also disclosed is a method for screening  
 CC compounds and/or potential therapies directed against HBV, and compounds  
 CC that modulate the expression and/or replication of HCV. The compounds and  
 CC methods of the invention are useful for the treatment of degenerative and  
 CC disease states related to HBV and HCV infection, replication and gene  
 CC expression such as cirrhosis, liver failure, and hepatocellular  
 CC carcinoma. The present sequence represents a substrate for one of the HCV  
 CC DNzyme or minus strand DNzyme sequences disclosed in the present  
 CC invention  
 XX  
 SQ Sequence 17 BP; 2 A; 7 C; 3 G; 0 T; 5 U; 0 Other;  
 Query Match 0.9%; Score 14; DB 1; Length 17;  
 Best Local Similarity 71.4%; Pred. No. 1.8e+02;  
 Matches 10; Conservative 4; Mismatches 0; Indels 0; Gaps 0;  
 QY 766 TCCAGCGCCATGTC 779  
 Db 4 UCCAGCGCAUGUUC 17  
 RESULT 272  
 ADI84295  
 ID ADI84295 standard; RNA; 17 BP.  
 XX  
 XX ADI84295;  
 XX  
 DT 03-JUN-2004 (first entry)  
 XX  
 DE HCV DNzyme substrate sequence #1541.  
 XX  
 XX ss; enzymatic nucleic acid; RNA cleavage; hepatitis C virus; HCV;  
 KW HCV infection; type I interferon; DNzyme.  
 XX  
 OS Hepatitis C virus.  
 XX  
 XX US2003125270-A1.  
 PN  
 PD 03-JUL-2003.  
 XX  
 XX 18-DEC-2000; 2000US-00740332.  
 PF  
 XX 18-DEC-2000; 2000US-00740332.  
 PR  
 XX (BLAT/) BLATT L.  
 PA (MCSW/) MCSWIGGEN J.  
 PA (ROBE/) ROBERTS E.  
 PA (PANC/) PAVCO P A.  
 PA (MACE/) MACEJACK D.  
 XX  
 XX Blatt L, Mcswiggen J, Roberts E, Pavco PA, Macejack D;  
 PI WPI; 2004-031273/03.  
 DR  
 XX Enzymatic nucleic acid molecules which specifically cleave RNA derived  
 PT from hepatitis C virus (HCV), useful for the treatment of HCV infections,

PT especially in combination with type I interferon therapy.  
 XX  
 XX Claim 1; SEQ ID NO 1541; 198pp; English.  
 XX The invention relates to an enzymatic nucleic acid molecule which  
 CC specifically cleaves RNA derived from hepatitis C virus (HCV), in which  
 CC the binding arms of the enzymatic nucleic acid molecule comprises  
 CC sequences complementary to any of the defined substrate sequences given  
 CC in the specification. The nucleic acid molecule may be administered for  
 CC the treatment of HCV infections, especially in combination with type I  
 CC interferons. The present sequence represents a HCV DNzyme substrate  
 CC sequence.  
 XX  
 SQ Sequence 17 BP; 2 A; 7 C; 3 G; 0 T; 5 U; 0 Other;  
 Query Match 0.9%; Score 14; DB 1; Length 17;  
 Best Local Similarity 71.4%; Pred. No. 1.8e+02;  
 Matches 10; Conservative 4; Mismatches 0; Indels 0; Gaps 0;  
 QY 766 TCCAGCGCCATGTC 779  
 Db 4 UCCAGCGCAUGUUC 17  
 RESULT 273  
 ADN44286/C  
 ID ADN44286 standard; DNA; 17 BP.  
 XX  
 XX AC ADN44286;  
 XX  
 DT 15-JUL-2004 (first entry)  
 XX  
 DE Mutant cell identification-related mutagenic oligonucleotide SeqID955.  
 XX  
 KW cell identification; oligonucleotide-directed sequence alteration;  
 KW selectable phenotype; transgenic plant; herbicide resistance;  
 KW sterile plant; abiotic stress tolerance; albino plant;  
 KW amino acid production; ss.  
 XX  
 OS Eucalyptus camaldulensis.  
 OS Synthetic.  
 XX  
 XX WO2004033708-A2.  
 PN  
 PD 22-APR-2004.  
 XX  
 XX 07-OCT-2003; 2003WO-US031862.  
 PF  
 XX 07-OCT-2002; 2002US-0416983P.  
 PR 07-MAR-2003; 2003US-0453360P.  
 XX  
 XX (UYDE ) UNIV DELAWARE.  
 PA (NAPR-) NAPRO BIO THERAPEUTICS INC.  
 XX  
 XX Kmiec EB, Van Brabant A;  
 PI WPI; 2004-340941/31.  
 DR  
 XX Identifying a cell with a desired oligonucleotide-directed sequence  
 PT alteration at a nucleic acid target site within the cell by identifying  
 PT the desired sequence alteration in cells selected for the presence of a  
 PT selectable phenotype.  
 XX  
 XX Example 25; SEQ ID NO 955; 303pp; English.  
 PS  
 XX This invention relates to a novel method of identifying a cell having a  
 CC desired oligonucleotide-directed sequence alteration at a first nucleic  
 CC acid target site within the cell. The method comprises identifying the  
 CC desired sequence alteration in cells that have been selected for the  
 CC presence of a selectable phenotype conferred by a concurrent  
 CC oligonucleotide-directed sequence alteration at a second nucleic acid  
 CC target site within the cells. The method is useful in identifying a cell  
 CC having a desired oligonucleotide-directed sequence alteration at a first

CC	nucleic acid target site within the cell. The method may be useful for	XX	Sequence 17 BP; 5 A; 4 C; 6 G; 2 T; 0 U; 0 Other;
CC	the production of plants with herbicide resistance, male or female	SQ	Query Match 0.9%; Score 14; DB 1; Length 17;
CC	sterile plants, abiotic stress tolerance, albino plants or plants with		Best Local Similarity 100.0%; Pred. No. 1.8e+02;
CC	altered amino acid production as well as for use in mammalian cell lines.		Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
CC	The present sequence is that of a mutagenic oligonucleotide which was		
CC	used in the exemplification of the invention.		
XX		QY	1202 GGTCCACCGGTGG 1215
SQ	Sequence 17 BP; 2 A; 6 C; 4 G; 5 T; 0 U; 0 Other;	Db	4 GGTCCACCGGTGG 17
		RESULT 275	
		AAT05231/c	
		ID AAT05231 standard; DNA; 17 BP.	
		XX	
		AC AAT05231;	
		XX	
		DT 13-JUN-1996 (first entry)	
		XX	
		DE Hepatitis C virus antisense oligonucleotide A377 (17).	
		XX	
		KW Inhibition; expression; hepatitis C virus; HCV; non-A; non-B; RNA;	
		KW translation; in vivo; ex vivo; in vitro; treatment; prevention;	
		KW infection; antisense; non coding; region; NCR; core region; ss.	
		XX	
		OS Synthetic.	
		XX	
		PN WO9530746-A1.	
		XX	
		PD 16-NOV-1995.	
		XX	
		PF 08-MAY-1995; 95WO-US005812.	
		XX	
		PR 10-MAY-1994; 94US-00240382.	
		XX	
		PA (GEO ) GEN HOSPITAL CORP.	
		XX	
		PI Wakita T, Wands JR;	
		XX	
		DR WPI; 1995-404113/51.	
		XX	
		PT New anti-sense hepatitis C virus oligonucleotide(s) - used for	
		PT inhibiting HCV RNA translation, for the treatment or prevention of HCV	
		PT infection.	
		XX	
		FS Claim 1; Page 31; 50pp; English.	
		XX	
		CC The present oligonucleotide (ON) inhibits the expression of hepatitis C	
		CC virus (HCV) RNA, specifically HCV type II protein synthesis is inhibited	
		CC by about 50%. The ONs of the invention inhibit translation of HCV types I	
		CC -V RNA in vivo, ex vivo or in vitro, and can therefore be used to treat	
		CC or prevent HCV infection. The antisense ONs comprise 10-28 nucleotides	
		CC complementary to the entire HCV 5'-non-coding and part of the core	
		CC region. The A or S in the ONs name denotes antisense or sense, and the	
		CC no. indicates the position of the 5'-end of the ON. The ON was tested at	
		CC 10 fold molar excess to HCV RNA	
		XX	
		SQ Sequence 17 BP; 1 A; 1 C; 4 G; 11 T; 0 U; 0 Other;	
		Query Match 0.8%; Score 13.8; DB 1; Length 17;	
		Best Local Similarity 88.2%; Pred. No. 1.9e+02;	
		Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;	
		QY 222 CTCATAGAAAAACAAA 238	
		Db 17 CTCAGAGAAACCAAA 1	
		RESULT 276	
		AAX75009	
		ID AAX75009 standard; RNA; 17 BP.	
		XX	

---

CC	nucleic acid target site within the cell. The method may be useful for	XX	Sequence 17 BP; 5 A; 4 C; 6 G; 2 T; 0 U; 0 Other;
CC	the production of plants with herbicide resistance, male or female	SQ	Query Match 0.9%; Score 14; DB 1; Length 17;
CC	sterile plants, abiotic stress tolerance, albino plants or plants with		Best Local Similarity 100.0%; Pred. No. 1.8e+02;
CC	altered amino acid production as well as for use in mammalian cell lines.		Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
CC	The present sequence is that of a mutagenic oligonucleotide which was		
CC	used in the exemplification of the invention.		
XX		QY	1202 GGTCCACCGGTGG 1215
SQ	Sequence 17 BP; 2 A; 6 C; 4 G; 5 T; 0 U; 0 Other;	Db	14 GGTCCACCGGTGG 1
		RESULT 274	
		ADN44287	
		ID ADN44287 standard; DNA; 17 BP.	
		XX	
		AC ADN44287;	
		XX	
		DT 15-JUL-2004 (first entry)	
		XX	
		DE Mutant cell identification-related mutagenic oligonucleotide SeqID956.	
		XX	
		KW cell identification; oligonucleotide-directed sequence alteration;	
		KW selectable phenotype; transgenic plant; herbicide resistance;	
		KW sterile plant; abiotic stress tolerance; albino plant;	
		KW amino acid production; ss.	
		XX	
		OS Eucalyptus camaldulensis.	
		OS Synthetic.	
		XX	
		PN WO2004033708-A2.	
		XX	
		PD 22-APR-2004.	
		XX	
		PF 07-OCT-2003; 2003WO-US031862.	
		XX	
		PR 07-OCT-2002; 2002US-0415983P.	
		PR 07-MAR-2003; 2003US-0453360P.	
		XX	
		PA (UYDE ) UNIV DELAWARE.	
		PA (NAPR-) NAPRO BIO THERAPEUTICS INC.	
		XX	
		PI Kmiec EB, Van Brabant A;	
		XX	
		DR WPI; 2004-340941/31.	
		XX	
		PT Identifying a cell with a desired oligonucleotide-directed sequence	
		PT alteration at a nucleic acid target site within the cell by identifying	
		PT the desired sequence alteration in cells selected for the presence of a	
		PT selectable phenotype.	
		XX	
		PS Example 25; SEQ ID NO 956; 303pp; English.	
		XX	
		CC This invention relates to a novel method of identifying a cell having a	
		CC desired oligonucleotide-directed sequence alteration at a first nucleic	
		CC acid target site within the cell. The method comprises identifying the	
		CC desired sequence alteration in cells that have been selected for the	
		CC presence of a selectable phenotype conferred by a concurrent	
		CC oligonucleotide-directed sequence alteration at a second nucleic acid	
		CC target site within the cells. The method is useful in identifying a cell	
		CC having a desired oligonucleotide-directed sequence alteration at a first	
		CC nucleic acid target site within the cell. The method may be useful for	
		CC the production of plants with herbicide resistance, male or female	
		CC sterile plants, abiotic stress tolerance, albino plants or plants with	
		CC altered amino acid production as well as for use in mammalian cell lines.	
		CC The present sequence is that of a mutagenic oligonucleotide which was	
		CC used in the exemplification of the invention.	

AC AAX75009;  
 XX  
 DT 28-JUL-1999 (first entry)  
 XX  
 DE Mouse flt-1 VEGF receptor hammerhead ribozyme substrate #537.  
 XX  
 KW Vascular endothelial growth factor receptor; VEGF receptor; flt-1; flk-1;  
 KW KDR; hammerhead ribozyme; hairpin ribozyme; cleavage;  
 KW tumour angiogenesis; psoriasis; rheumatoid arthritis; ocular disease;  
 KW fms-like tyrosine kinase 1; kinase insert domain containing receptor;  
 KW foetal liver kinase 1; ss.  
 XX  
 OS Mus sp.  
 XX  
 PN W09715662-A2.  
 XX  
 PD 01-MAY-1997.  
 XX  
 PF 25-OCT-1996; 96WO-US017480.  
 XX  
 PR 26-OCT-1995; 95US-0005974P.  
 PR 11-JAN-1996; 96US-00584040.  
 XX  
 XX (RIBO-) RIBOZYME PHARM INC.  
 PA (CHIR) CHIRON CORP.  
 XX  
 XX Pavco P, Mcswiggen J, Stinchcomb D, Escobedo J;  
 XX WPI; 1997-259017/23.  
 DR  
 XX Nucleic acid molecule modulating VEGF receptor(s) gene expression or mRNA  
 PT stability - useful for treating e.g. tumour angiogenesis, psoriasis,  
 PT rheumatoid arthritis, etc., in a human patient.  
 XX  
 PS Claim 4; Page 171; 218pp; English.  
 XX  
 CC The present invention describes nucleic acid molecules which modulate the  
 CC synthesis, expression and/or stability of a mRNA encoding 1 or more  
 CC receptors of vascular endothelial growth factor (VEGF). A patient  
 CC (preferably human) having a condition associated with the level of the  
 CC fms-like tyrosine kinase 1 (flt-1), kinase insert domain containing  
 CC receptor (KDR) and/or foetal liver kinase 1 (flk-1) (e.g. tumour  
 CC angiogenesis, ocular diseases, psoriasis and rheumatoid arthritis) can be  
 CC treated by administering the nucleic acid molecule or the expression  
 CC vector to the patient. AAX757275 to AAX75752 represent specific examples  
 CC of nucleic acid molecules from the present invention  
 XX  
 SQ Sequence 17 BP; 2 A; 8 C; 3 G; 0 T; 4 U; 0 Other;  
 Query Match 0.8%; Score 13.8; DB 1; Length 17;  
 Best Local Similarity 64.7%; Pred. No. 1.9e+02;  
 Matches 11; Conservative 4; Mismatches 2; Indels 0; Gaps 0;  
 QY 1112 CTCCTCTTGTGCGAGC 1128  
 Db 1 CUCCCCUUGCUGAGC 17  
 RESULT 277  
 AAX62812/c  
 ID AAX62812 standard; RNA; 17 BP.  
 XX  
 AC AAX62812;  
 XX  
 DT 16-JUL-1999 (first entry)  
 XX  
 DE Delta-9 desaturase hamerhead ribozyme target SEQ ID NO:687.  
 XX  
 KW Maize; corn; Zea mays; delta-9 desaturase; GBSS; target; substrate;  
 KW granule bound starch synthase; hammerhead ribozyme; hairpin ribozyme;  
 KW modulation; gene expression; transgenic plant; cleavage; canola plant;  
 KW caffeine synthesis; coffee plant; nicotine production; tobacco;  
 KW fruit ripening; flower pigmentation; lignin production; ss.

XX Zea mays.  
 OS W09710328-A2.  
 PN 20-MAR-1997.  
 PD  
 XX 12-JUL-1996; 96WO-US011689.  
 PF  
 XX 13-JUL-1995; 95US-0001135P.  
 PR  
 XX (RIBO-) RIBOZYME PHARM INC.  
 PA (DOWC) DOWELANCO.  
 XX  
 PI Zwick MG, Edington BE, Mcswiggen JA, Merlo PAO, Guo L, Skokut TA;  
 PI Young SA, Folkerts O, Merlo DJ;  
 XX WPI; 1997-202224/18.  
 DR  
 XX Ribozyme which modulates plant gene expression - preferably modulates  
 PT expression of DELTA-9 desaturase or granule bound starch synthase in  
 PT maize or canola.  
 PT  
 XX Claim 38; Page 85; 155pp; English.  
 PS  
 XX The present invention describes an enzymatic nucleic acid molecule (I)  
 CC with RNA cleaving activity, which modulates the expression of a plant  
 CC gene. Also described is a gene comprising a cDNA sequence encoding maize  
 CC Delta-9 desaturase. (I) can be used to modulate expression of a gene,  
 CC preferably Delta-9 desaturase or a granule bound starch synthase (GBSS)  
 CC gene, in a plant (preferably a maize or canola plant). (I) can be used to  
 CC modulate caffeine synthesis in a coffee plant, nicotine production in a  
 CC tobacco plant, fruit ripening processes in an apple, tomato, pear, plum  
 CC or peach plant, flower pigmentation in a rose, petunia, chrysanthemum or  
 CC marigold plant or lignin production in a tobacco, aspen, poplar or pine  
 CC plant  
 XX  
 SQ Sequence 17 BP; 5 A; 3 C; 6 G; 0 T; 3 U; 0 Other;  
 Query Match 0.8%; Score 13.8; DB 1; Length 17;  
 Best Local Similarity 88.2%; Pred. No. 1.9e+02;  
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 1213 TGGCTTCCACACTTCT 1229  
 Db 17 TGGCTGCCACACTTCT 1  
 RESULT 278  
 AAT69614  
 ID AAT69614 standard; DNA; 17 BP.  
 XX  
 AC AAT69614;  
 XX  
 DT 26-AUG-1997 (first entry)  
 XX  
 DE Murine obr gene forward primer.  
 XX  
 KW Ob receptor; ObR; cytokine receptor; signal transduction;  
 KW eating disorder; obesity; cachexia; anorexia; bulimia; diagnosis;  
 KW gene therapy; polymerase chain reaction; PCR; primer; ss.  
 XX  
 OS Synthetic.  
 XX  
 PN W09719952-A1.  
 XX  
 PD 05-JUN-1997.  
 XX  
 PF 27-NOV-1996; 96WO-US019128.  
 XX  
 PR 27-NOV-1995; 95US-00562663.  
 PR 04-DEC-1995; 95US-00566622.  
 PR 08-DEC-1995; 95US-00569485.

PR 11-DEC-1995; 95US-00570142.  
 PR 28-DEC-1995; 95US-00583153.  
 PR 22-JAN-1996; 96US-00599455.  
 PR 26-APR-1996; 96US-00638524.  
 PR 03-SEP-1996; 96US-00708123.  
 XX PA (MILL-) MILLENNIUM PHARM INC.  
 XX Tartaglia LA, Tepper RI, Culpepper JA, White DW;  
 XX WPI; 1997-310525/28.  
 DR Isolated Ob receptor genes and polypeptide(s) - useful to develop  
 PT products for diagnosis or treatment of body weight disorders, e.g.  
 PT obesity, cachexia, anorexia and bulimia.  
 XX Example; Page 122; 265pp; English.  
 XX Forward and reverse PCR primers (AAT69614 and AAT69615) are based on the  
 CC 3' sequence of mouse Ob receptor (OBR) cDNA clone famj5312 (see also  
 CC AAT69590). They revealed a polymorphism on SSCP gels between CS7B1/6J  
 CC genomic DNA and wild-derived Mus spretus strain SPRET/Ei DNA. The  
 CC polymorphism allowed the genetic mapping of famj5312 to murine chromosome  
 CC 4, approx. 2.2 cm distal to the marker D4Mit9 and 4.6 cm proximal to the  
 CC marker D4Mit46. This mapping confirmed the results obt'd. using another  
 CC primer pair (AAT69612-13) derived from famj5312  
 XX  
 SQ Sequence 17 BP; 3 A; 6 C; 2 G; 6 T; 0 U; 0 Other;  
 Query Match 0.8%; Score 13.8; DB 1; Length 17;  
 Best Local Similarity 88.2%; Pred. No. 1.9e+02;  
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 660 CACTACCTGCCCTTCAG 676  
 Db 1 CACTATTGCGCTTCAG 17  
 RESULT 279  
 AAV61074  
 ID AAV61074 standard; DNA; 17 BP.  
 XX AC AAV61074;  
 XX 09-DEC-1998 (first entry)  
 DT Synthetic DNA fragment from US5821058.  
 DE Electrophoretic analysis; DNA fragment; sequencing; chromophore;  
 XX fluorophore; tag; electrophoresis; primer; ss.  
 KW Synthetic.  
 OS US5821058-A.  
 XX PN 13-OCT-1998.  
 XX 21-DEC-1994; 94US-00361176.  
 XX 16-JAN-1984; 84US-00570973.  
 PR 02-JAN-1985; 85US-00689013.  
 PR 11-APR-1985; 85US-00722742.  
 PR 07-OCT-1987; 87US-00108232.  
 PR 21-FEB-1991; 91US-00660160.  
 PR 12-JUN-1992; 92US-00898019.  
 XX (CALY ) CALIFORNIA INST OF TECHNOLOGY.  
 XX Hood LE, Connell CR, Hunkapiller MW, Smith LM, Hunkapiller TJ;  
 PI WPI; 1998-567653/48.  
 DR Electrophoretic analysis of DNA fragments - tagged with chromophore or  
 PT

PT fluorophore.  
 XX Disclosure; Fig 1; 16pp; English.  
 XX A method has been developed of separating and detecting tagged  
 CC polynucleotides. The method comprises: providing a set of  
 CC polynucleotides, each tagged with a chromophore or fluorophore; resolving  
 CC to separate one of the tagged polynucleotides from other tagged  
 CC polynucleotides differing in length by a single nucleotide using an  
 CC electrophoretic procedure capable of resolving tagged polynucleotides  
 CC differing by a single nucleotide; and detecting the resolved tagged  
 CC polynucleotides by means of the chromophore or fluorophore. The present  
 CC invention also describes a method of determining the sequence of a  
 CC polynucleotide by analysing tagged polynucleotide fragments generated by  
 CC a polynucleotide sequencing technique which comprises: introducing the  
 CC tagged polynucleotide fragments into an electrophoretic medium;  
 CC separating the tagged polynucleotide fragments in the electrophoretic  
 CC medium using an electrophoretic procedure capable of resolving the  
 CC polynucleotide fragments differing in length by a single nucleotide;  
 CC detecting the separated tagged polynucleotide fragments by means of the  
 CC chromophore or fluorophore; and determining the polynucleotide sequence  
 CC from the polynucleotide fragments detected. The present sequence  
 CC represents a DNA fragment used in an example for end-labeling the DNA  
 CC fragment with a fluorescent tag  
 XX  
 SQ Sequence 17 BP; 5 A; 4 C; 4 G; 4 T; 0 U; 0 Other;  
 Query Match 0.8%; Score 13.8; DB 1; Length 17;  
 Best Local Similarity 88.2%; Pred. No. 1.9e+02;  
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 1357 AAGCGCTGCAGGAATAC 1373  
 Db 1 ATGCTCTGCAGGAATAC 17  
 RESULT 280  
 AAV47411/C  
 ID AAV47411 standard; DNA; 17 BP.  
 XX AC AAV47411;  
 XX 10-NOV-1998 (first entry)  
 DT Antisense oligonucleotide 911, targeting adenosine A1 receptor.  
 DE Secondary structure; mRNA; phosphorothioate backbone; G-protein;  
 XX bronchoconstriction; lung inflammation; asthma; pulmonary disease;  
 KW allergy; emphysema; cystic fibrosis; ss.  
 XX OS Synthetic.  
 OS Homo sapiens.  
 XX Key Location/Qualifiers  
 FH modified\_base 1..17  
 FT /\*tag= a  
 FT /note= "contains phosphorothioate internucleotide  
 FT linkages"  
 XX WO9823294-A1.  
 PN 04-JUN-1998.  
 PD 26-NOV-1997; 97WO-US022017.  
 PF 26-NOV-1996; 96US-00757024.  
 PR (UVEC-) UNIV EAST CAROLINA.  
 XX Nyce JW;  
 XX WPI; 1998-322464/28.  
 XX



PT Treating respiratory disease with antisense sequences directed against  
PT adenosine or bradykinin receptors - with localised delivery to the  
PT respiratory system, suitable for long term treatment of asthma, adult  
PT respiratory distress syndrome etc.

PS Claim 12; Page 8-24; 47pp; English.

XX Sequences AAV46501-VA7446 are anti-sense oligonucleotides that target the  
CC human adenosine A1 receptor, the design of which required the secondary  
CC structure of this target mRNA. The adenosine receptor mRNA secondary  
CC structure was both analysed and used to construct antisense  
CC oligonucleotides containing a phosphorothioate backbone. Once the  
CC antisense molecules are created they can be used to target their  
CC predetermined target, thus causing the gene product to decrease. The  
CC antisense oligonucleotides were targeted to specific mRNA regions  
CC containing either a junction between the intron and exon, or where they  
CC may overlap the initiation codon. The receptor is a member of the G-  
CC protein coupled family of cell surface receptors that have 7-  
CC transmembrane segments. These oligonucleotides can be used to treat or  
CC prevent conditions associated with bronchoconstriction and/or lung  
CC inflammation in humans or other animals e.g. asthma, pulmonary disease,  
CC allergy, emphysema and cystic fibrosis

XX Sequence 17 BP; 2 A; 5 C; 9 G; 1 T; 0 U; 0 Other;

Query Match 0.8%; Score 13.8; DB 1; Length 17;  
Best Local Similarity 88.2%; Pred. No. 1.9e+02;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1530 GCCACGCTCTCCCGC 1546  
|||||||  
DB 17 GCCACGCTGTGCCGC 1

RESULT 281

AAV46535/c  
ID AAV46535 standard; DNA; 17 BP.

AC AAV46535;

XX 10-NOV-1998 (first entry)

XX Antisense oligonucleotide 35, targeting adenosine A1 receptor.

XX Secondary structure; mRNA; phosphorothioate backbone; G-protein;  
KW bronchoconstriction; lung inflammation; asthma; pulmonary disease;  
KW allergy; emphysema; cystic fibrosis; ss.

XX Synthetic.

OS Homo sapiens.

XX Key Location/Qualifiers

FT modified\_base 1..17

FT /tag= a

FT /note= "contains phosphorothioate internucleotide  
FT linkages"

XX WO9823294-A1.

XX 04-JUN-1998.

XX 26-NOV-1997; 97WO-US022017.

XX 26-NOV-1996; 96US-00757024.

XX (UYEC-) UNIV EAST CAROLINA.

XX Nyce JW;

XX WPI; 1998-322464/28.

XX Treating respiratory disease with antisense sequences directed against  
PT adenosine or bradykinin receptors - with localised delivery to the

PT respiratory system, suitable for long term treatment of asthma, adult  
PT respiratory distress syndrome etc.

XX Claim 12; Page 8-24; 47pp; English.

XX Sequences AAV46501-VA7446 are anti-sense oligonucleotides that target the  
CC human adenosine A1 receptor, the design of which required the secondary  
CC structure of this target mRNA. The adenosine receptor mRNA secondary  
CC structure was both analysed and used to construct antisense  
CC oligonucleotides containing a phosphorothioate backbone. Once the  
CC antisense molecules are created they can be used to target their  
CC predetermined target, thus causing the gene product to decrease. The  
CC antisense oligonucleotides were targeted to specific mRNA regions  
CC containing either a junction between the intron and exon, or where they  
CC may overlap the initiation codon. The receptor is a member of the G-  
CC protein coupled family of cell surface receptors that have 7-  
CC transmembrane segments. These oligonucleotides can be used to treat or  
CC prevent conditions associated with bronchoconstriction and/or lung  
CC inflammation in humans or other animals e.g. asthma, pulmonary disease,  
CC allergy, emphysema and cystic fibrosis

XX Sequence 17 BP; 2 A; 5 C; 9 G; 1 T; 0 U; 0 Other;

Query Match 0.8%; Score 13.8; DB 1; Length 17;  
Best Local Similarity 88.2%; Pred. No. 1.9e+02;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1530 GCCACGCTCTCCCGC 1546

DB 17 GCCACGCTGTGCCGC 1

RESULT 282

AAV94804

ID AAV94804 standard; RNA; 17 BP.

XX AAV94804;

XX 24-FEB-1999 (first entry)

XX Human IL-2 receptor g-chain substrate position 1385.

XX Human; IL-2 receptor g-chain; interleukin 2 receptor gamma chain;  
KW hammerhead ribozyme; hairpin ribozyme; substrate; expression; cancer;  
KW autoimmune disease; psoriasis; allergy; inflammatory disease;  
KW graft rejection; ss.

XX Homo sapiens.

XX WO9824913-A2.

XX 11-JUN-1998.

XX 02-DEC-1997; 97WO-US021748.

XX 03-DEC-1996; 96US-00758306.

XX (RIBO-) RIBOZYME PHARM INC.

XX Stinchcomb DT, Mcswiggen JA;

XX WPI; 1998-333332/29.

XX Ribozymes targetted to interleukin 2 - useful for treating e.g. cancer,  
PT autoimmune disease and allergies.

XX Claim 4; Page 37; 61pp; English.

XX The present sequence invention describes ribozymes targeted to modulate  
CC the synthesis and/or expression of interleukin (IL)-2R gamma encoded RNA.  
CC AAV93889 to AAV94574 represent specifically claimed ribozymes, and  
CC AAV94575 to AAV95260 represent specifically claimed substrate sequences  
CC from the present invention. The ribozymes can be used for the treatment



CC diseases and conditions. Typical diseases and conditions are those  
 CC associated with impaired respiration and inflammation, including lung  
 CC diseases, pulmonary vasoconstriction, inflammation, allergic rhinitis,  
 CC acute asthma, allergies, asthma, impaired respiration, respiratory  
 CC distress syndrome, pain, cystic fibrosis, pulmonary hypertension,  
 CC pulmonary vasoconstriction, emphysema, chronic obstructive pulmonary  
 CC disease (COPD), and cancers such as leukemias, lymphomas, carcinomas e.g.  
 CC colon cancer, breast cancer, lung cancer, pancreatic cancer,  
 CC hepatocellular carcinoma, kidney cancer, melanoma, hepatic metastases, as  
 CC well as all types of cancers which may metastasize or have metastasized  
 CC to the lungs, including breast and prostate cancer  
 XX  
 SQ Sequence 17 BP; 2 A; 5 C; 9 G; 1 T; 0 U; 0 Other;

Query Match 0.8%; Score 13.8; DB 1; Length 17;  
 Best Local Similarity 88.2%; Pred. No. 1.9e+02;  
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1530 GCCCAGCCTCTCCCGC 1546  
 |||||  
 DB 17 GCCCAGCCTGTGCCGC 1

RESULT 285  
 AAX52912/C

ID AAX52912 standard; DNA; 17 BP.

XX  
 AC AAX52912;

XX  
 DT 05-JUL-1999 (first entry)

DE Human adenosine A1 receptor antisense oligonucleotide fragment.

XX Antisense oligonucleotide; multiple target; antisense treatment;

KW impaired respiration; inflammation; lung disease;

KW pulmonary vasoconstriction; inflammation; allergic rhinitis;

KW acute asthma; allergy; asthma; impaired respiration;

KW respiratory distress syndrome; pain; cystic fibrosis;

KW pulmonary hypertension; pulmonary vasoconstriction; emphysema;

KW chronic obstructive pulmonary disease; leukemia; lymphoma; carcinoma;

KW colon cancer; breast cancer; lung cancer; pancreatic cancer;

KW hepatocellular carcinoma; kidney cancer; melanoma; hepatic metastasis;

KW prostate cancer; ss.

XX Synthetic.

XX WO913886-A1.

XX  
 PD 25-MAR-1999.

XX  
 PF 17-SEP-1998; 98WO-US019419.

XX  
 PR 17-SEP-1997; 97US-0059160P.

XX  
 PR 09-JUN-1998; 98US-00093972.

XX (UYEC-) UNIV EAST CAROLINA.

XX Nyce JW;

XX WPI; 1999-229400/19.

XX New antisense oligonucleotides used in treatment of, e.g. pulmonary  
 PT vasoconstriction.

XX Disclosure; Page 28; 120pp; English.

XX The specification describes antisense oligonucleotides (AAX52869-X55271)  
 CC directed against at least 2 mRNAs selected from target genes, coding and  
 CC non-coding regions of RNAs corresponding to target genes, gene initiation  
 CC codons, genomic flanking regions, intron-exon borders, the 5'-end, the 3'-  
 CC end and the junction-section between coding and non-coding regions and all  
 CC segments of RNAs encoding proteins associated with one or more diseases,  
 CC conditions or mixtures. The antisense oligonucleotides may be derived

CC from sequences AAX55272-74. These multiple target oligonucleotides  
 CC (specifically AAX55180-271) can be used for the antisense treatment of  
 CC diseases and conditions. Typical diseases and conditions are those  
 CC associated with impaired respiration and inflammation, including lung  
 CC diseases, pulmonary vasoconstriction, inflammation, allergic rhinitis,  
 CC acute asthma, allergies, asthma, impaired respiration, respiratory  
 CC distress syndrome, pain, cystic fibrosis, pulmonary hypertension,  
 CC pulmonary vasoconstriction, emphysema, chronic obstructive pulmonary  
 CC disease (COPD), and cancers such as leukemias, lymphomas, carcinomas e.g.  
 CC colon cancer, breast cancer, lung cancer, pancreatic cancer,  
 CC hepatocellular carcinoma, kidney cancer, melanoma, hepatic metastases, as  
 CC well as all types of cancers which may metastasize or have metastasized  
 CC to the lungs, including breast and prostate cancer  
 XX

SQ Sequence 17 BP; 2 A; 5 C; 9 G; 1 T; 0 U; 0 Other;

Query Match 0.8%; Score 13.8; DB 1; Length 17;

Best Local Similarity 88.2%; Pred. No. 1.9e+02;

Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1530 GCCCAGCCTCTCCCGC 1546

|||||  
 DB 17 GCCCAGCCTGTGCCGC 1

RESULT 286

AAA33231/C

ID AAA33231 standard; DNA; 17 BP.

XX  
 AC AAA33231;

XX  
 DT 28-JUL-2000 (first entry)

XX Low adenosine antisense oligonucleotide SEQ ID NO:920.

XX Human; adenosine receptor; low adenosine antisense oligonucleotide;  
 KW phosphorothioate; impaired respiration; inflammation; allergy;  
 KW allergic disease; bronchoconstriction; inhibitor; anti-inflammatory;  
 KW anti-allergic; antiasthmatic; cytostatic; analgesic; impaired airway;  
 KW lung disease; ischaemic condition; pulmonary vasoconstriction; asthma;  
 KW respiratory distress syndrome; pain; cystic fibrosis; emphysema;  
 KW pulmonary hypertension; chronic obstructive pulmonary disease; COPD;  
 KW cancer; leukaemia; lymphoma; carcinoma; metastasis; ss.

XX Homo sapiens.

XX WO200009525-A2.

XX  
 PD 24-FEB-2000.

XX  
 PF 03-AUG-1999; 99WO-US017712.

XX  
 PR 03-AUG-1998; 98US-0095212P.

XX (UYEC-) UNIV EAST CAROLINA.

XX Nyce JW;

XX WPI; 2000-205971/18.

XX New antisense oligonucleotides useful for treating e.g. pulmonary  
 PT vasoconstriction, inflammation, allergies, asthma, hypertension,  
 PT bronchitis, emphysema, respiratory distress syndrome, ischemia or  
 PT cancers.

XX Claim 18; Page 380; 1343pp; English.

XX The present invention describes a new composition comprising an antisense  
 CC oligonucleotide (ON) with low adenosine (up to 15%), which targets  
 CC nucleic acids involved in bronchoconstriction, allergies, and/or  
 CC inflammation. The ON can have anti-inflammatory, anti-allergic,  
 CC antiasthmatic, cytostatic and analgesic activities. The compositions are  
 CC useful for the treatment of diseases associated with inflammation,

CC impaired airways, including lung disease and diseases whose secondary  
 CC effects afflict the lungs of a subject. They can be used for treating  
 CC e.g. ischaemic conditions, pulmonary vasoconstriction, allergies, asthma,  
 CC impeded respiration, respiratory distress syndrome, pain, cystic  
 CC fibrosis, pulmonary hypertension, emphysema, chronic obstructive  
 CC pulmonary disease (COPD), and cancers such as leukaemias, lymphomas,  
 CC carcinomas, and cancers which may metastasise to the lungs, including  
 CC breast and prostate cancer. The reduction of the adenosine content of the  
 CC ONS reduces side effects. The A-containing ONS break down with the  
 CC release of deoxyadenosine which activates adenosine receptors causing  
 CC bronchoconstriction and inflammation. AAA32313 to AAA35312 represent the  
 CC nucleotide sequences given in the sequence listing from the present  
 CC invention, which correspond to SEQ ID NO:1 to 2815, and then the last 185  
 CC sequences are also called SEQ ID NO:1 to 185, but the sequences differ  
 CC from the previously named sequences. SEQ ID NO:11 to 1680 (AAA32323 to  
 CC AAA3392) are specifically claimed ONS from the present invention. N.B.  
 CC Sequences given in the disclosure of the present invention do not match  
 CC up with their corresponding SEQ ID NO: sequences given in the sequence  
 CC listing  
 XX  
 SQ Sequence 17 BP; 2 A; 5 C; 9 G; 1 T; 0 U; 0 Other;  
 Query Match 0.8%; Score 13.8; DB 1; Length 17;  
 Best Local Similarity 88.2%; Pred. No. 1.9e+02;  
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 1530 GCCCAGCCTCTCCCGC 1546  
 DB 17 GCCCAGCCTGTGCCGC 1  
 RESULT 287  
 AAA32356/c  
 ID AAA32356 standard; DNA; 17 BP.  
 XX  
 AC AAA32356;  
 XX  
 DT 28-JUL-2000 (first entry)  
 XX  
 DE Low adenosine antisense oligonucleotide SEQ ID NO:44.  
 XX  
 KW Human; adenosine receptor; low adenosine antisense oligonucleotide;  
 KW phosphorothioate; impaired respiration; inflammation; allergy;  
 KW allergic disease; bronchoconstriction; inhibitor; antiinflammatory;  
 KW antiallergic; antiasthmatic; cytostatic; analgesic; impaired airway;  
 KW lung disease; ischaemic condition; pulmonary vasoconstriction; asthma;  
 KW respiratory distress syndrome; pain; cystic fibrosis; emphysema;  
 KW pulmonary hypertension; chronic obstructive pulmonary disease; COPD;  
 KW cancer; leukaemia; lymphoma; carcinoma; metastasis; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200009525-A2.  
 XX  
 PD 24-FEB-2000.  
 XX  
 PF 03-AUG-1999; 99WO-US017712.  
 XX  
 PR 03-AUG-1998; 98US-0095212P.  
 XX  
 PA (UYEC-) UNIV EAST CAROLINA.  
 XX  
 XX Nyce JW;  
 XX  
 XX WPI; 2000-205971/18.  
 XX  
 XX New antisense oligonucleotides useful for treating e.g. pulmonary  
 PT vasoconstriction, inflammation, allergies, asthma, hypertension,  
 PT bronchitis, emphysema, respiratory distress syndrome, ischemia or  
 PT cancers.  
 XX  
 PS Claim 18; Page 272; 1343pp; English.  
 XX

CC The present invention describes a new composition comprising an antisense  
 CC oligonucleotide (ON) with low adenosine (up to 15%), which targets  
 CC nucleic acids involved in bronchoconstriction, allergies, and/or  
 CC inflammation. The ON can have antiinflammatory, antiallergic,  
 CC antiasthmatic, cytostatic and analgesic activities. The compositions are  
 CC useful for the treatment of diseases associated with inflammation,  
 CC impaired airways, including lung disease and diseases whose secondary  
 CC effects afflict the lungs of a subject. They can be used for treating  
 CC e.g. ischaemic conditions, pulmonary vasoconstriction, allergies, asthma,  
 CC impeded respiration, respiratory distress syndrome, pain, cystic  
 CC fibrosis, pulmonary hypertension, emphysema, chronic obstructive  
 CC pulmonary disease (COPD), and cancers such as leukaemias, lymphomas,  
 CC carcinomas, and cancers which may metastasise to the lungs, including  
 CC breast and prostate cancer. The reduction of the adenosine content of the  
 CC ONS reduces side effects. The A-containing ONS break down with the  
 CC release of deoxyadenosine which activates adenosine receptors causing  
 CC bronchoconstriction and inflammation. AAA32313 to AAA35312 represent the  
 CC nucleotide sequences given in the sequence listing from the present  
 CC invention, which correspond to SEQ ID NO:1 to 2815, and then the last 185  
 CC sequences are also called SEQ ID NO:1 to 185, but the sequences differ  
 CC from the previously named sequences. SEQ ID NO:11 to 1680 (AAA32323 to  
 CC AAA3392) are specifically claimed ONS from the present invention. N.B.  
 CC Sequences given in the disclosure of the present invention do not match  
 CC up with their corresponding SEQ ID NO: sequences given in the sequence  
 CC listing  
 XX  
 SQ Sequence 17 BP; 2 A; 5 C; 9 G; 1 T; 0 U; 0 Other;  
 Query Match 0.8%; Score 13.8; DB 1; Length 17;  
 Best Local Similarity 88.2%; Pred. No. 1.9e+02;  
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 1530 GCCCAGCCTCTCCCGC 1546  
 DB 17 GCCCAGCCTGTGCCGC 1  
 RESULT 288  
 AA257766/c  
 ID AA257766 standard; DNA; 17 BP.  
 XX  
 AC AA257766;  
 XX  
 DT 05-APR-2000 (first entry)  
 XX  
 DE Hepatitis C virus antisense inhibitor oligonucleotide #21.  
 XX  
 KW Hepatitis C virus; HCV; antisense oligonucleotide; hepatotropic; ss;  
 KW anti-inflammatory; translation inhibition; HCV infection; virucide.  
 XX  
 OS Hepatitis C virus.  
 XX  
 PN US6001990-A.  
 XX  
 PD 14-DEC-1999.  
 XX  
 PF 07-JUN-1995; 95US-00474700.  
 XX  
 PR 10-MAY-1994; 94US-00240382.  
 XX  
 PA (GEHO) GEN HOSPITAL CORP.  
 XX  
 XX Moradpour D, Wands JR, Wakita T;  
 XX  
 XX WPI; 2000-104900/09.  
 XX  
 XX Antisense oligonucleotide to Hepatitis C virus RNA, useful for treating  
 PT Hepatitis C virus infections.  
 XX  
 PS Claim 24; Col 25; 31pp; English.  
 XX  
 CC This sequence is an antisense oligonucleotide that hybridises to  
 CC Hepatitis C virus (HCV) RNA, under physiological conditions. The

CC invention relates to HCV antisense oligonucleotides, and also for a  
 CC vector comprising a nucleotide sequence which is transcribed in an animal  
 CC cell to generate an antisense oligonucleotide. The oligonucleotides have  
 CC virucide, hepatotropic and anti-inflammatory activity, and are useful for  
 CC treating HCV infection by inhibiting translation of type I-V HCV RNA.  
 CC Hepatitis C virus is a positive strand RNA virus, and is the major  
 CC causative agent of post-transfusion hepatitis. Persistent HCV infection  
 CC can lead to chronic hepatitis, cirrhosis, and hepatocellular carcinoma  
 XX

Sequence 17 BP; 1 A; 1 C; 4 G; 11 T; 0 U; 0 Other;

Query Match 0.8%; Score 13.8; DB 1; Length 17;  
 Best Local Similarity 88.2%; Pred. No. 1.9e+02; Mismatches 2; Indels 0; Gaps 0;  
 Matches 15; Conservative 0;

QY 222 CTCATAGAAAAAACAAA 238

DB 17 CTCGAAGAAACACAAA 1

RESULT 289

AAA03590/c

ID AAA03590 standard; DNA; 17 BP.

XX

AC AAA03590;

XX 19-MAY-2000 (first entry)

DE Human adenosine A1 receptor antisense oligonucleotide SEQ ID NO:874.

XX Human; adenosine A1 receptor; antisense oligonucleotide; hypoxia;  
 KW adenosine A2a receptor; adenosine A3 receptor; adenosine A3 receptor;  
 KW phosphorothioate; cardiopulmonary failure; renal failure; ischaemia;  
 KW endotoxin release; ARDS; acute respiratory distress syndrome;  
 KW cytoprotective; anti-allergic; anti-inflammatory; anti-hypoxic;  
 KW supraventricular tachycardia; allergic rhinitis; acute inflammation;  
 KW chronic obstructive pulmonary disease; ss.

XX Homo sapiens.

OS Synthetic.

XX WO9963938-A2.

FN

PD 16-DEC-1999.

XX

XX

PF 08-JUN-1999; 99WO-US012775.

XX

XX

PR 08-JUN-1998; 98US-0088501P.

PR 09-JUN-1998; 98US-00093972.

PR 09-JUN-1998; 98US-0088657P.

XX

XX (EPIC-) EPIGENESIS PHARM INC.

PA

XX

XX

PI Nyce JW, Hill JL;

XX

XX WPI; 2000-116433/10.

DR

XX

XX

PT Novel composition for treating or preventing e.g. cardiopulmonary and

PT renal injury.

XX

XX Claim 17; Page 36; 252pp; English.

PS

XX

XX

XX The present invention describes a pharmaceutical composition, comprising

CC at least one agent (I) that prevents, alleviates and/or inhibits

CC adenosine-mediated cardiopulmonary and/or renal damage and/or failure.

CC (I) is an adenosine A2a receptor agonist (Ia), or an oligonucleotide

CC (Ib), containing less than 15% adenosine (A), that is antisense to target

CC genes or corresponding RNA, to genomic flanking regions (i.e. 5' or 3'

CC ends or segments between coding and non-coding sequences), or to all

CC segments of mRNA encoding the adenosine A1, A2a, A2b or A3 receptors, and

CC has A1, A2b or A3 agonist activity or A2a antagonist activity (or at

CC least no agonist activity at this receptor). (I) may be a mixture of (Ia)

CC and (Ib), and optionally also contains one or more surfactants. The

CC

CC compositions are used to prevent, alleviate and/or treat adenosine  
 CC receptor-mediated cardiac, lung and/or renal damage or failure  
 CC (particularly where associated with ischaemia, toxin release and/or  
 CC administration of drugs or imaging agents, e.g. adenosine for treating  
 CC supraventricular tachycardia); (adult) respiratory distress syndrome  
 CC (e.g. associated with sepsis); allergic rhinitis; chronic obstructive  
 CC pulmonary disease; cardiopulmonary hypoxia associated with administration  
 CC of stress-test agents, particularly where such conditions are associated  
 CC with acute inflammation. AAA02717, AAA02719, AAA02721 and AAA02723 to  
 CC AAA03715 represent specifically claimed phosphorothioate antisense  
 CC oligonucleotides for use in the composition of the present invention.  
 CC AAA02718, AAA02720, AAA02722 and AAA03716 to AAA03720 represent other  
 CC phosphorothioate oligonucleotides used in the exemplification of the  
 CC present invention  
 XX

Sequence 17 BP; 2 A; 5 C; 9 G; 1 T; 0 U; 0 Other;

Query Match 0.8%; Score 13.8; DB 1; Length 17;  
 Best Local Similarity 88.2%; Pred. No. 1.9e+02; Mismatches 2; Indels 0; Gaps 0;  
 Matches 15; Conservative 0;

QY 1530 GCCCAGCCTCTCCCGC 1546

DB 17 GCCCAGCCTGTGCCGC 1

RESULT 290

AAA03660/c

ID AAA03660 standard; DNA; 17 BP.

XX

AC AAA03660;

XX

DT 19-MAY-2000 (first entry)

XX

DE Human adenosine A1 receptor antisense oligonucleotide SEQ ID NO:944.

XX

KW Human; adenosine A1 receptor; antisense oligonucleotide; hypoxia;

KW adenosine A2a receptor; adenosine A3 receptor; adenosine A3 receptor;

KW phosphorothioate; cardiopulmonary failure; renal failure; ischaemia;

KW endotoxin release; ARDS; acute respiratory distress syndrome;

KW cytoprotective; anti-allergic; anti-inflammatory; anti-hypoxic;

KW supraventricular tachycardia; allergic rhinitis; acute inflammation;

KW chronic obstructive pulmonary disease; ss.

XX

OS Homo sapiens.

OS Synthetic.

XX

XX WO9963938-A2.

XX

PD 16-DEC-1999.

XX

XX

PF 08-JUN-1999; 99WO-US012775.

XX

XX

PR 08-JUN-1998; 98US-0088501P.

PR 09-JUN-1998; 98US-00093972.

PR 09-JUN-1998; 98US-0088657P.

XX

XX (EPIC-) EPIGENESIS PHARM INC.

PA

XX

XX

PI Nyce JW, Hill JL;

XX

XX WPI; 2000-116433/10.

XX

XX Novel composition for treating or preventing e.g. cardiopulmonary and

XX renal injury.

XX

XX Claim 17; Page 37; 252pp; English.

PS

XX

XX The present invention describes a pharmaceutical composition, comprising

CC at least one agent (I) that prevents, alleviates and/or inhibits

CC adenosine-mediated cardiopulmonary and/or renal damage and/or failure.

CC (I) is an adenosine A2a receptor agonist (Ia), or an oligonucleotide

CC (Ib), containing less than 15% adenosine (A), that is antisense to target

CC

CC genes or corresponding RNA, to genomic flanking regions (i.e. 5' or 3'  
 CC ends or segments between coding and non-coding sequences), or to all  
 CC segments of mRNA encoding the adenosine A1, A2a, A2b or A3 receptors, and  
 CC has A1, A2b or A3 agonist activity or A2a antagonist activity (or at  
 CC least no agonist activity at this receptor). (I) may be a mixture of (Ia)  
 CC and (Ib), and optionally also contains one or more surfactants. The  
 CC compositions are used to prevent, alleviate and/or treat adenosine  
 CC receptor-mediated cardiac, lung and/or renal damage or failure  
 CC (particularly where associated with ischaemia, toxin release and/or  
 CC administration of drugs or imaging agents, e.g. adenosine for treating  
 CC supraventricular tachycardia); (adult) respiratory distress syndrome  
 CC (e.g. associated with sepsis); allergic rhinitis; chronic obstructive  
 CC pulmonary disease; cardiopulmonary hypoxia associated with administration  
 CC of stress-test agents, particularly where such conditions are associated  
 CC with acute inflammation. AAA02717, AAA02719, AAA02721 and AAA02723 to  
 CC AAA03715 represent specifically claimed phosphorothioate antisense  
 CC oligonucleotides for use in the composition of the present invention.  
 CC AAA02718, AAA02720, AAA02722 and AAA03716 to AAA03720 represent other  
 CC phosphorothioate oligonucleotides used in the exemplification of the  
 CC present invention  
 XX SQ Sequence 17 BP; 2 A; 5 C; 9 G; 1 T; 0 U; 0 Other;

Query Match 0.8%; Score 13.8; DB 1; Length 17;  
 Best Local Similarity 88.2%; Pred. No. 1.9e+02;  
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1530 GCCCAGCCTCTCCCGC 1546  
 Db 17 GCCCAGCCTGTGCCGC 1

RESULT 291  
 AAF19353/c  
 ID AAF19353 standard; DNA; 17 BP.  
 XX AC AAF19353;  
 XX DT 14-MAR-2001 (first entry)  
 XX DE Human adenosine A1 receptor polynucleotide fragment #920.  
 XX KW Low adenosine antisense oligonucleotide; phosphorothioate; allergy;  
 KW human; airway disorder; bronchoconstriction; lung inflammation;  
 KW surfactant depletion; respiratory; bronchodilator; antiinflammatory;  
 KW immunosuppressive; antiasthmatic; analgesic; hypotensive; cytostatic;  
 KW respiratory obstruction; pulmonary obstruction; impeded respiration;  
 KW surfactant hypoproduction; pulmonary vasoconstriction; asthma; RDS;  
 KW respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis;  
 KW pulmonary hypertension; emphysema; pulmonary transplantation rejection;  
 KW chronic obstructive pulmonary disease; pulmonary infection; bronchitis;  
 KW cancer; SS.  
 XX OS Homo sapiens.  
 XX PN WO200062736-A2.  
 XX PD 26-OCT-2000.  
 XX PF 24-MAR-2000; 2000WO-US008020.  
 XX PR 06-APR-1999; 99US-0127958P.  
 XX PA (UYEC-) UNIV EAST CAROLINA.  
 XX PA (NYCE/) NYCE J W.  
 XX PI Nyce JW;  
 XX WI 2000-679539/66.  
 XX DR  
 XX PT Low adenosine (A) content antisense oligonucleotides which do not trigger  
 PT adenosine receptors during metabolism, useful e.g. for treating cancers  
 PT and respiratory obstructions.

XX Claim 14; Page 120; 1592pp; English.  
 PS The present invention describes low adenosine (A) content antisense  
 CC oligonucleotides and compositions (I) comprising them. In the antisense  
 CC oligonucleotides the A is replaced by a 'Universal' or alternative base.  
 CC (I) can have respiratory, bronchodilator, antiinflammatory, analgesic,  
 CC immunosuppressive, antiasthmatic, hypotensive and cytostatic activities.  
 CC The antisense oligonucleotides and (I) can be used to down-regulate the  
 CC expression and/or activity of target polypeptides associated with  
 CC lung/respiratory disorders and malignancies, such as stimulating and  
 CC activating peptide factors and transmitters, transcription factors and  
 CC immunoglobulins and antibodies, antibody receptors, cytokines and  
 CC chemokines, endogenously produced specific and non-specific enzymes,  
 CC binding proteins, adhesion molecules and their receptors, cytokine and  
 CC chemokine receptors, adenosine receptors, bradykinin receptors, central  
 CC nervous system (CNS) and peripheral nervous and non-nervous system  
 CC receptors, CNS and peripheral nervous and non-nervous system peptide  
 CC transmitters, defensins, growth factors, vasoactive peptides and  
 CC receptors, binding proteins and malignancy associated proteins. The  
 CC antisense oligonucleotides may be used in this way to treat disorders  
 CC including respiratory obstruction (especially pulmonary obstruction  
 CC and/or bronchoconstriction) and/or lung inflammation, allergy(ies) and/or  
 CC surfactant hypoproduction which are associated with a disease or  
 CC condition selected from pulmonary vasoconstriction, inflammation,  
 CC allergies, asthma, impeded respiration, respiratory distress syndrome  
 CC (RDS), pain, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary  
 CC hypertension, emphysema, chronic obstructive pulmonary disease (COPD),  
 CC pulmonary transplantation rejection, pulmonary infections, bronchitis,  
 CC and/or cancer. AAF18434 to AAF21543 represent human polynucleotide  
 CC fragments and antisense oligonucleotides used in the exemplification of  
 CC the present invention  
 XX SQ Sequence 17 BP; 2 A; 5 C; 9 G; 1 T; 0 U; 0 Other;

Query Match 0.8%; Score 13.8; DB 1; Length 17;  
 Best Local Similarity 88.2%; Pred. No. 1.9e+02;  
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1530 GCCCAGCCTCTCCCGC 1546  
 Db 17 GCCCAGCCTGTGCCGC 1

RESULT 292  
 AAF18477/c  
 ID AAF18477 standard; DNA; 17 BP.  
 XX AC AAF18477;  
 XX DT 14-MAR-2001 (first entry)  
 XX DE Human adenosine A1 receptor polynucleotide fragment #44.  
 XX KW Low adenosine antisense oligonucleotide; phosphorothioate; allergy;  
 KW human; airway disorder; bronchoconstriction; lung inflammation;  
 KW surfactant depletion; respiratory; bronchodilator; antiinflammatory;  
 KW immunosuppressive; antiasthmatic; analgesic; hypotensive; cytostatic;  
 KW respiratory obstruction; pulmonary obstruction; impeded respiration;  
 KW surfactant hypoproduction; pulmonary vasoconstriction; asthma; RDS;  
 KW respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis;  
 KW pulmonary hypertension; emphysema; pulmonary transplantation rejection;  
 KW chronic obstructive pulmonary disease; pulmonary infection; bronchitis;  
 KW cancer; SS.  
 XX OS Homo sapiens.  
 XX PN WO200062736-A2.  
 XX PD 26-OCT-2000.  
 XX PF 24-MAR-2000; 2000WO-US008020.  
 XX

PR 06-APR-1999; 99US-0127958P.  
 XX (UYEC-) UNIV EAST CAROLINA.  
 PA (NYCE/) NYCE J W.  
 XX Nyce JW;  
 XX WPI; 2000-679539/66.  
 XX  
 XX Low adenosine (A) content antisense oligonucleotides which do not trigger  
 PT adenosine receptors during metabolism, useful e.g. for treating cancers  
 PT and respiratory obstructions.  
 XX  
 PS Claim 14; Page 106; 1592pp; English.  
 XX  
 CC The present invention describes low adenosine (A) content antisense  
 CC oligonucleotides and compositions (I) comprising them. In the antisense  
 CC oligonucleotides the A is replaced by a 'Universal' or alternative base.  
 CC (I) can have respiratory, bronchodilator, antiinflammatory, analgesic,  
 CC immunosuppressive, antiasthmatic, hypotensive and cytostatic activities.  
 CC The antisense oligonucleotides and (I) can be used to down-regulate the  
 CC expression and/or activity of target polypeptides associated with  
 CC lung/respiratory disorders and malignancies, such as stimulating and  
 CC activating peptide factors and transmitters, transcription factors,  
 CC immunoglobulins and antibodies, antibody receptors, cytokines and  
 CC chemokines, endogenously produced specific and non-specific enzymes,  
 CC binding proteins, adhesion molecules and their receptors, cytokine and  
 CC chemokine receptors, adenosine receptors, bradykinin receptors, central  
 CC nervous system (CNS) and peripheral nervous and non-nervous system  
 CC receptors, CNS and peripheral nervous and non-nervous system peptide  
 CC transmitters, defensins, growth factors, vasoactive peptides and  
 CC receptors, binding proteins and malignancy associated proteins. The  
 CC antisense oligonucleotides may be used in this way to treat disorders  
 CC including respiratory obstruction (especially pulmonary obstruction  
 CC and/or bronchoconstriction) and/or lung inflammation, allergy(ies) and/or  
 CC surfactant hypoproduction which are associated with a disease or  
 CC condition selected from pulmonary vasoconstriction, inflammation,  
 CC allergies, asthma, impeded respiration, respiratory distress syndrome  
 CC (RDS), pain, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary  
 CC hypertension, emphysema, chronic obstructive pulmonary disease (COPD),  
 CC pulmonary transplantation rejection, pulmonary infections, bronchitis,  
 CC and/or cancer. AAF18434 to AAF21543 represent human polynucleotide  
 CC fragments and antisense oligonucleotides used in the exemplification of  
 CC the present invention  
 XX  
 SQ Sequence 17 BP; 2 A; 5 C; 9 G; 1 T; 0 U; 0 Other;  
 Query Match 0.8%; Score 13.8; DB 1; Length 17;  
 Best Local Similarity 88.2%; Pred. NO. 1.9e+02;  
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 1530 GCCCAGCCTCTCCCGC 1546  
 Db 17 GCCCAGCCTGTCCCGC 1  
 RESULT 293  
 AAF02647  
 ID AAF02647 standard; DNA; 17 BP.  
 XX AAF02647;  
 AC  
 XX 16-FEB-2001 (first entry)  
 DT  
 DE Hammerhead ribozyme substrate #942.  
 XX  
 KW Ribozyme; erythropoietin; granulocyte colony stimulating factor;  
 KW interferon alpha; ss.  
 XX Homo sapiens.  
 OS  
 XX WO200061729-A2.  
 PN

PD 19-OCT-2000.  
 XX  
 XX 11-APR-2000; 2000WO-US009721.  
 XX  
 PR 12-APR-1999; 99US-0129390P.  
 XX  
 XX (RIBO-) RIBOZYME PHARM INC.  
 XX  
 XX Blatt L, Zwick M, Pavco P, Mcswiggen J;  
 XX WPI; 2000-647423/62.  
 XX  
 XX Enzymatic and antisense nucleic acid inhibition of repressor genes,  
 PT useful for producing e.g. granulocyte colony stimulating factor protein,  
 PT interferon alpha and erythropoietin.  
 XX  
 PS Claim 37; Page 77; 164pp; English.  
 XX  
 CC The present invention relates to enzymatic and antisense nucleic acid  
 CC molecules that act as inhibitors of the expression of repressor genes  
 CC encoding the TR2 Orphan receptor, EAR3/COUP-TF-1, the GATA transcription  
 CC factor gene, IRF-2 and/or the CAAAT Displacement Protein (CDP).  
 CC Inhibition of the repressors removes prevents inhibition (and  
 CC consequently increases expression of) genes involved in the production of  
 CC erythropoietin, granulocyte colony stimulating factor protein and  
 CC interferon alpha  
 XX  
 SQ Sequence 17 BP; 4 A; 6 C; 3 G; 4 T; 0 U; 0 Other;  
 Query Match 0.8%; Score 13.8; DB 1; Length 17;  
 Best Local Similarity 88.2%; Pred. NO. 1.9e+02;  
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 116 CCAGACGCTCTCAGACA 132  
 Db 1 CCAGACGTTCTCAGTCA 17  
 RESULT 294  
 ASK01885/c  
 ID ASK01885 standard; RNA; 17 BP.  
 XX ASK01885;  
 AC  
 XX 12-MAR-2002 (first entry)  
 DT  
 DE Human NOGO Zinzyme #207.  
 XX  
 KW Human; ss; antisense therapy; cytostatic; antiinflammatory; haemostatic;  
 KW cerebroprotective; nootropic; neuroprotective; antiparkinsonian;  
 KW muscular; CD20; neurite growth inhibitor gene; NOGO; hammerhead ribozyme;  
 KW DNazyme; inozyme; G-cleaver; amberzyme; zinzyme; lymphoma; leukaemia;  
 KW B-cell lymphoma; non-Hodgkin's lymphoma; NHL; lymphocytic leukaemia;  
 KW human immunodeficiency virus; HIV associated NHL; mantle-cell lymphoma;  
 KW MCL; immunocytoma; IMC; immune thrombocytopaenia; stroke; dementia;  
 KW inflammatory arthropathy; central nervous system injury;  
 KW cerebrovascular accident; CVA; Alzheimer's disease; multiple sclerosis;  
 KW chemotherapy-induced neuropathy; amyotrophic lateral sclerosis; ALS;  
 KW Parkinson's disease; ataxia; Huntington's disease;  
 KW Creutzfeldt-Jakob disease; muscular dystrophy; neurodegenerative disease.  
 XX  
 OS Homo sapiens.  
 OS Synthetic.  
 XX  
 XX WO200159103-A2.  
 PN  
 XX 16-AUG-2001.  
 PD  
 XX 09-FEB-2001; 2001WO-US004273.  
 XX  
 XX 11-FEB-2000; 2000US-0181797P.  
 XX 28-FEB-2000; 2000US-0185516P.  
 XX 06-MAR-2000; 2000US-0187128P.  
 PR





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Query Match      0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.9e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1622 AATTAACCTGCTTGTG 1638
DB 17 AATTAACCTGCTTTTG 1

RESULT 296
AAD20527
ID AAD20527 standard; DNA; 17 BP.
AC AAD20527;
XX
XX 03-JAN-2002 (first entry)
XX
DE Mouse Obr genomic DNA amplifying forward PCR primer #2.
KW Mouse; obese receptor; Obr; anorectic; anabolic; body weight disorder;
KW therapy; obesity; cachexia; anorexia; PCR primer; ss.
XX
OS Mus sp.
XX
PN US6287782-B1.
XX
PD 11-SEP-2001.
XX
PF 29-APR-1998; 98US-00069781.
XX
PR 27-NOV-1995; 95US-00562663.
PR 04-DEC-1995; 95US-00566622.
PR 08-DEC-1995; 95US-00569485.
PR 11-DEC-1995; 95US-00570142.
PR 28-DEC-1995; 95US-00583153.
PR 22-JAN-1996; 96US-00599455.
PR 26-APR-1996; 96US-00638524.
PR 03-SEP-1996; 96US-00708123.
PR 28-MAY-1997; 97US-00864564.
XX
PA (MILL-) MILLENNIUM PHARM INC.
XX
PI Tartaglia LA, Tepper RI, Culpepper JA, White DW;
XX WPI; 2001-624489/72.
XX
PT Identifying compounds for treating body weight disorder, e.g. obesity,
PT anorexia or cachexia, comprises contacting cell expressing mammalian Ob
PT receptor protein, JAK2 protein and mammalian SOCS-1 protein with test
PT compound.
XX
PS Example; Col 62; 109pp; English.
XX
CC The patent discloses obese receptor (Obr) proteins and nucleic acids
CC encoding them. Obr protein participates in the regulation of mammalian
CC body weight. The invention also relates to a method of identifying
CC therapeutic compounds for the treatment of a body weight disorder. The
CC method involves contacting a cell that expresses a mammalian Obr protein,
CC a JAK2 protein and a mammalian SOCS-1 protein with a test compound. The
CC method is useful for identifying compounds which modulate Obr gene
CC expression and gene product activity, which can be used as agents to
CC control body weight particularly as therapeutic agents for treating body
CC weight disorders, including obesity, cachexia and anorexia. The present
CC DNA sequence is a forward PCR primer which is used for amplifying mouse
CC Obr genomic DNA
XX
SQ Sequence 17 BP; 3 A; 6 C; 2 G; 6 T; 0 U; 0 Other;

Query Match      0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.9e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 660 CACTACCTGCCCTTCAG 676
DB 1 CACTATTGGCCCTTCAG 17

RESULT 298
Query Match      0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.9e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 660 CACTACCTGCCCTTCAG 676
DB 1 CACTATTGGCCCTTCAG 17

RESULT 298
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AAF79852
ID  AAF79852 standard; DNA; 17 BP.
AC  AAF79852;
XX
XX  30-MAY-2001  (first entry)
XX
DE  DNA sequencing method DNA fragment.
XX
XX  DNA sequencing; sequence analysis; chromophore; fluorophore; ds.
XX
XX  Synthetic.
XX
XX  US6200748-B1.
XX
XX  13-MAR-2001.
XX
XX  07-JUN-1995; 95US-0048340.
XX
XX  16-JAN-1984; 84US-00570973.
XX
XX  02-JAN-1985; 85US-00689013.
XX
XX  11-APR-1985; 85US-00722742.
XX
XX  07-OCT-1987; 87US-00106232.
XX
XX  21-FEB-1991; 91US-00660160.
XX
XX  12-JUN-1992; 92US-00898019.
XX
XX  21-DEC-1994; 94US-00361176.
XX
XX  (CALY ) CALIFORNIA INST OF TECHNOLOGY.
XX
XX  Smith LM, Hood LE, Hunkapiller MW, Hunkapiller TJ, Connell CR;
XX
XX  WPI; 2001-256466/26.
XX
XX  Novel duplex useful in sequencing reactions, comprising an
XX  oligonucleotide primer covalently coupled to a chromophore or fluorophore
XX  so as to allow chain extension by a polymerase, and a template.
XX
XX  Disclosure; Fig 1A; 15pp; English.
XX
XX  The present invention describes a duplex comprising a template and a
XX  primer joined to a chromophore or fluorophore to enable chain extension
XX  by a polymerase. Also described is a method of sequencing a nucleic acid
XX  using said primer, where the chromophore or fluorophore is used to
XX  determine the sequence of the oligonucleotide. This is useful in sequence
XX  analysis. The present sequence was used to demonstrate the method of the
XX  invention
XX
XX  Sequence 17 BP; 5 A; 4 C; 4 G; 4 T; 0 U; 0 Other;
XX
XX  Query Match 0.8%; Score 13.8; DB 1; Length 17;
XX  Best Local Similarity 88.2%; Pred. No. 1.9e+02;
XX  Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX  1357 AAGCGCTCGAGGATAC 1373
XX  |||||
XX  1 ATGCTCTCGAGGATAC 17
XX
XX
XX
XX  RESULT 299
XX  ABL46807/c
XX  ID  ABL46807 standard; RNA; 17 BP.
XX
XX  ABL46807;
XX
XX  27-JUN-2003  (first entry)
XX
XX  Human GRID NCH ribozyme substrate oligonucleotide #261.
XX
XX  Human; Grb2-related with Insert Domain; GRID; T-cell;
XX  co-stimulatory adaptor protein; tissue rejection; graft rejection;
XX  leukaemia; cytostatic; ss.
XX
XX  Homo sapiens.
XX

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XX  WO200162911-A2.
XX
XX  30-AUG-2001.
XX
XX  23-FEB-2001; 2001WO-US005957.
XX
XX  24-FEB-2000; 2000US-0184594P.
XX
XX  (RIBO-) RIBOZYME PHARM INC.
XX  (GLAX ) GLAXO GROUP LTD.
XX
XX  Jarvis T, Von Carlowitz I, Mcswiggen JA, Hamblin PA, Ellis JH;
XX  WPI; 2001-550088/61.
XX
XX  New nucleic acid(s) for regulating the Grb2-related with Insert Domain
XX  (GRID) gene comprises using antisense and enzymatic nucleic acid
XX  molecules such as hammerhead ribozymes.
XX
XX  Claim 4; Page 67; 108pp; English.
XX
XX  The present invention relates to oligonucleotides that downregulate the
XX  expression of human Grb2-related with Insert Domain (GRID) gene. GRID is
XX  a T-cell co-stimulatory adaptor protein. The oligonucleotides are useful
XX  for modulating the expression of GRID, to treat conditions such as
XX  tissue/graft rejection and leukaemia. The oligonucleotides can also be
XX  administered in conjunction with other therapies such as radiation,
XX  chemotherapy and cyclosporin treatment. The present oligonucleotide was
XX  used to illustrate the invention
XX
XX  Sequence 17 BP; 3 A; 4 C; 8 G; 0 T; 2 U; 0 Other;
XX
XX  Query Match 0.8%; Score 13.8; DB 1; Length 17;
XX  Best Local Similarity 88.2%; Pred. No. 1.9e+02;
XX  Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX  1539 CTCGCCGCTCTGGATCC 1555
XX  |||||
XX  17 CTCGCCGCTCTGGAAACC 1
XX
XX  RESULT 300
XX  AAD41482
XX  ID  AAD41482 standard; DNA; 17 BP.
XX
XX  AAD41482;
XX
XX  30-OCT-2002  (first entry)
XX
XX  Mouse Ob receptor (Obr) gene amplifying forward PCR primer #2.
XX
XX  Mouse; obese receptor; Obr; receptor; body weight disorder; obesity;
XX  cachexia; anorexia; anorectic; anabolic; immunomodulator; PCR; primer;
XX  ss.
XX
XX  Mus sp.
XX
XX  US6395498-B1.
XX
XX  28-MAY-2002.
XX
XX  28-MAY-1997; 97US-00864564.
XX
XX  27-NOV-1995; 95US-00562663.
XX
XX  04-DEC-1995; 95US-00566622.
XX
XX  08-DEC-1995; 95US-00569485.
XX
XX  11-DEC-1995; 95US-00570142.
XX
XX  28-DEC-1995; 95US-00583153.
XX
XX  22-JAN-1996; 96US-00599455.
XX
XX  26-APR-1996; 96US-00638524.
XX
XX  03-SEP-1996; 96US-00708123.
XX

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PA (MILL-) MILLENNIUM PHARM INC.  
XX Tartaglia LA, Tepper RI, Culpepper JA, White DW;  
PI WPI; 2002-535640/57.  
XX  
XX Identifying candidate therapeutic agents for treating body weight  
PT disorders, comprises contacting test compound with cell expressing  
PT mammalian obese receptor and reporter protein, and measuring expression  
PT of reporter protein.  
XX  
XX Example; Col 119; 110pp; English.  
XX  
XX The present invention relates to novel obese (Ob) receptor (OBR) proteins  
CC and polynucleotides encoding them. The invention relates to a method of  
CC identifying candidate therapeutic agents to treat body weight disorder.  
CC The method involves providing a cell which expresses a mammalian OBR on  
CC the cell surface, binds leptin, the cell harbouring a reporter construct  
CC comprising a sequence encoding a reporter protein, contacting the cell  
CC with a test compound and measuring the expression of the reporter protein  
CC in the presence of the test compound. The method is useful to identify an  
CC agent, preferably a small molecule or antibody for the treatment of body  
CC weight disorders such as obesity, cachexia, and anorexia. The present DNA  
CC sequence is a PCR primer which is used for amplifying mouse OBR genomic  
CC DNA. This sequence is used in the exemplification of the invention  
XX  
SQ Sequence 17 BP; 3 A; 6 C; 2 G; 6 T; 0 U; 0 Other;  
Query Match 0.8%; Score 13.8; DB 1; Length 17;  
Best Local Similarity 88.2%; Pred. No. 1.9e+02;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 660 CACTACCTGCCCTTCAG 676  
Db 1 CACTATTGCCCTTCAG 17  
RESULT 301  
AAD41484  
ID AAD41484 standard; DNA; 17 BP.  
XX  
XX AAD41484;  
AC  
XX 30-OCT-2002 (first entry)  
DT  
XX Mouse Ob receptor (OBR) gene amplifying forward PCR primer #3.  
DE  
XX  
XX Mouse; obese receptor; OBR; receptor; body weight disorder; obesity;  
KW cachexia; anorexia; anorectic; anabolic; immunomodulator; PCR; primer;  
KW ss.  
XX  
XX Mus sp.  
OS  
XX US6395498-B1.  
FN  
XX 28-MAY-2002.  
PD  
XX 28-MAY-1997; 97US-00864564.  
PF  
XX 27-NOV-1995; 95US-00562663.  
PR  
XX 04-DEC-1995; 95US-00566622.  
PR  
XX 08-DEC-1995; 95US-00569485.  
PR  
XX 11-DEC-1995; 95US-00570142.  
PR  
XX 28-DEC-1995; 95US-00583153.  
PR  
XX 22-JAN-1996; 96US-00599455.  
PR  
XX 28-DEC-1995; 95US-00593153.  
PR  
XX 26-APR-1996; 96US-00638524.  
PR  
XX 03-SEP-1996; 96US-00708123.  
XX  
XX (MILL-) MILLENNIUM PHARM INC.  
PA  
XX Tartaglia LA, Tepper RI, Culpepper JA, White DW;  
PI WPI; 2002-535640/57.  
XX  
XX Identifying candidate therapeutic agents for treating body weight  
PT disorders, comprises contacting test compound with cell expressing  
PT mammalian obese receptor and reporter protein, and measuring expression  
PT of reporter protein.  
XX  
XX Example; Col 119; 110pp; English.  
XX  
XX The present invention relates to novel obese (Ob) receptor (OBR) proteins  
CC and polynucleotides encoding them. The invention relates to a method of  
CC identifying candidate therapeutic agents to treat body weight disorder.  
CC The method involves providing a cell which expresses a mammalian OBR on  
CC the cell surface, binds leptin, the cell harbouring a reporter construct  
CC comprising a sequence encoding a reporter protein, contacting the cell  
CC with a test compound and measuring the expression of the reporter protein  
CC in the presence of the test compound. The method is useful to identify an  
CC agent, preferably a small molecule or antibody for the treatment of body  
CC weight disorders such as obesity, cachexia, and anorexia. The present DNA  
CC sequence is a PCR primer which is used for amplifying mouse OBR genomic  
CC DNA. This sequence is used in the exemplification of the invention  
XX  
SQ Sequence 17 BP; 3 A; 6 C; 2 G; 6 T; 0 U; 0 Other;  
Query Match 0.8%; Score 13.8; DB 1; Length 17;  
Best Local Similarity 88.2%; Pred. No. 1.9e+02;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 660 CACTACCTGCCCTTCAG 676  
Db 1 CACTATTGCCCTTCAG 17  
RESULT 301  
AAD41484  
ID AAD41484 standard; DNA; 17 BP.  
XX  
XX AAD41484;  
AC  
XX 30-OCT-2002 (first entry)  
DT  
XX Mouse Ob receptor (OBR) gene amplifying forward PCR primer #3.  
DE  
XX  
XX Mouse; obese receptor; OBR; receptor; body weight disorder; obesity;  
KW cachexia; anorexia; anorectic; anabolic; immunomodulator; PCR; primer;  
KW ss.  
XX  
XX Mus sp.  
OS  
XX US6395498-B1.  
FN  
XX 28-MAY-2002.  
PD  
XX 28-MAY-1997; 97US-00864564.  
PF  
XX 27-NOV-1995; 95US-00562663.  
PR  
XX 04-DEC-1995; 95US-00566622.  
PR  
XX 08-DEC-1995; 95US-00569485.  
PR  
XX 11-DEC-1995; 95US-00570142.  
PR  
XX 28-DEC-1995; 95US-00583153.  
PR  
XX 22-JAN-1996; 96US-00599455.  
PR  
XX 26-APR-1996; 96US-00638524.  
PR  
XX 03-SEP-1996; 96US-00708123.  
XX  
XX (MILL-) MILLENNIUM PHARM INC.  
PA  
XX Tartaglia LA, Tepper RI, Culpepper JA, White DW;  
PI WPI; 2002-535640/57.  
XX  
XX Identifying candidate therapeutic agents for treating body weight  
PT disorders, comprises contacting test compound with cell expressing  
PT mammalian obese receptor and reporter protein, and measuring expression  
PT of reporter protein.  
XX  
XX Example; Col 121; 110pp; English.  
XX  
XX The present invention relates to novel obese (Ob) receptor (OBR) proteins  
CC and polynucleotides encoding them. The invention relates to a method of  
CC identifying candidate therapeutic agents to treat body weight disorder.  
CC The method involves providing a cell which expresses a mammalian OBR on  
CC the cell surface, binds leptin, the cell harbouring a reporter construct  
CC comprising a sequence encoding a reporter protein, contacting the cell  
CC with a test compound and measuring the expression of the reporter protein  
CC in the presence of the test compound. The method is useful to identify an  
CC agent, preferably a small molecule or antibody for the treatment of body  
CC weight disorders such as obesity, cachexia, and anorexia. The present DNA  
CC sequence is a PCR primer which is used for amplifying mouse OBR genomic  
CC DNA. This sequence is used in the exemplification of the invention  
XX  
SQ Sequence 17 BP; 3 A; 6 C; 2 G; 6 T; 0 U; 0 Other;  
Query Match 0.8%; Score 13.8; DB 1; Length 17;  
Best Local Similarity 88.2%; Pred. No. 1.9e+02;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 660 CACTACCTGCCCTTCAG 676  
Db 1 CACTATTGCCCTTCAG 17  
RESULT 302  
AAD42341  
ID AAD42341 standard; DNA; 17 BP.  
XX  
XX AAD42341;  
AC  
XX 04-NOV-2002 (first entry)  
DT  
XX Mouse obesity receptor (OBR) gene amplifying forward primer #3.  
DE  
XX  
XX Obesity receptor; OBR; body weight disorder; therapy; food intake;  
KW anorexia; cachexia; acquired immune deficiency syndrome; cytostatic;  
KW AIDS-related wasting; cancer-related wasting; metabolic; anti-HIV;  
KW immunomodulator; human immunodeficiency virus; mouse; PCR; primer; ss.  
XX  
XX Mus sp.  
OS  
XX US6403552-B1.  
FN  
XX 11-JUN-2002.  
PD  
XX 09-JUN-1998; 98US-00094410.  
PF  
XX 27-NOV-1995; 95US-00562663.  
PR  
XX 04-DEC-1995; 95US-00566622.  
PR  
XX 08-DEC-1995; 95US-00569485.  
PR  
XX 11-DEC-1995; 95US-00570142.  
PR  
XX 28-DEC-1995; 95US-00583153.  
PR  
XX 22-JAN-1996; 96US-00599455.  
PR  
XX 26-APR-1996; 96US-00638524.  
PR  
XX 03-SEP-1996; 96US-00708123.  
PR  
XX 28-MAY-1997; 97US-00864564.  
XX  
XX (MILL-) MILLENNIUM PHARM INC.  
PA  
XX Tartaglia LA, Tepper RI, Culpepper JA, White DW;  
PI WPI; 2002-536045/57.  
XX  
XX Increasing food intake in a mammal having a low body weight disorder such  
PT as anorexia, involves administering to the mammal a soluble polypeptide

comprising the extracellular domain of an obesity receptor protein.  
Example; Col 63; 114pp; English.  
The invention relates to obesity receptor (OBR) protein and its corresponding nucleic acid. The invention also relates to a method for the diagnosis and treatment of body weight disorders. The method is useful for increasing food intake in a mammal having a disorder characterised by low body weight, where the disorder is anorexia, cachexia, acquired immunodeficiency syndrome (AIDS)-related wasting or cancer-related wasting. The present sequence is a PCR primer used for amplifying mouse OBR gene. This sequence is used in the exemplification of the invention  
Sequence 17 BP; 3 A; 6 C; 2 G; 6 T; 0 U; 0 Other;  
Query Match 0.8%; Score 13.8; DB 1; Length 17;  
Best Local Similarity 88.2%; Pred. No. 1.9e+02;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 660 CACTACCTGCGCTTCAG 676  
DB 1 CACTATTGCGCTTCAG 17  
RESULT 304  
ABN01903/c  
ID AEN01903 standard; DNA; 17 BP.  
XX  
XX AEN01903;  
XX AC  
XX 29-MAY-2002 (first entry)  
XX Human GDMPL-1 17-mer scanning SEQ ID NO:4 sequence SEQ ID NO:1895.  
XX Human; genome-derived myosin-like protein 1; GDMPL-1; hGDMPL-1; heart;  
KW muscle; myosin; chromosome 22; gene therapy; vaccine; heart disease;  
KW skeletal muscle disorder; amplicon; screening; ss.  
XX Homo sapiens.  
XX  
XX WO200192524-A2.  
XX  
XX 06-DEC-2001.  
XX 25-MAY-2001; 2001WO-US016981.  
XX 26-MAY-2000; 2000US-0207456P.  
XX 21-SEP-2000; 2000US-0234687P.  
XX 27-SEP-2000; 2000US-0236359P.  
XX 04-OCT-2000; 2000GB-00024263.  
XX 30-JAN-2001; 2001WO-US000661.  
XX 30-JAN-2001; 2001WO-US000662.  
XX 30-JAN-2001; 2001WO-US000663.  
XX 30-JAN-2001; 2001WO-US000664.  
XX 30-JAN-2001; 2001WO-US000665.  
XX 30-JAN-2001; 2001WO-US000666.  
XX 30-JAN-2001; 2001WO-US000667.  
XX 30-JAN-2001; 2001WO-US000668.  
XX 30-JAN-2001; 2001WO-US000669.  
XX 05-FEB-2001; 2001US-0266860P.  
XX (AEOM-) AEOMICA INC.  
XX Gu Y, Ji Y, Penn SG, Hanzel DK, Rank DR, Chen W, Shannon ME;  
XX WPI; 2002-179446/23.  
XX New polypeptide, for raising antibodies that recognize hGDMPL-1 proteins,  
PT or as specific biomolecule capture probes for surface-enhanced laser  
PT desorption ionization, comprises human myosin-like protein hGDMPL-1.  
XX Disclosure; SEQ ID NO 1895; 214pp; English.  
XX The present invention describes a human genome-derived myosin-like  
XX protein 1 (hGDMPL-1). The protein and polynucleotide sequences of hGDMPL-  
CC 1 can be used in gene therapy and vaccine production. The hGDMPL-1  
CC nucleic acids can be used as probes to detect, characterise and quantify  
CC hGDMPL-1 nucleic acids in samples, as amplification substrates, to  
CC provide initial substrates for the recombinant engineering of hGDMPL-1

comprising the extracellular domain of an obesity receptor protein.  
Example; Col 63; 114pp; English.  
The invention relates to obesity receptor (OBR) protein and its corresponding nucleic acid. The invention also relates to a method for the diagnosis and treatment of body weight disorders. The method is useful for increasing food intake in a mammal having a disorder characterised by low body weight, where the disorder is anorexia, cachexia, acquired immunodeficiency syndrome (AIDS)-related wasting or cancer-related wasting. The present sequence is a PCR primer used for amplifying mouse OBR gene. This sequence is used in the exemplification of the invention  
Sequence 17 BP; 3 A; 6 C; 2 G; 6 T; 0 U; 0 Other;  
Query Match 0.8%; Score 13.8; DB 1; Length 17;  
Best Local Similarity 88.2%; Pred. NO. 1.9e+02;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 660 CACTACCTGCGCTTCAG 676  
DB 1 CACTATTGCGCTTCAG 17  
RESULT 303  
AAD42339  
ID AAD42339 standard; DNA; 17 BP.  
XX  
XX AAD42339;  
XX  
XX 04-NOV-2002 (first entry)  
XX Mouse obesity receptor (OBR) gene amplifying forward primer #2.  
XX Obesity receptor; OBR; body weight disorder; therapy; food intake;  
KW anorexia; cachexia; acquired immune deficiency syndrome; cytostatic;  
KW AIDS-related wasting; cancer-related wasting; metabolic; anti-HIV;  
KW immunomodulator; human immunodeficiency virus; mouse; PCR; primer; ss.  
XX Mus sp.  
XX US6403552-B1.  
XX 11-JUN-2002.  
XX 09-JUN-1998; 98US-00094410.  
XX 27-NOV-1995; 95US-00562663.  
XX 04-DEC-1995; 95US-00566622.  
XX 08-DEC-1995; 95US-00569485.  
XX 11-DEC-1995; 95US-00570142.  
XX 28-DEC-1995; 95US-00583153.  
XX 22-JAN-1996; 96US-00599455.  
XX 26-APR-1996; 96US-00638524.  
XX 03-SEP-1996; 96US-00708123.  
XX 28-MAY-1997; 97US-00864564.  
XX (MILL-) MILLENIUM PHARM INC.  
XX Tartaglia LA, Tepper RI, Culpepper JA, White DW;  
XX WPI; 2002-536045/57.  
XX Increasing food intake in a mammal having a low body weight disorder such  
PT as anorexia, involves administering to the mammal a soluble polypeptide  
PT comprising the extracellular domain of an obesity receptor protein.  
XX Example; Col 62; 114pp; English.  
XX The invention relates to obesity receptor (OBR) protein and its  
CC corresponding nucleic acid. The invention also relates to a method for  
CC the diagnosis and treatment of body weight disorders. The method is

CC protein variants having desired phenotypic improvements, and for  
CC expressing the proteins. The hGDMPLP-1 proteins or polypeptides may be  
CC used as immunogens to raise antibodies that specifically recognise hGDMPLP  
CC -1 proteins, as standards in assays used to determine the concentration  
CC and/or amount specifically of hGDMPLP proteins, as specific biomolecule  
CC capture probes for surface-enhanced laser desorption/ionisation, as  
CC therapeutic supplement in patients having specific deficiency in hGDMPLP-1  
CC production, and in vaccines or for replacement therapy. The  
CC polynucleotide sequences encoding hGDMPLP-1 may be used for diagnosing a  
CC disorder associated with the expression of hGDMPLP-1, in particular heart  
CC and skeletal muscle disorders. hGDMPLP-1 is localised to chromosome 22.  
CC The present sequence represents an oligomer used in the screening of the  
CC hGDMPLP-1 sequence in the exemplification of the present invention. N.B.  
CC The sequence data for this patent did not form part of the printed  
CC specification, but was obtained in electronic format directly from WIPO  
CC at ftp.wipo.int/pub/published\_pct\_sequence  
XX  
SQ Sequence 17 BP; 2 A; 7 C; 4 G; 4 T; 0 U; 0 Other;

Query Match 0.8%; Score 13.8; DB 1; Length 17;  
Best Local Similarity 88.2%; Pred. No. 1.9e+02;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 93 GAGAGTGGCAGGTCT 109

DB 17 GAGAGAGGCCAGGTCT 1

RESULT 305  
ABN07493/C

ID ABN07493 standard; DNA; 17 BP.

XX AC ABN07493;

XX 29-MAY-2002 (first entry)

DE Human GDMPLP-1 17-mer scanning SEQ ID NO:5 sequence SEQ ID NO:7485.  
XX Human; genome-derived myosin-like protein 1; GDMPLP-1; hGDMPLP-1; heart;  
KW muscle; myosin; chromosome 22; gene therapy; vaccine; heart disease;  
KW skeletal muscle disorder; amplicon; screening; ss.  
XX Homo sapiens.

OS

XX WO200192524-A2.

XX 06-DEC-2001.

XX 25-MAY-2001; 2001WO-US016981.

XX 26-MAY-2000; 2000US-0207456P.

XX 21-SEP-2000; 2000US-0234687P.

XX 27-SEP-2000; 2000US-0236359P.

XX 04-OCT-2000; 2000GB-00024263.

XX 30-JAN-2001; 2001WO-US000661.

XX 30-JAN-2001; 2001WO-US000662.

XX 30-JAN-2001; 2001WO-US000663.

XX 30-JAN-2001; 2001WO-US000664.

XX 30-JAN-2001; 2001WO-US000665.

XX 30-JAN-2001; 2001WO-US000666.

XX 30-JAN-2001; 2001WO-US000667.

XX 30-JAN-2001; 2001WO-US000668.

XX 30-JAN-2001; 2001WO-US000669.

XX 05-FEB-2001; 2001WO-US000670.

XX (AEOM-) AEOMICA INC.

XX Gu Y, Ji Y, Penn SG, Hanzel DK, Rank DR, Chen W, Shannon ME;  
XX WPI; 2002-179446/23.  
XX New polypeptide, for raising antibodies that recognize hGDMPLP-1 proteins,  
PT

PT or as specific biomolecule capture probes for surface-enhanced laser  
PT desorption/ionisation, comprises human myosin-like protein hGDMPLP-1.  
XX Disclosure; SEQ ID NO 7485; 214pp; English.

XX The present invention describes a human genome-derived myosin-like  
CC protein 1 (hGDMPLP-1). The protein and polynucleotide sequences of hGDMPLP-  
CC 1 can be used in gene therapy and vaccine production. The hGDMPLP-1  
CC nucleic acids can be used as probes to detect, characterise and quantify  
CC hGDMPLP-1 nucleic acids in samples, as amplification substrates, to  
CC provide initial substrates for the recombinant engineering of hGDMPLP-1  
CC protein variants having desired phenotypic improvements, and for  
CC expressing the proteins. The hGDMPLP-1 proteins or polypeptides may be  
CC used as immunogens to raise antibodies that specifically recognise hGDMPLP  
CC -1 proteins, as standards in assays used to determine the concentration  
CC and/or amount specifically of hGDMPLP proteins, as specific biomolecule  
CC capture probes for surface-enhanced laser desorption/ionisation, as  
CC therapeutic supplement in patients having specific deficiency in hGDMPLP-1  
CC production, and in vaccines or for replacement therapy. The  
CC polynucleotide sequences encoding hGDMPLP-1 may be used for diagnosing a  
CC disorder associated with the expression of hGDMPLP-1, in particular heart  
CC and skeletal muscle disorders. hGDMPLP-1 is localised to chromosome 22.  
CC The present sequence represents an oligomer used in the screening of the  
CC hGDMPLP-1 sequence in the exemplification of the present invention. N.B.  
CC The sequence data for this patent did not form part of the printed  
CC specification, but was obtained in electronic format directly from WIPO  
CC at ftp.wipo.int/pub/published\_pct\_sequence  
XX

SQ Sequence 17 BP; 4 A; 3 C; 9 G; 1 T; 0 U; 0 Other;

Query Match 0.8%; Score 13.8; DB 1; Length 17;  
Best Local Similarity 88.2%; Pred. No. 1.9e+02;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1530 GCCCAGCCTCTCCCGC 1546

DB 17 GTCCAGCCTCTCTCGC 1

RESULT 306

ABN08576

ID ABN08576 standard; DNA; 17 BP.

XX AC ABN08576;

XX 29-MAY-2002 (first entry)

XX Human GDMPLP-1 17-mer scanning SEQ ID NO:5 sequence SEQ ID NO:8568.

XX Human; genome-derived myosin-like protein 1; GDMPLP-1; hGDMPLP-1; heart;  
KW muscle; myosin; chromosome 22; gene therapy; vaccine; heart disease;  
KW skeletal muscle disorder; amplicon; screening; ss.

OS Homo sapiens.

XX WO200192524-A2.

XX 06-DEC-2001.

XX 25-MAY-2001; 2001WO-US016981.

XX 26-MAY-2000; 2000US-0207456P.

XX 21-SEP-2000; 2000US-0234687P.

XX 27-SEP-2000; 2000US-0236359P.

XX 04-OCT-2000; 2000GB-00024263.

XX 30-JAN-2001; 2001WO-US000661.

XX 30-JAN-2001; 2001WO-US000662.

XX 30-JAN-2001; 2001WO-US000663.

XX 30-JAN-2001; 2001WO-US000664.

XX 30-JAN-2001; 2001WO-US000665.

XX 30-JAN-2001; 2001WO-US000666.

XX 30-JAN-2001; 2001WO-US000667.

XX 30-JAN-2001; 2001WO-US000668.

PR	30-JAN-2001; 2001WO-US00069.
PR	30-JAN-2001; 2001WO-US000670.
PR	05-FEB-2001; 2001US-026866OP.
PA	(AEOM-) AEOMICA INC.
XX	
PI	Gu Y, Ji Y, Penn SG, Hanzel DK, Rank DR, Chen W, Shannon ME;
XX	
WI	PFI; 2002-179446/23.
XX	
PT	New polypeptide, for raising antibodies that recognize hGDMPLP-1 proteins,
PT	or as specific biomolecule capture probes for surface-enhanced laser
PT	desorption ionization, comprises human myosin-like protein hGDMPLP-1.
XX	
PS	Disclosure; SEQ ID NO 8568; 214pp; English.
XX	
CC	The present invention describes a human genome-derived myosin-like
CC	protein 1 (hGDMPLP-1). The protein and polynucleotide sequences of hGDMPLP-
CC	1 can be used in gene therapy and vaccine production. The hGDMPLP-1
CC	nucleic acids can be used as probes to detect, characterise and quantify
CC	hGDMPLP-1 nucleic acids in samples, as amplification substrates, to
CC	provide initial substrates for the recombinant engineering of hGDMPLP-1
CC	protein variants having desired phenotypic improvements, and for
CC	expressing the proteins. The hGDMPLP-1 proteins or polypeptides may be
CC	used as immunogens to raise antibodies that specifically recognise hGDMPLP
CC	-1 proteins, as standards in assays used to determine the concentration
CC	and/or amount specifically of hGDMPLP proteins, as specific biomolecule
CC	capture probes for surface-enhanced laser desorption/ionisation, as
CC	therapeutic supplement in patients having specific deficiency in hGDMPLP-1
CC	production, and in vaccines or for replacement therapy. The
CC	polynucleotide sequences encoding hGDMPLP-1 may be used for diagnosing a
CC	disorder associated with the expression of hGDMPLP-1, in particular heart
CC	and skeletal muscle disorders. hGDMPLP-1 is localised to chromosome 22.
CC	The present sequence represents an oligomer used in the screening of the
CC	hGDMPLP-1 sequence in the exemplification of the present invention. N.B.
CC	The sequence data for this patent did not form part of the printed
CC	specification, but was obtained in electronic format directly from WIPO
CC	at ftp.wipo.int/pub/published_pct_sequence
XX	
SQ	Sequence 17 BP; 6 A; 2 C; 6 G; 3 T; 0 U; 0 Other;
	Query Match 0.8%; Score 13.8; DB 1; Length 17;
	Best Local Similarity 88.2%; Pred. No. 1.9e+02;
	Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY	292 AGGATGCCCTAATAGAG 308
DB	1 AGGATGCACGTATGAG 17
RESULT 307	
ABN09695/C	
ID	ABN09695 standard; DNA; 17 BP.
XX	
AC	ABN09695;
XX	
DT	29-MAY-2002 (first entry)
XX	
DE	Human GDMLP-1 17-mer scanning SEQ ID NO:5 sequence SEQ ID NO:9687.
XX	
KW	Human; genome-derived myosin-like protein 1; GDMLP-1; hGDMPLP-1; heart;
KW	muscle; myosin; chromosome 22; gene therapy; vaccine; heart disease;
KW	skeletal muscle disorder; amplicon; screening; ss.
OS	Homo sapiens.
XX	
PN	WO200192524-A2.
XX	
PD	06-DEC-2001.
XX	
PF	25-MAY-2001; 2001WO-US016981.
XX	
PR	26-MAY-2000; 2000US-0207456P.

PR	21-SEP-2000; 2000US-0234687P.
PR	27-SEP-2000; 2000US-0236359P.
PR	04-OCT-2000; 2000GB-00024263.
PR	30-JAN-2001; 2001WO-US000661.
PR	30-JAN-2001; 2001WO-US000662.
PR	30-JAN-2001; 2001WO-US000663.
PR	30-JAN-2001; 2001WO-US000664.
PR	30-JAN-2001; 2001WO-US000665.
PR	30-JAN-2001; 2001WO-US000666.
PR	30-JAN-2001; 2001WO-US000667.
PR	30-JAN-2001; 2001WO-US000668.
PR	30-JAN-2001; 2001WO-US000669.
PR	05-FEB-2001; 2001US-026866OP.
XX	
PA	(AEOM-) AEOMICA INC.
XX	
PI	Gu Y, Ji Y, Penn SG, Hanzel DK, Rank DR, Chen W, Shannon ME;
XX	
WI	PFI; 2002-179446/23.
XX	
PT	New polypeptide, for raising antibodies that recognize hGDMPLP-1 proteins,
PT	or as specific biomolecule capture probes for surface-enhanced laser
PT	desorption ionization, comprises human myosin-like protein hGDMPLP-1.
XX	
PS	Disclosure; SEQ ID NO 9687; 214pp; English.
XX	
CC	The present invention describes a human genome-derived myosin-like
CC	protein 1 (hGDMPLP-1). The protein and polynucleotide sequences of hGDMPLP-
CC	1 can be used in gene therapy and vaccine production. The hGDMPLP-1
CC	nucleic acids can be used as probes to detect, characterise and quantify
CC	hGDMPLP-1 nucleic acids in samples, as amplification substrates, to
CC	provide initial substrates for the recombinant engineering of hGDMPLP-1
CC	protein variants having desired phenotypic improvements, and for
CC	expressing the proteins. The hGDMPLP-1 proteins or polypeptides may be
CC	used as immunogens to raise antibodies that specifically recognise hGDMPLP
CC	-1 proteins, as standards in assays used to determine the concentration
CC	and/or amount specifically of hGDMPLP proteins, as specific biomolecule
CC	capture probes for surface-enhanced laser desorption/ionisation, as
CC	therapeutic supplement in patients having specific deficiency in hGDMPLP-1
CC	production, and in vaccines or for replacement therapy. The
CC	polynucleotide sequences encoding hGDMPLP-1 may be used for diagnosing a
CC	disorder associated with the expression of hGDMPLP-1, in particular heart
CC	and skeletal muscle disorders. hGDMPLP-1 is localised to chromosome 22.
CC	The present sequence represents an oligomer used in the screening of the
CC	hGDMPLP-1 sequence in the exemplification of the present invention. N.B.
CC	The sequence data for this patent did not form part of the printed
CC	specification, but was obtained in electronic format directly from WIPO
CC	at ftp.wipo.int/pub/published_pct_sequence
XX	
SQ	Sequence 17 BP; 6 A; 2 C; 6 G; 3 T; 0 U; 0 Other;
	Query Match 0.8%; Score 13.8; DB 1; Length 17;
	Best Local Similarity 88.2%; Pred. No. 1.9e+02;
	Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY	292 AGGATGCCCTAATAGAG 308
DB	1 AGGATGCACGTATGAG 17
RESULT 307	
ABN09695/C	
ID	ABN09695 standard; DNA; 17 BP.
XX	
AC	ABN09695;
XX	
DT	29-MAY-2002 (first entry)
XX	
DE	Human GDMLP-1 17-mer scanning SEQ ID NO:5 sequence SEQ ID NO:9687.
XX	
KW	Human; genome-derived myosin-like protein 1; GDMLP-1; hGDMPLP-1; heart;
KW	muscle; myosin; chromosome 22; gene therapy; vaccine; heart disease;
KW	skeletal muscle disorder; amplicon; screening; ss.
OS	Homo sapiens.
XX	
PN	WO200192524-A2.
XX	
PD	06-DEC-2001.
XX	
PF	25-MAY-2001; 2001WO-US

KW skeletal muscle disorder; amplicon; screening; ss.  
XX Homo sapiens.  
XX WO200192524-A2.  
XX 06-DEC-2001.  
XX 25-MAY-2001; 2001WO-US016981.  
XX 26-MAY-2000; 2000US-0207456P.  
PR 21-SEP-2000; 2000US-0234687P.  
PR 27-SEP-2000; 2000US-0236359P.  
PR 04-OCT-2000; 2000GB-00024263.  
PR 30-JAN-2001; 2001WO-US000661.  
PR 30-JAN-2001; 2001WO-US000662.  
PR 30-JAN-2001; 2001WO-US000663.  
PR 30-JAN-2001; 2001WO-US000664.  
PR 30-JAN-2001; 2001WO-US000665.  
PR 30-JAN-2001; 2001WO-US000666.  
PR 30-JAN-2001; 2001WO-US000667.  
PR 30-JAN-2001; 2001WO-US000668.  
PR 30-JAN-2001; 2001WO-US000669.  
PR 05-FEB-2001; 2001WO-US000670.  
XX 05-FEB-2001; 2001US-0266860P.  
XX (AEOM-) AEOMICA INC.  
XX Gu Y, Ji Y, Penn SG, Hanzel DK, Rank DR, Chen W, Shannon MB;  
XX WPI; 2002-179446/23.  
XX New polypeptide, for raising antibodies that recognize hGDMPLP-1 proteins,  
PT or as specific biomolecule capture probes for surface-enhanced laser  
PT desorption ionization, comprises human myosin-like protein hGDMPLP-1.  
XX Disclosure; SEQ ID NO 8663; 214pp; English.  
XX The present invention describes a human genome-derived myosin-like  
CC protein 1 (hGDMPLP-1). The protein and polynucleotide sequences of hGDMPLP-  
CC 1 can be used in gene therapy and vaccine production. The hGDMPLP-1  
CC nucleic acids can be used as probes to detect, characterize and quantify  
CC hGDMPLP-1 nucleic acids in samples, as amplification substrates, to  
CC provide initial substrates for the recombinant engineering of hGDMPLP-1  
CC protein variants having desired phenotypic improvements, and for  
CC expressing the proteins. The hGDMPLP-1 proteins or polypeptides may be  
CC used as immunogens to raise antibodies that specifically recognise hGDMPLP  
CC -1 proteins, as standards in assays used to determine the concentration  
CC and/or amount specifically of hGDMPLP proteins, as specific biomolecule  
CC capture probes for surface-enhanced laser desorption/ionisation, as  
CC therapeutic supplement in patients having specific deficiency in hGDMPLP-1  
CC production, and in vaccines or for replacement therapy. The  
CC polynucleotide sequences encoding hGDMPLP-1 may be used for diagnosing a  
CC disorder associated with the expression of hGDMPLP-1, in particular heart  
CC and skeletal muscle disorders. hGDMPLP-1 is localised to chromosome 22.  
CC The present sequence represents an oligomer used in the screening of the  
CC hGDMPLP-1 sequence in the exemplification of the present invention. N.B.  
CC The sequence data for this patent did not form part of the printed  
CC specification, but was obtained in electronic format directly from WIPO  
CC at ftp.wipo.int/pub/published\_pct\_sequence  
XX Sequence 17 BP; 8 A; 2 C; 7 G; 0 T; 0 U; 0 Other;  
SQ  
Query Match 0.8%; Score 13.8; DB 1; Length 17;  
Best Local Similarity 88.2%; Pred. No. 1.9e+02;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 270 GAAGAACCAAGAA 286  
Db 1 GAGGAAGCCAGAGGA 17  
RESULT 309

ABN09696/c  
ID ABN09696 standard; DNA; 17 BP.  
XX  
XX AC ABN09696;  
XX  
XX DT 29-MAY-2002 (first entry)  
XX  
XX DE Human GDMPLP-1 17-mer scanning SEQ ID NO:5 sequence SEQ ID NO:9688.  
XX  
XX KW Human; genome-derived myosin-like protein 1; GDMPLP-1; heart;  
KW muscle; myosin; chromosome 22; gene therapy; vaccine; heart disease;  
KW skeletal muscle disorder; amplicon; screening; ss.  
XX  
XX OS Homo sapiens.  
XX  
XX PN WO200192524-A2.  
XX  
XX PD 06-DEC-2001.  
XX  
XX PF 25-MAY-2001; 2001WO-US016981.  
XX  
XX PR 26-MAY-2000; 2000US-0207456P.  
PR 21-SEP-2000; 2000US-0234687P.  
PR 27-SEP-2000; 2000US-0236359P.  
PR 04-OCT-2000; 2000GB-00024263.  
PR 30-JAN-2001; 2001WO-US000661.  
PR 30-JAN-2001; 2001WO-US000662.  
PR 30-JAN-2001; 2001WO-US000663.  
PR 30-JAN-2001; 2001WO-US000664.  
PR 30-JAN-2001; 2001WO-US000665.  
PR 30-JAN-2001; 2001WO-US000666.  
PR 30-JAN-2001; 2001WO-US000667.  
PR 30-JAN-2001; 2001WO-US000668.  
PR 30-JAN-2001; 2001WO-US000669.  
PR 30-JAN-2001; 2001WO-US000670.  
XX 05-FEB-2001; 2001US-0266860P.  
XX  
XX PA (AEOM-) AEOMICA INC.  
XX  
XX PI Gu Y, Ji Y, Penn SG, Hanzel DK, Rank DR, Chen W, Shannon MB;  
XX  
XX WPI; 2002-179446/23.  
XX  
XX New polypeptide, for raising antibodies that recognize hGDMPLP-1 proteins,  
PT or as specific biomolecule capture probes for surface-enhanced laser  
PT desorption ionization, comprises human myosin-like protein hGDMPLP-1.  
XX  
XX Disclosure; SEQ ID NO 9688; 214pp; English.  
XX The present invention describes a human genome-derived myosin-like  
CC protein 1 (hGDMPLP-1). The protein and polynucleotide sequences of hGDMPLP-  
CC 1 can be used in gene therapy and vaccine production. The hGDMPLP-1  
CC nucleic acids can be used as probes to detect, characterize and quantify  
CC hGDMPLP-1 nucleic acids in samples, as amplification substrates, to  
CC provide initial substrates for the recombinant engineering of hGDMPLP-1  
CC protein variants having desired phenotypic improvements, and for  
CC expressing the proteins. The hGDMPLP-1 proteins or polypeptides may be  
CC used as immunogens to raise antibodies that specifically recognise hGDMPLP  
CC -1 proteins, as standards in assays used to determine the concentration  
CC and/or amount specifically of hGDMPLP proteins, as specific biomolecule  
CC capture probes for surface-enhanced laser desorption/ionisation, as  
CC therapeutic supplement in patients having specific deficiency in hGDMPLP-1  
CC production, and in vaccines or for replacement therapy. The  
CC polynucleotide sequences encoding hGDMPLP-1 may be used for diagnosing a  
CC disorder associated with the expression of hGDMPLP-1, in particular heart  
CC and skeletal muscle disorders. hGDMPLP-1 is localised to chromosome 22.  
CC The present sequence represents an oligomer used in the screening of the  
CC hGDMPLP-1 sequence in the exemplification of the present invention. N.B.  
CC The sequence data for this patent did not form part of the printed  
CC specification, but was obtained in electronic format directly from WIPO  
CC at ftp.wipo.int/pub/published\_pct\_sequence  
XX  
XX Sequence 17 BP; 2 A; 8 C; 4 G; 3 T; 0 U; 0 Other;  
SQ

Query Match 0.8%; Score 13.8; DB 1; Length 17;  
Best Local Similarity 88.2%; Pred. No. 1.9e+02;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 92 GGAGAGTGGCAGGTC 108  
|||||  
Db 17 GGAGAGTGGCAGGTC 1

RESULT 310  
ABN09697/c  
ID ABN09697 standard; DNA; 17 BP.  
XX  
AC ABN09697;  
XX  
DT 29-MAY-2002 (first entry)  
XX  
DE Human GDMPLP-1 17-mer scanning SEQ ID NO:5 sequence SEQ ID NO:9689.  
XX  
KW Human; genome-derived myosin-like protein 1; GDMPLP-1; hGDMPLP-1; heart;  
KW muscle; myosin; chromosome 22; gene therapy; vaccine; heart disease;  
KW skeletal muscle disorder; amplicon; screening; ss.  
XX  
OS Homo sapiens.  
XX  
FN WO200192524-A2.  
XX  
PD 06-DEC-2001.  
XX  
PF 25-MAY-2001; 2001WO-US016981.  
XX  
PR 26-MAY-2000; 2000US-0207456P.  
PR 21-SEP-2000; 2000US-0234687P.  
PR 27-SEP-2000; 2000US-0236359P.  
PR 04-OCT-2000; 2000GB-00024263.  
PR 30-JAN-2001; 2001WO-US000661.  
PR 30-JAN-2001; 2001WO-US000662.  
PR 30-JAN-2001; 2001WO-US000663.  
PR 30-JAN-2001; 2001WO-US000664.  
PR 30-JAN-2001; 2001WO-US000665.  
PR 30-JAN-2001; 2001WO-US000666.  
PR 30-JAN-2001; 2001WO-US000667.  
PR 30-JAN-2001; 2001WO-US000668.  
PR 30-JAN-2001; 2001WO-US000669.  
PR 05-FEB-2001; 2001WO-US000670.  
XX  
PA (AEOM-) AEOMICA INC.  
XX  
PI Gu Y, Ji Y, Penn SG, Hanzel DK, Rank DR, Chen W, Shannon ME;  
XX  
DR WPI; 2002-179446/23.  
XX  
PT New polypeptide, for raising antibodies that recognize hGDMPLP-1 proteins,  
PT or as specific biomolecule capture probes for surface-enhanced laser  
PT desorption ionization, comprises human myosin-like protein hGDMPLP-1.  
XX  
PS Disclosure; SEQ ID NO 9689; 214pp; English.  
XX  
CC The present invention describes a human genome-derived myosin-like  
CC protein 1 (hGDMPLP-1). The protein and polynucleotide sequences of hGDMPLP-  
CC 1 can be used in gene therapy and vaccine production. The hGDMPLP-1  
CC nucleic acids can be used as probes to detect, characterise and quantify  
CC hGDMPLP-1 nucleic acids in samples, as amplification substrates, to  
CC provide initial substrates for the recombinant engineering of hGDMPLP-1  
CC protein variants having desired phenotypic improvements, and for  
CC expressing the proteins. The hGDMPLP-1 proteins or polypeptides may be  
CC used as immunogens to raise antibodies that specifically recognise hGDMPLP  
CC -1 proteins, as standards in assays used to determine the concentration  
CC and/or amount specifically of hGDMPLP proteins, as specific biomolecule  
CC capture probes for surface-enhanced laser desorption ionisation, as  
CC therapeutic supplement in patients having specific deficiency in hGDMPLP-1

CC production, and in vaccines or for replacement therapy. The  
CC polynucleotide sequences encoding hGDMPLP-1 may be used for diagnosing a  
CC disorder associated with the expression of hGDMPLP-1, in particular heart  
CC and skeletal muscle disorders. hGDMPLP-1 is localised to chromosome 22.  
CC The present sequence represents an oligomer used in the screening of the  
CC hGDMPLP-1 sequence in the exemplification of the present invention. N.B.  
CC The sequence data for this patent did not form part of the printed  
CC specification, but was obtained in electronic format directly from WIPO  
CC at ftp.wipo.int/pub/published\_pct\_sequence

XX  
SQ Sequence 17 BP; 2 A; 9 C; 3 G; 3 T; 0 U; 0 Other;  
XX  
Query Match 0.8%; Score 13.8; DB 1; Length 17;  
Best Local Similarity 88.2%; Pred. No. 1.9e+02;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 91 GGAGAGTGGCAGGTC 107  
|||||  
Db 17 GGAGAGTGGCAGGTC 1

RESULT 311  
ABN07363  
ID ABN07363 standard; DNA; 17 BP.  
XX  
AC ABN07363;  
XX  
DT 29-MAY-2002 (first entry)  
XX  
DE Human GDMPLP-1 17-mer scanning SEQ ID NO:5 sequence SEQ ID NO:7355.  
XX  
KW Human; genome-derived myosin-like protein 1; GDMPLP-1; hGDMPLP-1; heart;  
KW muscle; myosin; chromosome 22; gene therapy; vaccine; heart disease;  
KW skeletal muscle disorder; amplicon; screening; ss.  
XX  
OS Homo sapiens.  
XX  
FN WO200192524-A2.  
XX  
PD 06-DEC-2001.  
XX  
PF 25-MAY-2001; 2001WO-US016981.  
XX  
PR 26-MAY-2000; 2000US-0207456P.  
PR 21-SEP-2000; 2000US-0234687P.  
PR 27-SEP-2000; 2000US-0236359P.  
PR 04-OCT-2000; 2000GB-00024263.  
PR 30-JAN-2001; 2001WO-US000661.  
PR 30-JAN-2001; 2001WO-US000662.  
PR 30-JAN-2001; 2001WO-US000663.  
PR 30-JAN-2001; 2001WO-US000664.  
PR 30-JAN-2001; 2001WO-US000665.  
PR 30-JAN-2001; 2001WO-US000666.  
PR 30-JAN-2001; 2001WO-US000667.  
PR 30-JAN-2001; 2001WO-US000668.  
PR 30-JAN-2001; 2001WO-US000669.  
PR 05-FEB-2001; 2001WO-US000670.  
XX  
PA (AEOM-) AEOMICA INC.  
XX  
PI Gu Y, Ji Y, Penn SG, Hanzel DK, Rank DR, Chen W, Shannon ME;  
XX  
DR WPI; 2002-179446/23.  
XX  
PT New polypeptide, for raising antibodies that recognize hGDMPLP-1 proteins,  
PT or as specific biomolecule capture probes for surface-enhanced laser  
PT desorption ionization, comprises human myosin-like protein hGDMPLP-1.  
XX  
PS Disclosure; SEQ ID NO 7355; 214pp; English.  
XX  
CC The present invention describes a human genome-derived myosin-like  
CC protein 1 (hGDMPLP-1). The protein and polynucleotide sequences of hGDMPLP-1



CC 1 can be used in gene therapy and vaccine production. The hGDMPLP-1  
CC nucleic acids can be used as probes to detect, characterise and quantify  
CC hGDMPLP-1 nucleic acids in samples, as amplification substrates, to  
CC provide initial substrates for the recombinant engineering of hGDMPLP-1  
CC protein variants having desired phenotypic improvements, and for  
CC expressing the proteins. The hGDMPLP-1 proteins or polypeptides may be  
CC used as immunogens to raise antibodies that specifically recognise hGDMPLP  
CC -1 proteins, as standards in assays used to determine the concentration  
CC and/or amount specifically of hGDMPLP proteins, as specific biomolecule  
CC capture probes for surface-enhanced laser desorption/ionisation, as  
CC therapeutic supplement in patients having specific deficiency in hGDMPLP-1  
CC production, and in vaccines or for replacement therapy. The  
CC polynucleotide sequences encoding hGDMPLP-1 may be used for diagnosing a  
CC disorder associated with the expression of hGDMPLP-1, in particular heart  
CC and skeletal muscle disorders. hGDMPLP-1 is localised to chromosome 22.  
CC The present sequence represents an oligomer used in the screening of the  
CC hGDMPLP-1 sequence in the exemplification of the present invention. N.B.  
CC The sequence data for this patent did not form part of the printed  
CC specification, but was obtained in electronic format directly from WIPO  
CC at ftp.wipo.int/pub/published\_pct\_sequence  
XX SQ Sequence 17 BP; 8 A; 4 C; 5 G; 0 T; 0 U; 0 Other;

Query Match 0.8%; Score 13.8; DB 1; Length 17;  
Best Local Similarity 88.2%; Pred. No. 1.9e+02;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 270 GAAGAAGCCCAAGAGAA 286  
|||||||  
DB 1 GAAGAAGCCCAAGAGAA 17

RESULT 312  
ABN08672  
ID ABN08672 standard; DNA; 17 BP.  
XX AC ABN08672;  
XX 29-MAY-2002 (first entry)  
XX Human GDMPLP-1 17-mer scanning SEQ ID NO:5 sequence SEQ ID NO:8664.  
XX Human; genome-derived myosin-like protein 1; GDMPLP-1; hGDMPLP-1; heart;  
KW muscle; myosin; chromosome 22; gene therapy; vaccine; heart disease;  
KW skeletal muscle disorder; amplicon; screening; ss.  
XX Homo sapiens.  
XX WO200192524-A2.  
XX 06-DEC-2001.  
XX 25-MAY-2001; 2001WO-US016981.  
XX 26-MAY-2000; 2000US-0207456P.  
PR 21-SEP-2000; 2000US-0234687P.  
PR 27-SEP-2000; 2000US-0236359P.  
PR 04-OCT-2000; 2000GB-00024263.  
PR 30-JAN-2001; 2001WO-US000661.  
PR 30-JAN-2001; 2001WO-US000662.  
PR 30-JAN-2001; 2001WO-US000663.  
PR 30-JAN-2001; 2001WO-US000664.  
PR 30-JAN-2001; 2001WO-US000665.  
PR 30-JAN-2001; 2001WO-US000666.  
PR 30-JAN-2001; 2001WO-US000667.  
PR 30-JAN-2001; 2001WO-US000668.  
PR 30-JAN-2001; 2001WO-US000669.  
PR 30-JAN-2001; 2001WO-US000670.  
PR 05-FEB-2001; 2001US-0266860P.  
XX (AEOM-) AEOMICA INC.  
XX Gu Y, Ji Y, Penn SG, Hanzel DK, Rank DR, Chen W, Shannon ME;  
PI

XX WPI; 2002-179446/23.  
XX New polypeptide, for raising antibodies that recognize hGDMPLP-1 proteins,  
PT or as specific biomolecule capture probes for surface-enhanced laser  
PT desorption/ionization, comprises human myosin-like protein hGDMPLP-1.  
XX Disclosure; SEQ ID NO 8664; 214pp; English.  
XX The present invention describes a human genome-derived myosin-like  
CC protein 1 (hGDMPLP-1). The protein and polynucleotide sequences of hGDMPLP-  
CC 1 can be used in gene therapy and vaccine production. The hGDMPLP-1  
CC nucleic acids can be used as probes to detect, characterise and quantify  
CC hGDMPLP-1 nucleic acids in samples, as amplification substrates, to  
CC provide initial substrates for the recombinant engineering of hGDMPLP-1  
CC protein variants having desired phenotypic improvements, and for  
CC expressing the proteins. The hGDMPLP-1 proteins or polypeptides may be  
CC used as immunogens to raise antibodies that specifically recognise hGDMPLP  
CC -1 proteins, as standards in assays used to determine the concentration  
CC and/or amount specifically of hGDMPLP proteins, as specific biomolecule  
CC capture probes for surface-enhanced laser desorption/ionisation, as  
CC therapeutic supplement in patients having specific deficiency in hGDMPLP-1  
CC production, and in vaccines or for replacement therapy. The  
CC polynucleotide sequences encoding hGDMPLP-1 may be used for diagnosing a  
CC disorder associated with the expression of hGDMPLP-1, in particular heart  
CC and skeletal muscle disorders. hGDMPLP-1 is localised to chromosome 22.  
CC The present sequence represents an oligomer used in the screening of the  
CC hGDMPLP-1 sequence in the exemplification of the present invention. N.B.  
CC The sequence data for this patent did not form part of the printed  
CC specification, but was obtained in electronic format directly from WIPO  
CC at ftp.wipo.int/pub/published\_pct\_sequence  
XX SQ Sequence 17 BP; 8 A; 2 C; 7 G; 0 T; 0 U; 0 Other;

Query Match 0.8%; Score 13.8; DB 1; Length 17;  
Best Local Similarity 88.2%; Pred. No. 1.9e+02;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 271 AAGAAGCCCAAGAGAA 287  
|||||||  
DB 1 AGGAAGCCCAAGAGAG 17

RESULT 313  
ABN08669  
ID ABN08669 standard; DNA; 17 BP.  
XX AC ABN08669;  
XX 29-MAY-2002 (first entry)  
XX Human GDMPLP-1 17-mer scanning SEQ ID NO:5 sequence SEQ ID NO:8661.  
XX Human; genome-derived myosin-like protein 1; GDMPLP-1; hGDMPLP-1; heart;  
KW muscle; myosin; chromosome 22; gene therapy; vaccine; heart disease;  
KW skeletal muscle disorder; amplicon; screening; ss.  
XX Homo sapiens.  
XX WO200192524-A2.  
XX 06-DEC-2001.  
XX 25-MAY-2001; 2001WO-US016981.  
XX 26-MAY-2000; 2000US-0207456P.  
PR 21-SEP-2000; 2000US-0234687P.  
PR 27-SEP-2000; 2000US-0236359P.  
PR 04-OCT-2000; 2000GB-00024263.  
PR 30-JAN-2001; 2001WO-US000661.  
PR 30-JAN-2001; 2001WO-US000662.  
PR 30-JAN-2001; 2001WO-US000663.  
PR 30-JAN-2001; 2001WO-US000664.

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PR 30-JAN-2001; 2001WO-US000665.
PR 30-JAN-2001; 2001WO-US000666.
PR 30-JAN-2001; 2001WO-US000667.
PR 30-JAN-2001; 2001WO-US000668.
PR 30-JAN-2001; 2001WO-US000669.
PR 30-JAN-2001; 2001WO-US000670.
PR 05-FEB-2001; 2001US-026860P.
XX
XX (AEOM-) AEOMICA INC.
XX
XX Gu Y, Ji Y, Penn SG, Hanzel DK, Rank DR, Chen W, Shannon ME;
XX WPI; 2002-179446/23.
XX
XX New polypeptide, for raising antibodies that recognize hGDMPLP-1 proteins,
XX or as specific biomolecule capture probes for surface-enhanced laser
XX desorption ionization, comprises human myosin-like protein hGDMPLP-1.
XX
XX Disclosure; SEQ ID NO 8661; 214pp; English.
XX
XX The present invention describes a human genome-derived myosin-like
XX protein 1 (hGDMPLP-1). The protein and polynucleotide sequences of hGDMPLP-
XX 1 can be used in gene therapy and vaccine production. The hGDMPLP-1
XX nucleic acids can be used as probes to detect, characterise and quantify
XX hGDMPLP-1 nucleic acids in samples, as amplification substrates, to
XX provide initial substrates for the recombinant engineering of hGDMPLP-1
XX protein variants having desired phenotypic improvements, and for
XX expressing the proteins. The hGDMPLP-1 proteins or polypeptides may be
XX used as immunogens to raise antibodies that specifically recognise hGDMPLP
XX -1 proteins, as standards in assays used to determine the concentration
XX and/or amount specifically of hGDMPLP proteins, as specific biomolecule
XX capture probes for surface-enhanced laser desorption ionisation, as
XX therapeutic supplement in patients having specific deficiency in hGDMPLP-1
XX production, and in vaccines or for replacement therapy. The
XX polynucleotide sequences encoding hGDMPLP-1 may be used for diagnosing a
XX disorder associated with the expression of hGDMPLP-1, in particular heart
XX and skeletal muscle disorders. hGDMPLP-1 is localised to chromosome 22.
XX The present sequence represents an oligomer used in the screening of the
XX hGDMPLP-1 sequence in the exemplification of the present invention. N.B.
XX The sequence data for this patent did not form part of the printed
XX specification, but was obtained in electronic format directly from WIPO
XX at ftp.wipo.int/pub/published_pct_sequence
XX
XX Sequence 17 BP; 7 A; 2 C; 7 G; 1 T; 0 U; 0 Other;
XX
XX Query Match 0.8%; Score 13.8; DB 1; Length 17;
XX Best Local Similarity 88.2%; Pred. No. 1.9e+02;
XX Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX QY 268 TAGAAGAAGCCCAAGAG 284
XX |||||
XX 1 TGGAGGAAGCCCAAGAG 17
XX
XX RESULT 314
XX ABN02651/c
XX ID ABN02651 standard; DNA; 17 BP.
XX AC ABN02651;
XX
XX 29-MAY-2002 (first entry)
XX
XX Human GDMPLP-1 17-mer scanning SEQ ID NO:4 sequence SEQ ID NO:2643.
XX
XX Human; genome-derived myosin-like protein 1; GDMPLP-1; hGDMPLP-1; heart;
XX muscle; myosin; chromosome 22; gene therapy; vaccine; heart disease;
XX skeletal muscle disorder; amplicon; screening; ss.
XX
XX Homo sapiens.
XX
XX WO200192524-A2.
XX
XX 06-DEC-2001.
XX
XX 25-MAY-2001; 2001WO-US016981.
XX
XX 26-MAY-2000; 2000US-0207456P.
XX
XX 21-SEP-2000; 2000US-0234687P.
XX
XX 27-SEP-2000; 2000US-0236359P.
XX
XX 04-OCT-2000; 2000GB-00024263.
XX
XX 30-JAN-2001; 2001WO-US000661.
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XX 30-JAN-2001; 2001WO-US000662.
XX
XX 30-JAN-2001; 2001WO-US000663.
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XX 30-JAN-2001; 2001WO-US000664.
XX
XX 30-JAN-2001; 2001WO-US000665.
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XX 30-JAN-2001; 2001WO-US000666.
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XX 30-JAN-2001; 2001WO-US000667.
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XX 30-JAN-2001; 2001WO-US000668.
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XX 30-JAN-2001; 2001WO-US000669.
XX
XX 30-JAN-2001; 2001WO-US000670.
XX
XX 05-FEB-2001; 2001US-026860P.
XX
XX (AEOM-) AEOMICA INC.
XX
XX Gu Y, Ji Y, Penn SG, Hanzel DK, Rank DR, Chen W, Shannon ME;
XX WPI; 2002-179446/23.
XX
XX New polypeptide, for raising antibodies that recognize hGDMPLP-1 proteins,
XX or as specific biomolecule capture probes for surface-enhanced laser
XX desorption ionization, comprises human myosin-like protein hGDMPLP-1.
XX
XX Disclosure; SEQ ID NO 2643; 214pp; English.
XX
XX The present invention describes a human genome-derived myosin-like
XX protein 1 (hGDMPLP-1). The protein and polynucleotide sequences of hGDMPLP-
XX 1 can be used in gene therapy and vaccine production. The hGDMPLP-1
XX nucleic acids can be used as probes to detect, characterise and quantify
XX hGDMPLP-1 nucleic acids in samples, as amplification substrates, to
XX provide initial substrates for the recombinant engineering of hGDMPLP-1
XX protein variants having desired phenotypic improvements, and for
XX expressing the proteins. The hGDMPLP-1 proteins or polypeptides may be
XX used as immunogens to raise antibodies that specifically recognise hGDMPLP
XX -1 proteins, as standards in assays used to determine the concentration
XX and/or amount specifically of hGDMPLP proteins, as specific biomolecule
XX capture probes for surface-enhanced laser desorption ionisation, as
XX therapeutic supplement in patients having specific deficiency in hGDMPLP-1
XX production, and in vaccines or for replacement therapy. The
XX polynucleotide sequences encoding hGDMPLP-1 may be used for diagnosing a
XX disorder associated with the expression of hGDMPLP-1, in particular heart
XX and skeletal muscle disorders. hGDMPLP-1 is localised to chromosome 22.
XX The present sequence represents an oligomer used in the screening of the
XX hGDMPLP-1 sequence in the exemplification of the present invention. N.B.
XX The sequence data for this patent did not form part of the printed
XX specification, but was obtained in electronic format directly from WIPO
XX at ftp.wipo.int/pub/published_pct_sequence
XX
XX Sequence 17 BP; 1 A; 4 C; 8 G; 4 T; 0 U; 0 Other;
XX
XX Query Match 0.8%; Score 13.8; DB 1; Length 17;
XX Best Local Similarity 88.2%; Pred. No. 1.9e+02;
XX Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX QY 845 CTTCCAGACCCGCCCAA 861
XX |||||
XX 17 CTGCCAGACCCGCCCAA 1
XX
XX RESULT 315
XX ABN08668
XX ID ABN08668 standard; DNA; 17 BP.
XX
XX AC ABN08668;
XX
XX 29-MAY-2002 (first entry)
XX
XX

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DE Human GDMPLP-1 17-mer scanning SEQ ID NO:5 sequence SEQ ID NO:8660.  
XX Human; genome-derived myosin-like protein 1; GDMPLP-1; hGDMPLP-1; heart;  
KW muscle; myosin; chromosome 22; gene therapy; vaccine; heart disease;  
KW skeletal muscle disorder; amplicon; screening; ss.  
XX Homo sapiens.  
XX WO200192524-A2.  
XX 06-DEC-2001.  
XX 25-MAY-2001; 2001WO-US016981.  
XX 26-MAY-2000; 2000US-0207456P.  
PR 21-SEP-2000; 2000US-0234687P.  
PR 27-SEP-2000; 2000US-0236359P.  
PR 04-OCT-2000; 2000GB-00024263.  
PR 30-JAN-2001; 2001WO-US000661.  
PR 30-JAN-2001; 2001WO-US000662.  
PR 30-JAN-2001; 2001WO-US000663.  
PR 30-JAN-2001; 2001WO-US000664.  
PR 30-JAN-2001; 2001WO-US000665.  
PR 30-JAN-2001; 2001WO-US000666.  
PR 30-JAN-2001; 2001WO-US000667.  
PR 30-JAN-2001; 2001WO-US000668.  
PR 30-JAN-2001; 2001WO-US000669.  
PR 30-JAN-2001; 2001WO-US000670.  
PR 05-FEB-2001; 2001US-0266860P.  
XX (AEOM-) AEOMICA INC.  
XX Gu Y, Ji Y, Penn SG, Hanzel DK, Rank DR, Chen W, Shannon ME;  
XX WPI; 2002-179446/23.  
XX New polypeptide, for raising antibodies that recognize hGDMPLP-1 proteins,  
PT or as specific biomolecule capture probes for surface-enhanced laser  
PT desorption ionization, comprises human myosin-like protein hGDMPLP-1.  
XX Disclosure; SEQ ID NO 8660; 214pp; English.  
XX The present invention describes a human genome-derived myosin-like  
CC protein 1 (hGDMPLP-1). The protein and polynucleotide sequences of hGDMPLP-  
CC 1 can be used in gene therapy and vaccine production. The hGDMPLP-1  
CC nucleic acids can be used as probes to detect, characterize and quantify  
CC hGDMPLP-1 nucleic acids in samples, as amplification substrates, to  
CC provide initial substrates for the recombinant engineering of hGDMPLP-1  
CC protein variants having desired phenotypic improvements, and for  
CC expressing the proteins. The hGDMPLP-1 proteins or polypeptides may be  
CC used as immunogens to raise antibodies that specifically recognise hGDMPLP  
CC -1 proteins, as standards in assays used to determine the concentration  
CC and/or amount specifically of hGDMPLP proteins, as specific biomolecule  
CC capture probes for surface-enhanced laser desorption/ionisation, as  
CC therapeutic supplement in patients having specific deficiency in hGDMPLP-1  
CC production, and in vaccines or for replacement therapy. The  
CC polynucleotide sequences encoding hGDMPLP-1 may be used for diagnosing a  
CC disorder associated with the expression of hGDMPLP-1, in particular heart  
CC and skeletal muscle disorders. hGDMPLP-1 is localised to chromosome 22.  
CC The present sequence represents an oligomer used in the screening of the  
CC hGDMPLP-1 sequence in the exemplification of the present invention. N.B.  
CC The sequence data for this patent did not form part of the printed  
CC specification, but was obtained in electronic format directly from WIPO  
CC at ftp.wipo.int/pub/published\_pct\_sequence  
XX Sequence 17 BP; 7 A; 3 C; 6 G; 1 T; 0 U; 0 Other;  
SQ Query Match 0.8%; Score 13.8; DB 1; Length 17;  
Best Local Similarity 88.2%; Pred. No. 1.9e+02;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

267 CTGAGAGAGCAAGAA 283  
||| |||||

Db 1 CTGAGAGAGCAAGAA 17  
RESULT 316  
ABQ63736  
ID ABQ63736 standard; DNA; 17 BP.  
XX  
XX AC ABQ63736;  
XX 20-AUG-2002 (first entry)  
XX Human KTOM1a portion (ABQ63232) probe # 449.  
XX Human; KTOM1a; KTOM1; kidney tumor overexpressed membrane; cytosstatic;  
KW gene therapy; cancer; kidney; liver; bone marrow; brain; heart; lung;  
KW kidney; colon; skeletal muscle; testis; uterus; placenta; probe; ss.  
OS Homo sapiens.  
XX WO200224750-A2.  
XX 28-MAR-2002.  
XX 21-SEP-2001; 2001WO-US029656.  
XX 21-SEP-2000; 2000US-0234687P.  
PR 27-SEP-2000; 2000US-0236359P.  
PR 04-OCT-2000; 2000GB-00024263.  
PR 30-JAN-2001; 2001WO-US000661.  
PR 30-JAN-2001; 2001WO-US000662.  
PR 30-JAN-2001; 2001WO-US000663.  
PR 30-JAN-2001; 2001WO-US000664.  
PR 30-JAN-2001; 2001WO-US000665.  
PR 30-JAN-2001; 2001WO-US000666.  
PR 30-JAN-2001; 2001WO-US000667.  
PR 30-JAN-2001; 2001WO-US000668.  
PR 30-JAN-2001; 2001WO-US000669.  
PR 30-JAN-2001; 2001WO-US000670.  
PR 23-MAY-2001; 2001US-00864761.  
PR 28-AUG-2001; 2001US-0315676P.  
XX (AEOM-) AEOMICA INC.  
XX Zhang J;  
XX WPI; 2002-479509/51.  
XX New human kidney tumor overexpressed membrane (KTOM1) protein and nucleic  
PT acids encoding the protein, useful for treating subjects having defects  
PT in KTOM1 which can manifest as cancer of the kidney, or as a disorder of  
PT e.g., liver or bone.  
XX Example 2; Page 216; 418pp; English.  
XX The invention relates to a novel isolated nucleic acid encoding human  
CC KTOM1 (kidney tumor overexpressed membrane) protein. The protein of the  
CC invention has cytostatic activity. The nucleotide may have a use in gene  
CC therapy. The KTOM1 nucleic acids may be used to diagnose, treat or  
CC monitor a disease caused by altered expression of human KTOM1.  
CC Compositions comprising the nucleic acids, proteins or antibodies may be  
CC used to treat subjects having defects in KTOM1 which can manifest as  
CC cancer of the kidney, as well as a disorder of liver, bone marrow, brain,  
CC heart, lung, kidney, colon, skeletal muscle, testis, uterus and placenta  
CC function. The sequence represents a probe used in the invention to scan  
CC the nt 1-1001 portion of human KTOM1a (ABQ63232)  
XX Sequence 17 BP; 4 A; 6 C; 4 G; 3 T; 0 U; 0 Other;  
SQ Query Match 0.8%; Score 13.8; DB 1; Length 17;  
Best Local Similarity 88.2%; Pred. No. 1.9e+02;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

524 CGACTCCCTGCTGGAGA 540



```
QY      520 GCATCGACTCCCTGCTGG 536
      ||||| ||||| |||||
Db      1 GCATCTACTCCCAGCTG 17

RESULT 319
ABQ63733
ID ABQ63733 standard; DNA; 17 BP.
XX
AC ABQ63733;
XX
DT 20-AUG-2002 (first entry)
XX
DE Human KTOM1a portion (ABQ63232) probe # 446.
XX
KW Human; KTOM1a; KTOM1; kidney tumour overexpressed membrane; cytostatic;
KW gene therapy; cancer; kidney; liver; bone marrow; brain; heart; lung;
KW kidney; colon; skeletal muscle; testis; uterus; placenta; probe; ss.
XX
OS Homo sapiens.
XX
PN WO200224750-A2.
XX
PD 28-MAR-2002.
XX
PF 21-SEP-2001; 2001WO-US029656.
XX
PR 21-SEP-2000; 2000US-0234687P.
XX
PR 27-SEP-2000; 2000US-0236359P.
XX
PR 04-OCT-2000; 2000GB-00024263.
XX
PR 30-JAN-2001; 2001WO-US000661.
XX
PR 30-JAN-2001; 2001WO-US000662.
XX
PR 30-JAN-2001; 2001WO-US000663.
XX
PR 30-JAN-2001; 2001WO-US000664.
XX
PR 30-JAN-2001; 2001WO-US000665.
XX
PR 30-JAN-2001; 2001WO-US000666.
XX
PR 30-JAN-2001; 2001WO-US000667.
XX
PR 30-JAN-2001; 2001WO-US000668.
XX
PR 30-JAN-2001; 2001WO-US000669.
XX
PR 30-JAN-2001; 2001WO-US000670.
XX
PR 23-MAY-2001; 2001US-00864761.
XX
PR 28-AUG-2001; 2001US-0315676P.
XX
PA (AEOM-) AEOMICA INC.
XX
PI Zhang J;
XX
WPI; 2002-479509/51.
XX
New human kidney tumor overexpressed membrane (KTOM1) protein and nucleic
PT acids encoding the protein, useful for treating subjects having defects
PT in KTOM1 which can manifest as cancer of the kidney, or as a disorder of
PT e.g., liver or bone.
XX
Example 2; Page 216; 418pp; English.
XX
PS The invention relates to a novel isolated nucleic acid encoding human
XX KTOM1 (kidney tumour overexpressed membrane) protein. The protein of the
CC invention has cytostatic activity. The nucleotide may have a use in gene
CC therapy. The KTOM1 nucleic acids may be used to diagnose, treat or
CC monitor a disease caused by altered expression of human KTOM1.
CC Compositions comprising the nucleic acids, proteins or antibodies may be
CC used to treat subjects having defects in KTOM1 which can manifest as
CC cancer of the kidney, as well as a disorder of liver, bone marrow, brain,
CC heart, lung, kidney, colon, skeletal muscle, testis, uterus and placenta
CC function. The sequence represents a probe used in the invention to scan
CC the nt 1-1001 portion of human KTOM1a (ABQ63232)
XX
SQ Sequence 17 BP; 3 A; 7 C; 3 G; 4 T; 0 U; 0 Other;
Query Match 0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.9e+02;
```

```
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY      521 CATCGACTCCCTGCTGG 537
      ||||| ||||| |||||
Db      1 CATCTACTCCCAGCTGG 17

RESULT 320
ABQ63735
ID ABQ63735 standard; DNA; 17 BP.
XX
AC ABQ63735;
XX
DT 20-AUG-2002 (first entry)
XX
DE Human KTOM1a portion (ABQ63232) probe # 448.
XX
KW Human; KTOM1a; KTOM1; kidney tumour overexpressed membrane; cytostatic;
KW gene therapy; cancer; kidney; liver; bone marrow; brain; heart; lung;
KW kidney; colon; skeletal muscle; testis; uterus; placenta; probe; ss.
XX
OS Homo sapiens.
XX
PN WO200224750-A2.
XX
PD 28-MAR-2002.
XX
PF 21-SEP-2001; 2001WO-US029656.
XX
PR 21-SEP-2000; 2000US-0234687P.
XX
PR 27-SEP-2000; 2000US-0236359P.
XX
PR 04-OCT-2000; 2000GB-00024263.
XX
PR 30-JAN-2001; 2001WO-US000661.
XX
PR 30-JAN-2001; 2001WO-US000662.
XX
PR 30-JAN-2001; 2001WO-US000663.
XX
PR 30-JAN-2001; 2001WO-US000664.
XX
PR 30-JAN-2001; 2001WO-US000665.
XX
PR 30-JAN-2001; 2001WO-US000666.
XX
PR 30-JAN-2001; 2001WO-US000667.
XX
PR 30-JAN-2001; 2001WO-US000668.
XX
PR 30-JAN-2001; 2001WO-US000669.
XX
PR 30-JAN-2001; 2001WO-US000670.
XX
PR 23-MAY-2001; 2001US-00864761.
XX
PR 28-AUG-2001; 2001US-0315676P.
XX
PA (AEOM-) AEOMICA INC.
XX
PI Zhang J;
XX
WPI; 2002-479509/51.
XX
New human kidney tumor overexpressed membrane (KTOM1) protein and nucleic
PT acids encoding the protein, useful for treating subjects having defects
PT in KTOM1 which can manifest as cancer of the kidney, or as a disorder of
PT e.g., liver or bone.
XX
Example 2; Page 216; 418pp; English.
XX
PS The invention relates to a novel isolated nucleic acid encoding human
XX KTOM1 (kidney tumour overexpressed membrane) protein. The protein of the
CC invention has cytostatic activity. The nucleotide may have a use in gene
CC therapy. The KTOM1 nucleic acids may be used to diagnose, treat or
CC monitor a disease caused by altered expression of human KTOM1.
CC Compositions comprising the nucleic acids, proteins or antibodies may be
CC used to treat subjects having defects in KTOM1 which can manifest as
CC cancer of the kidney, as well as a disorder of liver, bone marrow, brain,
CC heart, lung, kidney, colon, skeletal muscle, testis, uterus and placenta
CC function. The sequence represents a probe used in the invention to scan
CC the nt 1-1001 portion of human KTOM1a (ABQ63232)
XX
SQ Sequence 17 BP; 3 A; 6 C; 4 G; 4 T; 0 U; 0 Other;
Query Match 0.8%; Score 13.8; DB 1; Length 17;
```

```

Best Local Similarity 88.2%; Pred. No. 1.9e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 523 TCGACTCCCTGCTGGAG 539
Db 1 TCTACTCCAGCTGGAG 17

Query Match 0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.9e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 526 ACTCCCTGCTGGAGAAC 542
Db 1 ACTCCAGCTGGAGACC 17

RESULT 322
ABQ64165
ID ABQ64165 standard; DNA; 17 BP.
XX
AC ABQ64165;
XX
DT 20-AUG-2002 (first entry)
XX
DE Human KTOM1a portion (ABQ63232) probe # 878.
XX
KW Human; KTOM1a; KTOM1; kidney tumour overexpressed membrane; cytostatic;
KW gene therapy; cancer; kidney; liver; bone marrow; brain; heart; lung;
KW kidney; colon; skeletal muscle; testis; uterus; placenta; probe; ss.
XX
OS Homo sapiens.
XX
PN WO200224750-A2.
XX
PD 28-MAR-2002.
XX
PF 21-SEP-2001; 2001WO-US029656.
XX
PR 21-SEP-2000; 2000US-0234687P.
PR 27-SEP-2000; 2000US-0236359P.
PR 04-OCT-2000; 2000GB-00024263.
PR 30-JAN-2001; 2001WO-US000661.
PR 30-JAN-2001; 2001WO-US000662.
PR 30-JAN-2001; 2001WO-US000663.
PR 30-JAN-2001; 2001WO-US000664.
PR 30-JAN-2001; 2001WO-US000665.
PR 30-JAN-2001; 2001WO-US000666.
PR 30-JAN-2001; 2001WO-US000667.
PR 30-JAN-2001; 2001WO-US000668.
PR 30-JAN-2001; 2001WO-US000669.
PR 30-JAN-2001; 2001WO-US000670.
PR 23-MAY-2001; 2001US-00864761.
PR 28-AUG-2001; 2001US-0315676P.
XX
PA (ABOM-) AEOMICA INC.
XX
PI Zhang J;
XX
PI WPI; 2002-479509/51.
XX
DR New human kidney tumor overexpressed membrane (KTOM1) protein and nucleic
PT acids encoding the protein, useful for treating subjects having defects
PT in KTOM1 which can manifest as cancer of the kidney, or as a disorder of
PT e.g., liver or bone.
XX
PS Example 2; Page 216; 418pp; English.
XX
CC The invention relates to a novel isolated nucleic acid encoding human
CC KTOM1 (kidney tumour overexpressed membrane) protein. The protein of the
CC invention has cytostatic activity. The nucleotide may have a use in gene
CC therapy. The KTOM1 nucleic acids may be used to diagnose, treat or
CC monitor a disease caused by altered expression of human KTOM1.
CC Compositions comprising the nucleic acids, proteins or antibodies may be
CC used to treat subjects having defects in KTOM1 which can manifest as
CC cancer of the kidney, as well as a disorder of liver, bone marrow, brain,
CC heart, lung, kidney, colon, skeletal muscle, testis, uterus and placenta
CC function. The sequence represents a probe used in the invention to scan
CC the nt 1-1001 portion of human KTOM1a (ABQ63232)
XX
SQ Sequence 17 BP; 4 A; 7 C; 4 G; 2 T; 0 U; 0 Other;
```

```
Query Match      0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.9e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1203 GTCACACCGTGGCTTC 1219
    ||||| |||||
Db 1 GTCACCACTGTGGCTGC 17

RESULT 323
ABV79503
ID ABV79503 standard; DNA; 17 BP.
AC ABV79503;
XX
DT 03-JAN-2003 (first entry)
XX
DE Human HTPL scanning oligonucleotide SEQ ID 749.
XX
KW Human; gene therapy; tumour suppressor; HTPL; chromosome 10p12.1;
KW human testis expressed Patched like protein; testis; adrenal; liver;
KW male germ cell development; bone marrow; brain; kidney; lung; placenta;
KW prostate; skeletal muscle; colon; male infertility; cancer; ss.
XX
OS Homo sapiens.
XX
PN EP1229046-A2.
XX
PD 07-AUG-2002.
XX
PF 28-JAN-2002; 2002EP-00001167.
XX
PR 30-JAN-2001; 2001WO-US000663.
PR 30-JAN-2001; 2001WO-US000664.
PR 30-JAN-2001; 2001WO-US000665.
PR 30-JAN-2001; 2001WO-US000667.
PR 30-JAN-2001; 2001WO-US000668.
PR 30-JAN-2001; 2001WO-US000669.
PR 23-MAY-2001; 2001US-00864761.
PR 09-OCT-2001; 2001US-0327898P.
XX
PA (AEOM-) AEOMICA INC.
XX
PI Zhan J;
XX
WPI; 2002-676582/73.

Novel isolated human testis expressed Patched like protein (HTPL), useful
for identifying agonist and antagonist and specific binding partners, and
for treating subjects having defects in HTPL.

Example 2; Page 162; 718pp; English.

The present invention relates to human testis expressed Patched like
protein (HTPL, see ABV78759 to ABV78762 and AB98519 to AB98520). HTPL
has two isoforms, with a few single base pair differences between the
two. One of the single base pair changes introduces a premature stop
codon in HTPL-S (S for short) compared to HTPL-L (L for long). HTPL
shares an overall structure organisation with the Patched protein. The
shared structural features strongly imply that HTPL plays a role similar
to that of Patched, and is a potential tumour suppressor. HTPL is
important in regulating male germ cell development, and the HTPL gene was
mapped to human chromosome 10p12.1. HTPL and its coding sequence are
useful for diagnosing a disorder caused by mutation in HTPL, and in
therapy and manufacture of a medicament for treatment or prevention of
such disorder associated with decreased expression or activity of human
HTPL. Such disorders include disorders of testis, or adrenal, adult and
foetal liver, bone marrow, brain, kidney, lung, placenta, prostate,
skeletal muscle or colon function. HTPL proteins and nucleic acids are
clinically useful diagnostic markers and potential therapeutic agents for
male infertility and cancer. The present oligonucleotide was used in an
example from the invention
```

```
XX
SQ Sequence 17 BP; 4 A; 5 C; 5 G; 3 T; 0 U; 0 Other;
Query Match      0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.9e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 522 ATCGACTCCCTGCTGGA 538
    ||||| |||||
Db 1 AGCGACTCACTGCTGGA 17

RESULT 324
ABV79992
ID ABV79992 standard; DNA; 17 BP.
XX
AC ABV79992;
XX
DT 03-JAN-2003 (first entry)
XX
DE Human HTPL scanning oligonucleotide SEQ ID 1238.
XX
KW Human; gene therapy; tumour suppressor; HTPL; chromosome 10p12.1;
KW human testis expressed Patched like protein; testis; adrenal; liver;
KW male germ cell development; bone marrow; brain; kidney; lung; placenta;
KW prostate; skeletal muscle; colon; male infertility; cancer; ss.
XX
OS Homo sapiens.
XX
PN EP1229046-A2.
XX
PD 07-AUG-2002.
XX
PF 28-JAN-2002; 2002EP-00001167.
XX
PR 30-JAN-2001; 2001WO-US000663.
PR 30-JAN-2001; 2001WO-US000664.
PR 30-JAN-2001; 2001WO-US000665.
PR 30-JAN-2001; 2001WO-US000667.
PR 30-JAN-2001; 2001WO-US000668.
PR 30-JAN-2001; 2001WO-US000669.
PR 23-MAY-2001; 2001US-00864761.
PR 09-OCT-2001; 2001US-0327898P.
XX
PA (AEOM-) AEOMICA INC.
XX
PI Zhan J;
XX
WPI; 2002-676582/73.

Novel isolated human testis expressed Patched like protein (HTPL), useful
for identifying agonist and antagonist and specific binding partners, and
for treating subjects having defects in HTPL.

Example 2; Page 226; 718pp; English.

The present invention relates to human testis expressed Patched like
protein (HTPL, see ABV78759 to ABV78762 and AB98519 to AB98520). HTPL
has two isoforms, with a few single base pair differences between the
two. One of the single base pair changes introduces a premature stop
codon in HTPL-S (S for short) compared to HTPL-L (L for long). HTPL
shares an overall structure organisation with the Patched protein. The
shared structural features strongly imply that HTPL plays a role similar
to that of Patched, and is a potential tumour suppressor. HTPL is
important in regulating male germ cell development, and the HTPL gene was
mapped to human chromosome 10p12.1. HTPL and its coding sequence are
useful for diagnosing a disorder caused by mutation in HTPL, and in
therapy and manufacture of a medicament for treatment or prevention of
such disorder associated with decreased expression or activity of human
HTPL. Such disorders include disorders of testis, or adrenal, adult and
foetal liver, bone marrow, brain, kidney, lung, placenta, prostate,
skeletal muscle or colon function. HTPL proteins and nucleic acids are
clinically useful diagnostic markers and potential therapeutic agents for
male infertility and cancer. The present oligonucleotide was used in an
example from the invention
```

CC	male infertility and cancer. The present oligonucleotide was used in an	CC	skeletal muscle or colon function. HTPL proteins and nucleic acids are
CC	example from the invention	CC	clinically useful diagnostic markers and potential therapeutic agents for
XX		CC	male infertility and cancer. The present oligonucleotide was used in an
SQ	Sequence 17 BP; 2 A; 5 C; 4 G; 6 T; 0 U; 0 Other;	XX	example from the invention
	Query Match 0.8%; Score 13.8; DB 1; Length 17;	SQ	Sequence 17 BP; 3 A; 6 C; 5 G; 3 T; 0 U; 0 Other;
	Best Local Similarity 88.2%; Pred. No. 1.9e+02;		Query Match 0.8%; Score 13.8; DB 1; Length 17;
	Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;		Best Local Similarity 88.2%; Pred. No. 1.9e+02;
			Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY	1273 TCTTGTGACTCTGATCCC 1289	QY	521 CATCGACTCCCTGCTGG 537
DB	1 TCTGTGACTGTGATCCC 17	DB	1 CAGCGACTCACTGCTGG 17
RESULT 325		RESULT 326	
ID	ABV79502 standard; DNA; 17 BP.	ID	ABK18229 standard; RNA; 17 BP.
XX		XX	
AC	ABV79502;	AC	ABK18229;
DT		DT	
XX	03-JAN-2003 (first entry)	XX	09-APR-2002 (first entry)
DE	Human HTPL scanning oligonucleotide SEQ ID 748.	DE	Human ERG hammerhead ribozyme target sequence, Seq ID No 876.
XX		XX	
KW	Human; gene therapy; tumour suppressor; HTPL; chromosome 10p12.1;	XX	Human; hammerhead ribozyme; cytostatic; antitumour; antidiabetic;
KW	human testis expressed Patched like protein; testis; adrenal; liver;	KW	ophthalmological; antiarthritic; antipsoriatic; virucide; osteopathic;
KW	male germ cell development; bone marrow; brain; kidney; lung; placenta;	KW	tumour; cancer; lymphoma; Ewing's sarcoma; melanoma; psoriasis;
XX	prostate; skeletal muscle; colon; male infertility; cancer; ss.	KW	vulvar; angiogenesis; diabetic retinopathy; macular degeneration;
OS	Homo sapiens.	KW	neovascular glaucoma; myopic degeneration; arthritis; verruca vulgaris;
XX		KW	angiofibroma of tuberosus sclerosis; port-wine stain; wound healing;
PN	EP1229046-A2.	KW	Sturge Weber syndrome; Kippel-Trenaunay-Weber syndrome; leukaemia; ss;
XX		KW	Osler-Weber-rendu syndrome; leukaemia; osteoporosis; inozyme;
PD	07-AUG-2002.	KW	ambrzyme.
XX		XX	
PF	28-JAN-2002; 2002EP-00001167.	OS	Homo sapiens.
XX		XX	
PR	30-JAN-2001; 2001WO-US000663.	PN	WO200188124-A2.
PR	30-JAN-2001; 2001WO-US000664.	XX	
PR	30-JAN-2001; 2001WO-US000665.	PD	22-NOV-2001.
PR	30-JAN-2001; 2001WO-US000667.	XX	
PR	30-JAN-2001; 2001WO-US000668.	PF	16-MAY-2001; 2001WO-US015866.
PR	30-JAN-2001; 2001WO-US000669.	XX	
PR	23-MAY-2001; 2001US-00864761.	PR	16-MAY-2000; 2000US-00572021.
PR	09-OCT-2001; 2001US-0327898P.	XX	
XX		PA	(RIBO-) RIBOZYME PHARM INC.
PA	(AEOM-) AEOMICA INC.	PA	(GLAX ) GLAXO GROUP LTD.
XX		XX	
PI	Zhan J;	PI	Jarvis T, Von Carlowitz I, Mcswiggen JA, McLaughlin F, Randi AM;
XX		XX	
DR	WPI; 2002-676582/73.	DR	WPI; 2002-082995/11.
XX		XX	
PT	Novel isolated human testis expressed Patched like protein (HTPL), useful	PT	Novel polynucleotide which down regulates expression of Ets-related gene,
PT	for identifying agonist and antagonist and specific binding partners, and	PT	useful for treating cancer, diabetic retinopathy, macular degeneration,
PT	for treating subjects having defects in HTPL.	PT	arthritis, psoriasis, verruca vulgaris and Sturge Weber syndrome.
XX		XX	
PS	Example 2; Page 161; 718pp; English.	PS	Claim 4; Page 74; 149pp; English.
XX		XX	
CC	The present invention relates to human testis expressed Patched like	CC	The invention relates to a nucleic acid molecule (I) which down regulates
CC	protein (HTPL), see ABV78759 to ABV78762 and ABB98519 to ABB98520). HTPL	CC	expression of an Ets-related gene (ERG). (I) is useful for treating
CC	has two isoforms, with a few single base pair differences between the	CC	conditions selected from cancer, lymphoma, Ewing's sarcoma, melanoma,
CC	two. One of the single base pair changes introduces a premature stop	CC	tumour angiogenesis, diabetic retinopathy, macular degeneration,
CC	codon in HTPL-S (S for short) compared to HTPL-L (L for long). HTPL	CC	neovascular glaucoma, myopic degeneration, arthritis, psoriasis, verruca
CC	shares an overall structure organisation with the Patched protein. The	CC	vulgaris, angiofibroma of tuberosus sclerosis, port-wine stains, Sturge
CC	shared structural features strongly imply that HTPL plays a role similar	CC	Weber syndrome, Kippel-Trenaunay-Weber syndrome, Osler-Weber-rendu
CC	to that of Patched, and is a potential tumour suppressor. HTPL is	CC	syndrome, leukaemia, osteoporosis and wound healing. (I) is useful for
CC	important in regulating male germ cell development, and the HTPL gene was	CC	treating a patient having a condition associated with the level of ERG,
CC	mapped to human chromosome 10p12.1. HTPL and its coding sequence are	CC	by contacting cells of the patient with (I) under conditions suitable for
CC	useful for diagnosing a disorder caused by mutation in HTPL, and in	CC	the treatment. The method comprises the use of one or more therapies
CC	therapy and manufacture of a medicament for treatment or prevention of	CC	under conditions suitable for the treatment. Leukaemia or tumour
CC	such disorder associated with decreased expression or activity of human	CC	angiogenesis is treated by administering (I) to the patient in
CC	HTPL. Such disorders include disorders of testis, or adrenal, adult and	CC	conjunction with one or more of other therapies such as radiation or
CC	fetal liver, bone marrow, brain, kidney, lung, placenta, prostate,		



CC chemotherapy treatment. (I) is useful for reducing ERG activity in a  
 CC cell, by contacting the cell with (I). (I) is useful for cleaving RNA of  
 CC ERG gene, by contacting (I) with RNA, in the presence of a divalent  
 CC cation such as Mg<sup>2+</sup>. (I) is useful for diagnosis of conditions and  
 CC diseases related to the expression of ERG, and as diagnostic tool to  
 CC examine genetic drift and mutations within diseased cells or to detect  
 CC the presence of ERG RNA in a cell. (I) is useful for specifically  
 CC targeting genes that share homology with ERG gene or ERG fusion genes.  
 CC ABK17354-ABK22719 represent nucleic acids, including antisense and  
 CC enzymatic nucleic acid molecules which regulate expression of ERG, and  
 CC related PCR primers of the invention  
 XX  
 SQ Sequence 17 BP; 2 A; 12 C; 2 G; 0 T; 1 U; 0 Other;  
 Query Match 0.8%; Score 13.8; DB 1; Length 17;  
 Best Local Similarity 82.4%; Pred. No. 1.9e+02;  
 Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
 QY 1504 GCCCGAGCTCCAGGCC 1520  
 DB 1 GCCCCACCCUCCAGGCC 17  
 RESULT 327  
 ABK19135  
 ID ABK19135 standard; RNA; 17 BP.  
 AC ABK19135;  
 XX  
 DT 09-APR-2002 (first entry)  
 XX  
 DE Human ERG Amberzyme target sequence Seq ID No 1782.  
 XX  
 KW Human; hammerhead ribozyme; cytostatic; antitumour; antidiabetic;  
 KW ophthalmological; antiarthritic; antipsoriatic; virucide; osteopathic;  
 KW vulvar; cancer; lymphoma; Ewing's sarcoma; melanoma; psoriasis;  
 KW tumour angiogenesis; diabetic retinopathy; macular degeneration;  
 KW neovascular glaucoma; myopic degeneration; arthritis; verruca vulgaris;  
 KW angiofibroma of tuberous sclerosis; port-wine stain; wound healing;  
 KW Sturge Weber syndrome; Kippel-Trenaunay-Weber syndrome; leukaemia; ss;  
 KW Osler-Weber-rendu syndrome; leukaemia; osteoporosis; DNazyme; inozyme;  
 KW amberzyme.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200188124-A2.  
 XX  
 PD 22-NOV-2001.  
 XX  
 PF 16-MAY-2001; 2001WO-US015866.  
 XX  
 PR 16-MAY-2000; 2000US-00572021.  
 XX  
 PA (RIBO-) RIBOZYME PHARM INC.  
 PA (GLAX) GLAXO GROUP LTD.  
 XX  
 PI Jarvis T, Von Carlowitz I, Mcswiggen JA, McLaughlin F, Randi AM;  
 XX WPI; 2002-082995/11.  
 DR  
 XX Novel polynucleotide which down regulates expression of Ets-related gene,  
 PT useful for treating cancer, diabetic retinopathy, macular degeneration,  
 PT arthritis, psoriasis, verruca vulgaris and Sturge Weber syndrome.  
 XX  
 PS Claim 4; Page 120; 149pp; English.  
 XX  
 CC The invention relates to a nucleic acid molecule (I) which down regulates  
 CC expression of an Ets-related gene (ERG). (I) is useful for treating  
 CC conditions selected from cancer, lymphoma, Ewing's sarcoma, melanoma,  
 CC tumour angiogenesis, diabetic retinopathy, macular degeneration,  
 CC neovascular glaucoma, myopic degeneration, arthritis, psoriasis, verruca  
 CC vulgaris, angiofibroma of tuberous sclerosis, port-wine stains, Sturge  
 CC Weber syndrome, Kippel-Trenaunay-Weber syndrome, Osler-Weber-rendu

CC syndrome, leukaemia, osteoporosis and wound healing. (I) is useful for  
 CC treating a patient having a condition associated with the level of ERG,  
 CC by contacting cells of the patient with (I) under conditions suitable for  
 CC the treatment. The method comprises the use of one or more therapies  
 CC under conditions suitable for the treatment. Leukaemia or tumour  
 CC angiogenesis is treated by administering (I) to the patient in  
 CC conjunction with one or more of other therapies such as radiation or  
 CC chemotherapy treatment. (I) is useful for reducing ERG activity in a  
 CC cell, by contacting the cell with (I). (I) is useful for cleaving RNA of  
 CC ERG gene, by contacting (I) with RNA, in the presence of a divalent  
 CC cation such as Mg<sup>2+</sup>. (I) is useful for diagnosis of conditions and  
 CC diseases related to the expression of ERG, and as diagnostic tool to  
 CC examine genetic drift and mutations within diseased cells or to detect  
 CC the presence of ERG RNA in a cell. (I) is useful for specifically  
 CC targeting genes that share homology with ERG gene or ERG fusion genes.  
 CC ABK17354-ABK22719 represent nucleic acids, including antisense and  
 CC enzymatic nucleic acid molecules which regulate expression of ERG, and  
 CC related PCR primers of the invention  
 XX  
 SQ Sequence 17 BP; 10 A; 3 C; 3 G; 0 T; 1 U; 0 Other;  
 Query Match 0.8%; Score 13.8; DB 1; Length 17;  
 Best Local Similarity 82.4%; Pred. No. 1.9e+02;  
 Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
 QY 218 GACTCTCATAGAAAAA 234  
 DB 1 GACUCACAGAGAAAAA 17  
 RESULT 328  
 AAD38269  
 ID AAD38269 standard; DNA; 17 BP.  
 XX  
 AC AAD38269;  
 XX  
 DT 10-SEP-2002 (first entry)  
 XX  
 DE Mouse Ob receptor genomic DNA amplifying forward PCR primer #2.  
 XX  
 KW Mouse; Ob receptor; ObR; leptin; body weight disorder; drug screening;  
 KW gene therapy; obesity; cachexia; anorexia; anorectic; anabolic; PCR;  
 KW primer; ss.  
 XX  
 OS Mus sp.  
 XX  
 PN US6380363-B1.  
 XX  
 PD 30-APR-2002.  
 XX  
 PF 19-AUG-1998; 98US-00137132.  
 XX  
 PR 27-NOV-1995; 95US-00562663.  
 PR 04-DEC-1995; 95US-00566622.  
 PR 08-DEC-1995; 95US-00569485.  
 PR 11-DEC-1995; 95US-00570142.  
 PR 28-DEC-1995; 95US-00583153.  
 PR 22-JAN-1996; 96US-00599455.  
 PR 26-APR-1996; 96US-00638524.  
 PR 03-SEP-1996; 96US-00708123.  
 PR 28-MAY-1997; 97US-00864584.  
 XX  
 PA (TART/) TARTAGLIA L A.  
 PA (TEPP/) TEPPER R I.  
 PA (CULP/) CULPEPPER J A.  
 PA (WHIT/) WHITE D W.  
 XX  
 PI Tartaglia LA, Tepper RI, Culpepper JA, White DW;  
 XX WPI; 2002-413726/44.  
 DR  
 XX Antibodies which selectively bind mammalian Ob receptors and inhibits the  
 PT binding of leptin to the mammalian Ob receptor, useful for diagnosing and

```

PT treating weight disorders.
PS Example; Col 62; 108pp; English.
XX
XX The present invention relates to novel antibodies which selectively bind
XX mammalian Ob receptors (OBR) and inhibit the binding of leptin to the
XX mammalian Ob receptor. OBR sequences are novel receptor proteins that
XX participate in the control of mammalian body weight. The antibodies of
XX the invention may be used to detect of Ob receptor in a biological sample
XX and utilised as a part of diagnostic or prognostic technique in which
XX patients may be tested for abnormal amounts of Ob receptors. They may be
XX utilised in conjunction with, for example, compound screening schemes for
XX the evaluation of the effect of test compounds on expression and/or
XX activity of the Ob receptor gene product. The antibodies can be used in
XX conjunction with the gene therapy techniques, for example, to evaluate
XX the normal and/or engineered Ob receptor-expressing cells prior to their
XX introduction into the patient. They may be used in the method for the
XX screening of abnormal Ob receptor activity and can be used for drug
XX disorders, including but not limited to obesity, cachexia and anorexia.
XX The present DNA sequence is a PCR primer which is used for amplifying
XX mouse OBR genomic DNA. This sequence is used in the exemplification of
XX the invention
XX
XX Sequence 17 BP; 3 A; 6 C; 2 G; 6 T; 0 U; 0 Other;
SQ
Query Match 0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.9e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 660 CACTACCTGCCTTCAG 676
Db 1 CACTATTTCCTTCAG 17
RESULT 329
AAD38271
ID AAD38271 standard; DNA; 17 BP.
XX
XX AAD38271;
XX
XX 10-SEP-2002 (first entry)
XX
XX Mouse Ob receptor genomic DNA amplifying forward PCR primer #3.
XX
XX Mouse; Ob receptor; OBR; leptin; body weight disorder; drug screening;
XX gene therapy; obesity; cachexia; anorexia; anorectic; anabolic; PCR;
XX primer; ss.
XX
XX Mus sp.
XX
XX US6380363-B1.
XX
XX 30-APR-2002.
XX
XX 19-AUG-1998; 98US-00137132.
XX
XX 27-NOV-1995; 95US-00562663.
XX 04-DEC-1995; 95US-00566622.
XX 08-DEC-1995; 95US-00569485.
XX 11-DEC-1995; 95US-00570142.
XX 28-DEC-1995; 95US-00583153.
XX 22-JAN-1996; 96US-00599455.
XX 26-APR-1996; 96US-00638524.
XX 03-SEP-1996; 96US-00708123.
XX 28-MAY-1997; 97US-00864564.
XX
XX (TART/) TARTAGLIA L A.
XX (TEPP/) TEPPER R I.
XX (CULP/) CULPEPPER J A.
XX (WHIT/) WHITE D W.
XX
XX Tartaglia LA, Tepper RI, Culpepper JA, White DW;
PI

```

---

```

XX WPI; 2002-413726/44.
XX
XX Antibodies which selectively bind mammalian Ob receptors and inhibits the
XX binding of leptin to the mammalian Ob receptor, useful for diagnosing and
XX treating weight disorders.
XX
XX Example; Col 62; 108pp; English.
XX
XX The present invention relates to novel antibodies which selectively bind
XX mammalian Ob receptors (OBR) and inhibit the binding of leptin to the
XX mammalian Ob receptor. OBR sequences are novel receptor proteins that
XX participate in the control of mammalian body weight. The antibodies of
XX the invention may be used to detect of Ob receptor in a biological sample
XX and utilised as a part of diagnostic or prognostic technique in which
XX patients may be tested for abnormal amounts of Ob receptors. They may be
XX utilised in conjunction with, for example, compound screening schemes for
XX the evaluation of the effect of test compounds on expression and/or
XX activity of the Ob receptor gene product. The antibodies can be used in
XX conjunction with the gene therapy techniques, for example, to evaluate
XX the normal and/or engineered Ob receptor-expressing cells prior to their
XX introduction into the patient. They may be used in the method for the
XX screening of abnormal Ob receptor activity and can be used for drug
XX disorders, including but not limited to obesity, cachexia and anorexia.
XX The present DNA sequence is a PCR primer which is used for amplifying
XX mouse OBR genomic DNA. This sequence is used in the exemplification of
XX the invention
XX
XX Sequence 17 BP; 3 A; 6 C; 2 G; 6 T; 0 U; 0 Other;
SQ
Query Match 0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.9e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 660 CACTACCTGCCTTCAG 676
Db 1 CACTATTTCCTTCAG 17
RESULT 330
ACN05936/C
ID ACN05936 standard; RNA; 17 BP.
XX
XX ACN05936;
XX
XX 22-APR-2004 (first entry)
XX
XX WNV Amberzyme substrate SEQ ID NO 5939.
XX
XX WNV; West Nile Virus; antiinflammatory; cytostatic; hepatotropic;
XX virucide; neuroprotective; antibacterial; replication; pancreatitis;
XX encephalitis; myocarditis; meningitis; infection; hepatitis;
XX liver failure; cancer; cirrhosis; Hammerhead; Inozyme; DNazyme;
XX Amberzyme; Zinzyne; ss.
XX
XX West Nile Virus.
XX
XX WO200268637-A2.
XX
XX 06-SEP-2002.
XX
XX 19-OCT-2001; 2001WO-US048350.
XX
XX 20-OCT-2000; 2000US-0242411P.
XX
XX (RIBO-) RIBOZYME PHARM INC.
XX (BLAT/) BLATT L.
XX (MCSW/) MCSWIGGEN J A.
XX
XX Blatt L, Mcswiggen JA;
XX
XX WPI; 2002-706994/76.
XX

```

XX New nucleic acid molecule that modulates replication of West Nile Virus  
PT (WNV), useful for treating a condition related to WNV infection e.g.  
PT pancreatitis, meningitis, hepatocellular carcinoma or cirrhosis.  
XX  
PS Claim 23; SEQ ID NO 5939; 495pp; English.  
XX  
CC The invention relates to nucleic acid molecules that modulate replication  
CC of the West Nile Virus (WNV). The nucleic acid molecules are useful for  
CC treating a condition related to WNV infection e.g. pancreatitis,  
CC encephalitis, myocarditis, meningitis, neurologic infection, hepatitis,  
CC liver failure, hepatocellular carcinoma or cirrhosis. The nucleic acid  
CC molecule is selected from the group of ribozymes consisting of  
CC Hammerhead, Inozyme, G-cleaver, DNazyme, Amberzyme and Zinzyme. The  
CC nucleic acid molecules further comprise at least five ribose residues, at  
CC least ten 2'-O-methyl modifications, phosphorothioate linkages on at  
CC least three of the 5' terminal nucleotides and a 3' end modification of a  
CC 3'-3' inverted abasic moiety. Nucleic acid molecules SEQ ID NO 1 to 37080  
CC are claimed; however, SEQ ID NO 2194-2206 and 17502-17514 are not given  
CC in the specification. The present sequence is that of a nucleic acid  
CC molecule of the invention  
XX  
SQ Sequence 17 BP; 6 A; 4 C; 4 G; 0 T; 3 U; 0 Other;  
  
Query Match 0.8%; Score 13.8; DB 1; Length 17;  
Best Local Similarity 88.2%; Pred. No. 1.9e+02;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
  
QY 1226 TTCTGACTCGGAGTTC 1242  
DB 17 TTCTGAGTCGGACATTC 1  
  
RESULT 331  
ACN08391  
ID ACN08391 standard; RNA; 17 BP.  
XX  
AC ACN08391;  
XX  
DT 22-APR-2004 (first entry)  
XX  
DE WNV minus strand Hammerhead Ribozyme substrate SEQ ID NO 8394.  
XX  
KW WNV; West Nile Virus; antiinflammatory; cytostatic; hepatotropic;  
KW viricide; neuroprotective; antibacterial; replication; pancreatitis;  
KW encephalitis; myocarditis; meningitis; infection; hepatitis;  
KW liver failure; cancer; cirrhosis; Hammerhead; Inozyme; DNazyme;  
KW Amberzyme; Zinzyme; ss.  
XX  
OS West Nile Virus.  
XX  
PN WO200268637-A2.  
XX  
PD 06-SEP-2002.  
XX  
PF 19-OCT-2001; 2001WO-US048350.  
XX  
PR 20-OCT-2000; 2000US-024241P.  
XX  
PA (RIBO-) RIBOZYME PHARM INC.  
PA (BLAT/) BLATT L.  
PA (MCSW/) MCSWIGGEN J A.  
XX  
PI Blatt L, Mcswiggen JA;  
XX  
DR WPI; 2002-706994/76.  
XX  
CC New nucleic acid molecule that modulates replication of West Nile Virus  
PT (WNV), useful for treating a condition related to WNV infection e.g.  
PT pancreatitis, meningitis, hepatocellular carcinoma or cirrhosis.  
XX  
PS Claim 23; SEQ ID NO 8394; 495pp; English.  
XX

CC The invention relates to nucleic acid molecules that modulate replication  
CC of the West Nile Virus (WNV). The nucleic acid molecules are useful for  
CC treating a condition related to WNV infection e.g. pancreatitis,  
CC encephalitis, myocarditis, meningitis, neurologic infection, hepatitis,  
CC liver failure, hepatocellular carcinoma or cirrhosis. The nucleic acid  
CC molecule is selected from the group of ribozymes consisting of  
CC Hammerhead, Inozyme, G-cleaver, DNazyme, Amberzyme and Zinzyme. The  
CC nucleic acid molecules further comprise at least five ribose residues, at  
CC least ten 2'-O-methyl modifications, phosphorothioate linkages on at  
CC least three of the 5' terminal nucleotides and a 3' end modification of a  
CC 3'-3' inverted abasic moiety. Nucleic acid molecules SEQ ID NO 1 to 37080  
CC are claimed; however, SEQ ID NO 2194-2206 and 17502-17514 are not given  
CC in the specification. The present sequence is that of a nucleic acid  
CC molecule of the invention  
XX  
SQ Sequence 17 BP; 0 A; 9 C; 0 G; 0 T; 8 U; 0 Other;  
  
Query Match 0.8%; Score 13.8; DB 1; Length 17;  
Best Local Similarity 47.1%; Pred. No. 1.9e+02;  
Matches 8; Conservative 7; Mismatches 2; Indels 0; Gaps 0;  
  
QY 488 CTCGCCCTTCTACTTCT 504  
DB 1 CUCUCCUUCUUCUUCU 17  
  
RESULT 332  
ACN15008  
ID ACN15008 standard; RNA; 17 BP.  
XX  
AC ACN15008;  
XX  
DT 22-APR-2004 (first entry)  
XX  
DE WNV minus strand Amberzyme substrate SEQ ID NO 15011.  
XX  
KW WNV; West Nile Virus; antiinflammatory; cytostatic; hepatotropic;  
KW viricide; neuroprotective; antibacterial; replication; pancreatitis;  
KW encephalitis; myocarditis; meningitis; infection; hepatitis;  
KW liver failure; cancer; cirrhosis; Hammerhead; Inozyme; DNazyme;  
KW Amberzyme; Zinzyme; ss.  
XX  
OS West Nile Virus.  
XX  
PN WO200268637-A2.  
XX  
PD 06-SEP-2002.  
XX  
PF 19-OCT-2001; 2001WO-US048350.  
XX  
PR 20-OCT-2000; 2000US-024241P.  
XX  
PA (RIBO-) RIBOZYME PHARM INC.  
PA (BLAT/) BLATT L.  
PA (MCSW/) MCSWIGGEN J A.  
XX  
PI Blatt L, Mcswiggen JA;  
XX  
DR WPI; 2002-706994/76.  
XX  
CC New nucleic acid molecule that modulates replication of West Nile Virus  
PT (WNV), useful for treating a condition related to WNV infection e.g.  
PT pancreatitis, meningitis, hepatocellular carcinoma or cirrhosis.  
XX  
PS Claim 23; SEQ ID NO 15011; 495pp; English.  
XX  
CC The invention relates to nucleic acid molecules that modulate replication  
CC of the West Nile Virus (WNV). The nucleic acid molecules are useful for  
CC treating a condition related to WNV infection e.g. pancreatitis,  
CC encephalitis, myocarditis, meningitis, neurologic infection, hepatitis,  
CC liver failure, hepatocellular carcinoma or cirrhosis. The nucleic acid  
CC molecule is selected from the group of ribozymes consisting of  
CC Hammerhead, Inozyme, G-cleaver, DNazyme, Amberzyme and Zinzyme. The

XX		Sequence	17 BP; 5 A; 4 C; 5 G; 0 T; 3 U; 0 Other;	
SQL		Query Match	0.8%; Score 13.8; DB 1; Length 17;	
		Best Local Similarity	88.2%; Pred. NO. 1.9e+02;	
		Matches	15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;	
QY	1228	CTGACTCGGACGTTCCT	1244	
DB	17	CTGATCGGCATTCCT	1	
RESULT	334			
ACN14016				
ID	ACN14016	standard; RNA; 17 BP.		
XX	AC			
XX	ACN14016;			
XX	DT			
XX	22-APR-2004	(first entry)		
DE	NNV minus strand DNAzyme substrate SEQ ID NO 14019.			
XX	NNV; West Nile Virus; antiinflammatory; cytostatic; hepatotropic;			
KW	virucide; neuroprotective; antibacterial; replication; pancreatitis;			
KW	encephalitis; myocarditis; meningitis; infection; hepatitis;			
KW	liver failure; cancer; cirrhosis; Hammerhead; Inozyme; DNAzyme;			
XX	Amberzyme; Zinzyne; ss.			
XX	West Nile Virus.			
OS	West Nile Virus.			
XX	WO200268637-A2.			
FN	06-SEP-2002.			
PD	19-OCT-2001; 2001WO-US048350.			
PF	20-OCT-2000; 2000US-024241P.			
XX	(RIBO-) RIBOZYME PHARM INC.			
PA	(BLAT/) BLATT L.			
PA	(MCSW/) MCSWIGGEN J A.			
XX	Blatt L, Mcswiggen JA;			
PI	WPI; 2002-706994/76.			
DR	New nucleic acid molecule that modulates replication of West Nile Virus			
XX	(NNV), useful for treating a condition related to WNV infection e.g.			
PT	pancreatitis, meningitis, hepatocellular carcinoma or cirrhosis.			
PT	Claim 23; SEQ ID NO 14019; 495pp; English.			
PS	The invention relates to nucleic acid molecules that modulate replication			
XX	of the West Nile Virus (NNV). The nucleic acid molecules are useful for			
CC	treating a condition related to WNV infection e.g. pancreatitis,			
CC	encephalitis, myocarditis, meningitis, neurologic infection, hepatitis,			
CC	liver failure, hepatocellular carcinoma or cirrhosis. The nucleic acid			
CC	molecule is selected from the group of ribozymes consisting of			
CC	Hammerhead, Inozyme, G-cleaver, DNAzyme, Amberzyme and Zinzyne. The			
CC	nucleic acid molecules further comprise at least five ribose residues, at			
CC	least ten 2'-O-methyl modifications, phosphorothioate linkages on at			
CC	least three of the 5' terminal nucleotides and a 3' end modification of a			
CC	3'-3', inverted abasic moiety. Nucleic acid molecules SEQ ID NO 1 to 37080			
CC	are claimed; however, SEQ ID NO 2194-2206 and 17502-17514 are not given			
CC	in the specification. The present sequence is that of a nucleic acid			
CC	molecule of the invention			
XX	Sequence 17 BP; 3 A; 4 C; 4 G; 0 T; 6 U; 0 Other;			
SQL	Query Match	0.8%; Score 13.8; DB 1; Length 17;		
	Best Local Similarity	52.9%; Pred. NO. 1.9e+02;		
	Matches	9; Conservative 6; Mismatches 2; Indels 0; Gaps 0;		

QY 1229 TGACTCGGACGTTCCT 1245  
:|||||:|:|:  
Db 1 UGAGUCGGACAUCCU 17

## RESULT 335

ACN15009  
ID ACN15009 standard; RNA; 17 BP.

AC ACN15009;

XX 22-APR-2004 (first entry)

XX WNV minus strand Amberzyme substrate SEQ ID NO 15012.  
DE

XX WNV; West Nile Virus; antiinflammatory; cytostatic; hepatotropic;  
KW virucide; neuroprotective; antibacterial; replication; pancreatitis;  
KW encephalitis; myocarditis; meningitis; infection; hepatitis;  
KW liver failure; cancer; cirrhosis; Hammerhead; Inozyme; DNazyme;  
KW Amberzyme; Zinzyme; ss.

XX West Nile Virus.

XX WO200268637-A2.

XX 06-SEP-2002.

XX 19-OCT-2001; 2001WO-US048350.

XX 20-OCT-2000; 2000US-0242411P.

XX (RIBO-) RIBOZYME PHARM INC.

XX (BLAT/) BLATT L.

XX (MCSW/) MCSWIGGEN J A.

XX Blatt L, Mcswiggen JA;

XX WPI; 2002-706994/76.

XX New nucleic acid molecule that modulates replication of West Nile Virus  
(WNV), useful for treating a condition related to WNV infection e.g.

XX pancreatitis, meningitis, hepatocellular carcinoma or cirrhosis.

XX Claim 23; SEQ ID NO 15012; 495pp; English.

XX The invention relates to nucleic acid molecules that modulate replication  
of the West Nile Virus (WNV). The nucleic acid molecules are useful for  
treating a condition related to WNV infection e.g. pancreatitis,  
encephalitis, myocarditis, meningitis, neurologic infection, hepatitis,  
liver failure, hepatocellular carcinoma or cirrhosis. The nucleic acid  
molecule is selected from the group of ribozymes consisting of  
Hammerhead, Inozyme, G-cleaver, DNazyme, Amberzyme and Zinzyme. The  
nucleic acid molecules further comprise at least five ribose residues, at  
least ten 2'-O-methyl modifications, phosphorothioate linkages on at  
least three of the 5' terminal nucleotides and a 3' end modification of a  
3'-3' inverted abasic moiety. Nucleic acid molecules SEQ ID NO 1 to 37080  
are claimed; however, SEQ ID NO 2194-2206 and 17502-17514 are not given  
in the specification. The present sequence is that of a nucleic acid  
molecule of the invention

XX Sequence 17 BP; 3 A; 5 C; 4 G; 0 T; 5 U; 0 Other;

XX Query Match 0.8%; Score 13.8; DB 1; Length 17;  
Best Local Similarity 58.8%; Pred. No. 1.9e+02;

XX Matches 10; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 1228 CTGACTCGGACGTTCCT 1244  
:|||||:|:|:

Db 1 CUGAGUCGGACAUCCU 17

## RESULT 336

ACN06460/c

ID ACN06460 standard; RNA; 17 BP.

XX ACN06460;

XX 22-APR-2004 (first entry)

XX WNV Amberzyme substrate SEQ ID NO 6463.

XX WNV; West Nile Virus; antiinflammatory; cytostatic; hepatotropic;  
KW virucide; neuroprotective; antibacterial; replication; pancreatitis;  
KW encephalitis; myocarditis; meningitis; infection; hepatitis;  
KW liver failure; cancer; cirrhosis; Hammerhead; Inozyme; DNazyme;  
KW Amberzyme; Zinzyme; ss.

XX West Nile Virus.

XX WO200268637-A2.

XX 06-SEP-2002.

XX 19-OCT-2001; 2001WO-US048350.

XX 20-OCT-2000; 2000US-0242411P.

XX (RIBO-) RIBOZYME PHARM INC.

XX (BLAT/) BLATT L.

XX (MCSW/) MCSWIGGEN J A.

XX Blatt L, Mcswiggen JA;

XX WPI; 2002-706994/76.

XX New nucleic acid molecule that modulates replication of West Nile Virus  
(WNV), useful for treating a condition related to WNV infection e.g.

XX pancreatitis, meningitis, hepatocellular carcinoma or cirrhosis.

XX Claim 23; SEQ ID NO 6463; 495pp; English.

XX The invention relates to nucleic acid molecules that modulate replication  
of the West Nile Virus (WNV). The nucleic acid molecules are useful for  
treating a condition related to WNV infection e.g. pancreatitis,  
encephalitis, myocarditis, meningitis, neurologic infection, hepatitis,  
liver failure, hepatocellular carcinoma or cirrhosis. The nucleic acid  
molecule is selected from the group of ribozymes consisting of  
Hammerhead, Inozyme, G-cleaver, DNazyme, Amberzyme and Zinzyme. The  
nucleic acid molecules further comprise at least five ribose residues, at  
least ten 2'-O-methyl modifications, phosphorothioate linkages on at  
least three of the 5' terminal nucleotides and a 3' end modification of a  
3'-3' inverted abasic moiety. Nucleic acid molecules SEQ ID NO 1 to 37080  
are claimed; however, SEQ ID NO 2194-2206 and 17502-17514 are not given  
in the specification. The present sequence is that of a nucleic acid  
molecule of the invention

XX Sequence 17 BP; 8 A; 1 C; 8 G; 0 T; 0 U; 0 Other;

XX Query Match 0.8%; Score 13.8; DB 1; Length 17;  
Best Local Similarity 88.2%; Pred. No. 1.9e+02;

XX Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 489 TCGCCCTTCTACTTCTG 505  
||| ||||| |||||

Db 17 TCTCCCTTCTCTCTG 1

## RESULT 337

ACN01953/c

ID ACN01953 standard; RNA; 17 BP.

XX ACN01953;

XX 22-APR-2004 (first entry)

XX WNV Inozyme substrate SEQ ID NO 1943.

```
XX WNV; West Nile Virus; antiinflammatory; cytostatic; hepatotropic;
KW virucide; neuroprotective; antibacterial; replication; pancreatitis;
KW encephalitis; myocarditis; meningitis; infection; hepatitis;
KW liver failure; cancer; cirrhosis; Hammerhead; Inozyme; DNazyme;
KW Amberzyme; Zinzyme; ss.
XX
OS West Nile Virus.
XX
PN WO200268637-A2.
XX
PD 06-SEP-2002.
XX
PF 19-OCT-2001; 2001WO-US048350.
XX
PR 20-OCT-2000; 2000US-0242411P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
PA (BLAT/) BLATT L.
PA (MCSW/) MCSWIGGEN J A.
XX
PI Blatt L, Mcswiggen JA;
XX
PS WPI; 2002-706994/76.
XX
DR
XX
XX New nucleic acid molecule that modulates replication of West Nile Virus
PT (WNV), useful for treating a condition related to WNV infection e.g.
PT pancreatitis, meningitis, hepatocellular carcinoma or cirrhosis.
XX
XX Claim 23; SEQ ID NO 1943; 495pp; English.
XX
XX The invention relates to nucleic acid molecules that modulate replication
CC of the West Nile Virus (WNV). The nucleic acid molecules are useful for
CC treating a condition related to WNV infection e.g. pancreatitis,
CC encephalitis, myocarditis, meningitis, neurologic infection, hepatitis,
CC liver failure, hepatocellular carcinoma or cirrhosis. The nucleic acid
CC molecule is selected from the group of ribozymes consisting of
CC Hammerhead, Inozyme, G-cleaver, DNazyme, Amberzyme and Zinzyme. The
CC nucleic acid molecules further comprise at least five ribose residues, at
CC least ten 2'-O-methyl modifications, phosphorothioate linkages on at
CC least three of the 5' terminal nucleotides and a 3' end modification of a
CC 3'-3' inverted abasic moiety. Nucleic acid molecules SEQ ID NO 1 to 37080
CC are claimed; however, SEQ ID NO 2194-2206 and 17502-17514 are not given
CC in the specification. The present sequence is that of a nucleic acid
CC molecule of the invention
XX
SQ Sequence 17 BP; 5 A; 4 C; 5 G; 0 T; 3 U; 0 Other;
Query Match 0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.9e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1227 TCTGACTCGGAGCTTCC 1243
DB 17 TCTGACTCGGACATCC 1
RESULT 338
ACN08392
ID ACN08392 standard; RNA; 17 BP.
XX
XX ACN08392;
AC
XX
XX 22-APR-2004 (first entry)
DT
XX
XX WNV minus strand Hammerhead Ribozyme substrate SEQ ID NO 8395.
DE
XX
XX WNV; West Nile Virus; antiinflammatory; cytostatic; hepatotropic;
KW virucide; neuroprotective; antibacterial; replication; pancreatitis;
KW encephalitis; myocarditis; meningitis; infection; hepatitis;
KW liver failure; cancer; cirrhosis; Hammerhead; Inozyme; DNazyme;
KW Amberzyme; Zinzyme; ss.
XX
```

```
OS West Nile Virus.
XX
PN WO200268637-A2.
XX
PD 06-SEP-2002.
XX
PF 19-OCT-2001; 2001WO-US048350.
XX
PR 20-OCT-2000; 2000US-0242411P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
PA (BLAT/) BLATT L.
PA (MCSW/) MCSWIGGEN J A.
XX
PI Blatt L, Mcswiggen JA;
XX
PS WPI; 2002-706994/76.
XX
XX New nucleic acid molecule that modulates replication of West Nile Virus
PT (WNV), useful for treating a condition related to WNV infection e.g.
PT pancreatitis, meningitis, hepatocellular carcinoma or cirrhosis.
XX
XX Claim 23; SEQ ID NO 8395; 495pp; English.
XX
XX The invention relates to nucleic acid molecules that modulate replication
CC of the West Nile Virus (WNV). The nucleic acid molecules are useful for
CC treating a condition related to WNV infection e.g. pancreatitis,
CC encephalitis, myocarditis, meningitis, neurologic infection, hepatitis,
CC liver failure, hepatocellular carcinoma or cirrhosis. The nucleic acid
CC molecule is selected from the group of ribozymes consisting of
CC Hammerhead, Inozyme, G-cleaver, DNazyme, Amberzyme and Zinzyme. The
CC nucleic acid molecules further comprise at least five ribose residues, at
CC least ten 2'-O-methyl modifications, phosphorothioate linkages on at
CC least three of the 5' terminal nucleotides and a 3' end modification of a
CC 3'-3' inverted abasic moiety. Nucleic acid molecules SEQ ID NO 1 to 37080
CC are claimed; however, SEQ ID NO 2194-2206 and 17502-17514 are not given
CC in the specification. The present sequence is that of a nucleic acid
CC molecule of the invention
XX
SQ Sequence 17 BP; 0 A; 8 C; 1 G; 0 T; 8 U; 0 Other;
Query Match 0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 47.1%; Pred. No. 1.9e+02;
Matches 8; Conservative 7; Mismatches 2; Indels 0; Gaps 0;
QY 489 TCGCCCTTCTACTCTG 505
DB 1 UCUCUCCUUCUCCUUCUG 17
RESULT 339
ACN11835/C
ID ACN11835 standard; RNA; 17 BP.
XX
XX ACN11835;
AC
XX
XX 22-APR-2004 (first entry)
DT
XX
XX WNV minus strand Inozyme substrate SEQ ID NO 11838.
DE
XX
XX WNV; West Nile Virus; antiinflammatory; cytostatic; hepatotropic;
KW virucide; neuroprotective; antibacterial; replication; pancreatitis;
KW encephalitis; myocarditis; meningitis; infection; hepatitis;
KW liver failure; cancer; cirrhosis; Hammerhead; Inozyme; DNazyme;
KW Amberzyme; Zinzyme; ss.
XX
XX West Nile Virus.
OS
XX
XX WO200268637-A2.
PN
XX
XX 06-SEP-2002.
PD
XX
XX 19-OCT-2001; 2001WO-US048350.
PF
XX
XX 20-OCT-2000; 2000US-0242411P.
PR
XX
XX (RIBO-) RIBOZYME PHARM INC.
PA
XX
XX (BLAT/) BLATT L.
PA
XX
XX (MCSW/) MCSWIGGEN J A.
PA
XX
XX Blatt L, Mcswiggen JA;
PI
XX
XX WPI; 2002-706994/76.
PS
XX
XX The invention relates to nucleic acid molecules that modulate replication
CC of the West Nile Virus (WNV). The nucleic acid molecules are useful for
CC treating a condition related to WNV infection e.g. pancreatitis,
CC encephalitis, myocarditis, meningitis, neurologic infection, hepatitis,
CC liver failure, hepatocellular carcinoma or cirrhosis. The nucleic acid
CC molecule is selected from the group of ribozymes consisting of
CC Hammerhead, Inozyme, G-cleaver, DNazyme, Amberzyme and Zinzyme. The
CC nucleic acid molecules further comprise at least five ribose residues, at
CC least ten 2'-O-methyl modifications, phosphorothioate linkages on at
CC least three of the 5' terminal nucleotides and a 3' end modification of a
CC 3'-3' inverted abasic moiety. Nucleic acid molecules SEQ ID NO 1 to 37080
CC are claimed; however, SEQ ID NO 2194-2206 and 17502-17514 are not given
CC in the specification. The present sequence is that of a nucleic acid
CC molecule of the invention
XX
SQ Sequence 17 BP; 0 A; 8 C; 1 G; 0 T; 8 U; 0 Other;
```

XX 20-OCT-2000; 2000US-0242411P.  
PR (RIBO-) RIBOZYME PHARM INC.  
XX (BLAT/) BLATT L.  
PA (MCSW/) MCSWIGGEN J A.  
PA  
XX Blatt L, Mcswiggen JA;  
PI WPI; 2002-706994/76.  
XX  
DR  
XX  
XX The invention relates to nucleic acid molecules that modulate replication  
CC of the West Nile Virus (WNV). The nucleic acid molecules are useful for  
CC treating a condition related to WNV infection e.g. pancreatitis,  
CC encephalitis, myocarditis, meningitis, neurologic infection, hepatitis,  
CC liver failure, hepatocellular carcinoma or cirrhosis. The nucleic acid  
CC molecule is selected from the group of ribozymes consisting of  
CC Hammerhead, Inozyme, G-cleaver, DNazyme, Amberzyme and Zinzyme. The  
CC nucleic acid molecules further comprise at least five ribose residues, at  
CC least ten 2'-O-methyl modifications, phosphorothioate linkages on at  
CC least three of the 5' terminal nucleotides and a 3' end modification of a  
CC 3'-3' inverted abasic moiety. Nucleic acid molecules SEQ ID NO 1 to 37080  
CC are claimed; however, SEQ ID NO 2194-2206 and 17502-17514 are not given  
CC in the specification. The present sequence is that of a nucleic acid  
CC molecule of the invention  
XX  
SQ Sequence 17 BP; 2 A; 6 C; 4 G; 0 T; 5 U; 0 Other;  
Query Match 0.8%; Score 13.8; DB 1; Length 17;  
Best Local Similarity 88.2%; Pred. No. 1.9e+02;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 1470 CCAGAGAGAGCTCTGCA 1486  
DB 17 CAAGAGGGAGCTCTGCA 1  
RESULT 340  
ACN05385/c  
ID ACN05385 standard; RNA; 17 BP.  
XX  
AC ACN05385;  
XX  
DT 22-APR-2004 (first entry)  
XX  
XX WNV DNazyme substrate SEQ ID NO 5388.  
DE  
XX WNV; West Nile Virus; antiinflammatory; cytostatic; hepatotropic;  
KW virucide; neuroprotective; antibacterial; replication; pancreatitis;  
KW encephalitis; myocarditis; meningitis; infection; hepatitis;  
KW liver failure; cancer; cirrhosis; Hammerhead; Inozyme; DNazyme;  
KW Amberzyme; Zinzyme; ss.  
XX  
OS West Nile Virus.  
XX  
PN WO200268637-A2.  
XX  
PD 06-SEP-2002.  
XX  
PF 19-OCT-2001; 2001WO-US048350.  
XX  
PR 20-OCT-2000; 2000US-0242411P.  
XX  
PA (RIBO-) RIBOZYME PHARM INC.  
PA (BLAT/) BLATT L.  
XX (MCSW/) MCSWIGGEN J A.  
XX

PI Blatt L, Mcswiggen JA;  
XX WPI; 2002-706994/76.  
XX  
PT New nucleic acid molecule that modulates replication of West Nile Virus  
PT (WNV), useful for treating a condition related to WNV infection e.g.  
PT pancreatitis, meningitis, hepatocellular carcinoma or cirrhosis.  
XX  
PS Claim 23; SEQ ID NO 5388; 495pp; English.  
XX  
CC The invention relates to nucleic acid molecules that modulate replication  
CC of the West Nile Virus (WNV). The nucleic acid molecules are useful for  
CC treating a condition related to WNV infection e.g. pancreatitis,  
CC encephalitis, myocarditis, meningitis, neurologic infection, hepatitis,  
CC liver failure, hepatocellular carcinoma or cirrhosis. The nucleic acid  
CC molecule is selected from the group of ribozymes consisting of  
CC Hammerhead, Inozyme, G-cleaver, DNazyme, Amberzyme and Zinzyme. The  
CC nucleic acid molecules further comprise at least five ribose residues, at  
CC least ten 2'-O-methyl modifications, phosphorothioate linkages on at  
CC least three of the 5' terminal nucleotides and a 3' end modification of a  
CC 3'-3' inverted abasic moiety. Nucleic acid molecules SEQ ID NO 1 to 37080  
CC are claimed; however, SEQ ID NO 2194-2206 and 17502-17514 are not given  
CC in the specification. The present sequence is that of a nucleic acid  
CC molecule of the invention  
XX  
SQ Sequence 17 BP; 3 A; 5 C; 7 G; 0 T; 2 U; 0 Other;  
Query Match 0.8%; Score 13.8; DB 1; Length 17;  
Best Local Similarity 88.2%; Pred. No. 1.9e+02;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 1232 CTCGGACGTTCTCCG 1248  
DB 17 CGCGGACGTTCCATCCG 1  
RESULT 341  
ACN08973  
ID ACN08973 standard; RNA; 17 BP.  
XX  
AC ACN08973;  
XX  
DT 22-APR-2004 (first entry)  
XX  
XX WNV minus strand Hammerhead Ribozyme substrate SEQ ID NO 8976.  
DE  
XX WNV; West Nile Virus; antiinflammatory; cytostatic; hepatotropic;  
KW virucide; neuroprotective; antibacterial; replication; pancreatitis;  
KW encephalitis; myocarditis; meningitis; infection; hepatitis;  
KW liver failure; cancer; cirrhosis; Hammerhead; Inozyme; DNazyme;  
KW Amberzyme; Zinzyme; ss.  
XX  
OS West Nile Virus.  
XX  
PN WO200268637-A2.  
XX  
PD 06-SEP-2002.  
XX  
PF 19-OCT-2001; 2001WO-US048350.  
XX  
PR 20-OCT-2000; 2000US-0242411P.  
XX  
PA (RIBO-) RIBOZYME PHARM INC.  
PA (BLAT/) BLATT L.  
XX (MCSW/) MCSWIGGEN J A.  
XX  
PI Blatt L, Mcswiggen JA;  
XX WPI; 2002-706994/76.  
XX  
PT New nucleic acid molecule that modulates replication of West Nile Virus  
PT (WNV), useful for treating a condition related to WNV infection e.g.  
PT pancreatitis, meningitis, hepatocellular carcinoma or cirrhosis.  
XX

XX	PS	Claim 23; SEQ ID NO 8976; 495pp; English.	CC	identifying, quantifying and/or amplifying a nucleic acid, e.g. as one component of a gene chip, in vitro as (anti)sense reagents, and for
XX	CC	The invention relates to nucleic acid molecules that modulate replication of the West Nile Virus (WNV). The nucleic acid molecules are useful for	CC	production of recombinant polypeptides. Any of the nucleic acids, and for
CC	CC	treating a condition related to WNV infection e.g. pancreatitis, encephalitis, myocarditis, meningitis, neurologic infection, hepatitis, liver failure, hepatocellular carcinoma or cirrhosis. The nucleic acid	CC	polypeptides, vectors containing the nucleic acids, cells containing the
CC	CC	molecule is selected from the group of ribozymes consisting of Hammerhead, inozyme, G-cleaver, DNazyme, Amberzyme and zincyme. The	CC	vector or antibodies directed against the polypeptides are useful for
CC	CC	nucleic acid molecules further comprise at least five ribose residues, at least ten 2'-O-methyl modifications, phosphorothioate linkages on at	CC	preparation of pharmaceuticals for prevention and/or treatment of viral
CC	CC	least three of the 5' terminal nucleotides and a 3' end modification of a 3'-3' inverted abasic moiety. Nucleic acid molecules SEQ ID NO 1 to 37080	CC	diseases that are characterised by development of tumours or cell
CC	CC	are claimed; however, SEQ ID NO 2194-2206 and 17502-17514 are not given in the specification. The present sequence is that of a nucleic acid	CC	diseases that are characterised by development of tumours or cell
CC	CC	molecule of the invention	CC	degeneration, specifically cancer but also Alzheimer's disease and
XX	SQ	Sequence 17 BP; 3 A; 4 C; 4 G; 0 T; 6 U; 0 Other;	CC	schizophrenia. Analysis of the expression of the 17 mer nucleic acids in
			CC	patient samples is useful for diagnosis and/or prognosis of these
			CC	diseases. The polypeptides can also be used to generate antibodies, and
			CC	both the polypeptide and antibodies are useful as components of protein
			CC	chips. The nucleic acid sequences of the invention can be used in gene
			CC	therapy. This polynucleotide sequence represents a tumour suppression
			CC	related human fukutin oligonucleotide of the invention
			XX	
			SQ	Sequence 17 BP; 4 A; 7 C; 2 G; 4 T; 0 U; 0 Other;
			Query Match	0.8%; Score 13.8; DB 1; Length 17;
			Best Local Similarity	88.2%; Pred. No. 1.9e+02;
			Matches	15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY	1226	TTCTGACTCGGACGTTTC 1242	QY	374 CTGGGAAGAGTGTAAGC 390
DB	1	UUCUGAGUGGACAUUC 17	DB	17 CTGGGAAGAGTGTAAGC 1
			RESULT 343	
			ABT37737	
ID	ABT34420/c		ID	ABT37737 standard; DNA; 17 BP.
XX	AC	ABT34420 standard; DNA; 17 BP.	XX	ABT37737;
AC	ABT34420;		XX	12-JUN-2003 (first entry)
XX	XX		XX	Tumour suppression related human fukutin oligo SEQ ID No 3374.
DT	12-JUN-2003 (first entry)		DT	
DE	Tumour suppression related human fukutin oligo SEQ ID No 57.		DE	
XX	Cytostatic; virucide; neuroprotective; nootropic; neuroleptic; gene chip;		XX	Cytostatic; virucide; neuroprotective; nootropic; neuroleptic; gene chip;
XX	antisense; sense; tumour; cell degeneration; cancer; Alzheimer's disease;		XX	antisense; sense; tumour; cell degeneration; cancer; Alzheimer's disease;
XX	schizophrenia; protein chip; gene therapy; tumour suppression;		XX	schizophrenia; protein chip; gene therapy; tumour suppression;
XX	human fukutin; ds.		XX	human fukutin; ds.
XX	Homo sapiens.		XX	Homo sapiens.
XX	WO2003025175-A2.		XX	WO2003025175-A2.
XX	27-MAR-2003.		XX	27-MAR-2003.
XX	17-SEP-2002; 2002WO-IB004208.		XX	17-SEP-2002; 2002WO-IB004208.
XX	17-SEP-2001; 2001FR-00011978.		XX	17-SEP-2001; 2001FR-00011978.
XX	(MOLE-) MOLECULAR ENGINES LAB.		XX	(MOLE-) MOLECULAR ENGINES LAB.
XX	Telerman A, Amson R, Tuijnder M;		XX	Telerman A, Amson R, Tuijnder M;
XX	WPI; 2003-313353/30.		XX	WPI; 2003-313353/30.
XX	New isolated nucleic acid, useful for treating viral diseases associated		XX	New isolated nucleic acid, useful for treating viral diseases associated
XX	with tumors and cell degeneration, also related polypeptides, antibodies		XX	with tumors and cell degeneration, also related polypeptides, antibodies
XX	and transfected cells.		XX	and transfected cells.
XX	Disclosure; Page 40; 720pp; French.		XX	Disclosure; Page 428; 720pp; French.
XX	The invention relates to a novel isolated 17 mer nucleic acid sequence,		XX	The invention relates to a novel isolated 17 mer nucleic acid sequence,
XX	given in the specification, a sequence containing at least 15 consecutive		XX	given in the specification, a sequence containing at least 15 consecutive
XX	nucleotides from the 17 mer sequence, a sequence with, after optimal		XX	nucleotides from the 17 mer sequence, a sequence with, after optimal
XX	alignment, at least 80 % identity to the 17 mer sequence, a sequence that		XX	alignment, at least 80 % identity to the 17 mer sequence, a sequence that
XX	hybridizes to them under highly stringent conditions, or the complement		XX	hybridizes to them under highly stringent conditions, or the complement
XX	of any of them, or the corresponding RNA. The novel isolated nucleic		XX	of any of them, or the corresponding RNA. The novel isolated nucleic
XX	acids of the invention are useful as probes and primers for detecting,		XX	acids of the invention are useful as probes and primers for detecting,





PR	15-AUG-1994;	9AUS-00291932.	
PR	23-DEC-1996;	96US-00777916.	
XX	(STIN/) STINCHOMB D T.		
PA	(MCSW/) MCSWIGGEN J.		
PA	(DRAP/) DRAPER K G.		
XX	Stinchcomb DT, Mcswiggen J, Draper KG;		
XX	WPI; 2003-340953/32.		
XX	Novel enzymatic nucleic acid molecules which down regulates expression of		
PT	a sequence encoding a subunit of nuclear factor kappa B useful for		
PT	treating cancer, inflammatory disorders and autoimmune diseases.		
XX	Claim 3; Page 39; 72pp; English.		
XX	The invention describes an enzymatic nucleic acid molecule (I) which down		
CC	regulates expression of a sequence encoding a subunit of nuclear factor		
CC	kappa B (NFkB), where (I) is an inozyme, zinzyme, G-cleaver or amberzyme		
CC	configuration. The enzymatic nucleic acid molecule is adapted to treat		
CC	cancer and is useful for down-regulating REL-A activity in a cell, for		
CC	treating a patient having a condition associated with the level of REL-A.		
CC	(I) is useful for cleaving RNA comprising a sequence of REL-A gene, in		
CC	the presence of a divalent cation, especially Mg <sup>2+</sup> . The enzymatic and		
CC	antisense nucleic acid molecules are useful for treating breast, lung,		
CC	prostate, colorectal, brain, oesophageal, stomach, bladder, pancreatic,		
CC	cervical, head and neck, ovarian cancer, melanoma, lymphoma, glioma or		
CC	multidrug resistant cancer. The method involves use of other drug		
CC	therapies such as monoclonal antibodies, REL-A-specific inhibitors or		
CC	chemotherapy including paclitaxel, docetaxel, cisplatin, methotrexate,		
CC	cyclophosphamide, doxorubin, fluorouracil carboplatin, edatrexate,		
CC	acid molecules are also useful for treating inflammatory disease such as		
CC	rheumatoid arthritis, restenosis, asthma, Crohn's disease, diabetes,		
CC	obesity, autoimmune disease, lupus, multiple sclerosis, transplant/graft		
CC	rejection, gene therapy applications, ischaemia/reperfusion injury		
CC	(central nervous system (CNS) and myocardial), glomerulonephritis,		
CC	sepsis, allergic airway inflammation, inflammatory bowel disease or		
CC	infection. This sequence represents the substrate of a novel enzymatic		
CC	nucleic acid molecule		
XX	Sequence 17 BP; 4 A; 7 C; 5 G; 0 T; 1 U; 0 Other;		
SQ			
	Query Match 0.8%; Score 13.8; DB 1; Length 17;		
	Best Local Similarity 82.4%; Pred. No. 1.9e+02;		
	Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;		
OY	1502 AGCCCCCAGCTCCAGG 1518		
DB	1 AGACCCCGCUGCAGG 17		
	RESULT 346		
ACAO7701			
ID	ACAO7701 standard; RNA; 17 BP.		
XX	ACA07701;		
XX	03-JUN-2003 (first entry)		
DE	NFKB sub-unit modulating zinzyme substrate #100.		
XX	Enzymatic nucleic acid; nuclear factor kappa B; NFKB; inozyme; zinzyme;		
KW	G-cleaver; amberzyme; cancer; REL-A activity; breast cancer; human;		
KW	lung cancer; prostate cancer; colorectal cancer; brain cancer;		
KW	oesophageal cancer; stomach cancer; bladder cancer; pancreatic cancer;		
KW	cervical cancer; head and neck cancer; ovarian cancer; melanoma;		
KW	lymphoma; glioma; multidrug resistant cancer; REL-A-specific inhibitor;		
KW	chemotherapy; paclitaxel; docetaxel; cisplatin; methotrexate;		
KW	cyclophosphamide; doxorubin; fluorouracil carboplatin; edatrexate;		
KW	gemcitabine; radiation therapy; inflammatory disease; asthma; diabetes;		
KW	rheumatoid arthritis; restenosis; Crohn's disease; obesity; ischaemia;		
KW	gene therapy; autoimmune disease; lupus; multiple sclerosis; sepsis;		
KW	transplant/graft rejection; reperfusion injury; glomerulonephritis;		
KW	allergic airway inflammation; inflammatory bowel disease; infection; ss.		
OS	Homo sapiens.		
XX	US2002177568-A1.		
XX	28-NOV-2002.		
XX	23-MAY-2001; 2001US-00864785.		
XX	07-DEC-1992; 92US-00987132.		
PR	18-MAY-1994; 94US-00245466.		
PR	15-AUG-1994; 94US-00291932.		
PR	23-DEC-1996; 96US-00777916.		
XX	(STIN/) STINCHOMB D T.		
PA	(MCSW/) MCSWIGGEN J.		
PA	(DRAP/) DRAPER K G.		
XX	Stinchcomb DT, Mcswiggen J, Draper KG;		
XX	WPI; 2003-340953/32.		
XX	Novel enzymatic nucleic acid molecules which down regulates expression of		
PT	a sequence encoding a subunit of nuclear factor kappa B useful for		
PT	treating cancer, inflammatory disorders and autoimmune diseases.		
XX	Claim 3; Page 39; 72pp; English.		
XX	The invention describes an enzymatic nucleic acid molecule (I) which down		
CC	regulates expression of a sequence encoding a subunit of nuclear factor		
CC	kappa B (NFkB), where (I) is an inozyme, zinzyme, G-cleaver or amberzyme		
CC	configuration. The enzymatic nucleic acid molecule is adapted to treat		
CC	cancer and is useful for down-regulating REL-A activity in a cell, for		
CC	treating a patient having a condition associated with the level of REL-A.		
CC	(I) is useful for cleaving RNA comprising a sequence of REL-A gene, in		
CC	the presence of a divalent cation, especially Mg <sup>2+</sup> . The enzymatic and		
CC	antisense nucleic acid molecules are useful for treating breast, lung,		
CC	prostate, colorectal, brain, oesophageal, stomach, bladder, pancreatic,		
CC	cervical, head and neck, ovarian cancer, melanoma, lymphoma, glioma or		
CC	multidrug resistant cancer. The method involves use of other drug		
CC	therapies such as monoclonal antibodies, REL-A-specific inhibitors or		
CC	chemotherapy including paclitaxel, docetaxel, cisplatin, methotrexate,		
CC	cyclophosphamide, doxorubin, fluorouracil carboplatin, edatrexate,		
CC	gemcitabine or radiation therapy. The enzymatic and antisense nucleic		
CC	acid molecules are also useful for treating inflammatory disease such as		
CC	rheumatoid arthritis, restenosis, asthma, Crohn's disease, diabetes,		
CC	obesity, autoimmune disease, lupus, multiple sclerosis, transplant/graft		
CC	rejection, gene therapy applications, ischaemia/reperfusion injury		
CC	(central nervous system (CNS) and myocardial), glomerulonephritis,		
CC	sepsis, allergic airway inflammation, inflammatory bowel disease or		
CC	infection. This sequence represents the substrate of a novel enzymatic		
CC	nucleic acid molecule		
XX	Sequence 17 BP; 2 A; 9 C; 4 G; 0 T; 2 U; 0 Other;		
SQ			
	Query Match 0.8%; Score 13.8; DB 1; Length 17;		
	Best Local Similarity 82.4%; Pred. No. 1.9e+02;		
	Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;		
OY	1506 CCCAGCCTCCACGCCCC 1522		
DB	1 CCCAGCUGCAGGCCUCC 17		
	RESULT 347		
ACAO8217			
ID	ACAO8217 standard; RNA; 17 BP.		
XX	ACA08217;		
XX	ACA08217;		

DT 03-JUN-2003 (first entry)  
DE NFKB sub-unit modulating DNazyme substrate #24.  
XX  
XX Enzymatic nucleic acid; nuclear factor kappa B; NFKB; inozyme; zinzyme;  
KW G-cleaver; amberzyme; cancer; REL-A activity; breast cancer; human;  
KW lung cancer; prostate cancer; colorectal cancer; brain cancer;  
KW oesophageal cancer; stomach cancer; bladder cancer; pancreatic cancer;  
KW cervical cancer; head and neck cancer; ovarian cancer; melanoma;  
KW lymphoma; glioma; multidrug resistant cancer; REL-A-specific inhibitor;  
KW chemotherapy; paclitaxel; docetaxel; cisplatin; methotrexate;  
KW cyclophosphamide; doxorubicin; fluorouracil carboplatin; edatrexate;  
KW gemcitabine; radiation therapy; inflammatory disease; asthma; diabetes;  
KW rheumatoid arthritis; restenosis; Crohn's disease; obesity; ischaemia;  
KW gene therapy; autoimmune disease; lupus; multiple sclerosis; sepsis;  
KW transplant/graft rejection; reperfusion injury; glomerulonephritis;  
KW allergic airway inflammation; inflammatory bowel disease; infection; ss.  
XX  
XX Homo sapiens.  
XX  
XX US2002177568-A1.  
XX  
XX 28-NOV-2002.  
XX  
XX 23-MAY-2001; 2001US-00864785.  
XX  
XX 07-DEC-1992; 92US-00987132.  
XX 18-MAY-1994; 94US-00245466.  
XX 15-AUG-1994; 94US-00291932.  
XX 23-DEC-1996; 96US-00777916.  
XX  
XX (STIN/) STINCHCOMB D T.  
XX (MCSW/) MCSWIGGEN J.  
XX (DRAP/) DRAPER K G.  
XX  
XX Stinchcomb DT, Mcswiggen J, Draper KG;  
XX WPI; 2003-340953/32.  
XX  
XX Novel enzymatic nucleic acid molecules which down regulates expression of  
XX a sequence encoding a subunit of nuclear factor kappa B useful for  
XX treating cancer, inflammatory disorders and autoimmune diseases.  
XX  
XX Claim 3; Page 43; 72pp; English.  
XX  
XX The invention describes an enzymatic nucleic acid molecule (I) which down  
XX regulates expression of a sequence encoding a subunit of nuclear factor  
XX kappa B (NFKB), where (I) is an inozyme, zinzyme, G-cleaver or amberzyme  
XX configuration. The enzymatic nucleic acid molecule is adapted to treat  
XX cancer and is useful for down-regulating REL-A activity in a cell, for  
XX treating a patient having a condition associated with the level of REL-A.  
XX (I) is useful for cleaving RNA comprising a sequence of REL-A gene, in  
XX the presence of a divalent cation, especially Mg<sup>2+</sup>. The enzymatic and  
XX antisense nucleic acid molecules are useful for treating breast, lung,  
XX prostate, colorectal, brain, oesophageal, stomach, bladder, pancreatic,  
XX cervical, head and neck, ovarian cancer, melanoma, lymphoma, glioma or  
XX multidrug resistant cancer. The method involves use of other drug  
XX therapies such as monoclonal antibodies, REL-A-specific inhibitors or  
XX chemotherapy including paclitaxel, docetaxel, cisplatin, methotrexate,  
XX cyclophosphamide, doxorubicin, fluorouracil carboplatin, edatrexate,  
XX gemcitabine or radiation therapy. The enzymatic and antisense nucleic  
XX acid molecules are also useful for treating inflammatory disease such as  
XX rheumatoid arthritis, restenosis, asthma, Crohn's disease, diabetes,  
XX obesity, autoimmune disease, lupus, multiple sclerosis, transplant/graft  
XX rejection, gene therapy applications, ischaemia/reperfusion injury  
XX (central nervous system (CNS) and myocardial), glomerulonephritis,  
XX sepsis, allergic airway inflammation, inflammatory bowel disease or  
XX infection. This sequence represents the substrate of a novel enzymatic  
XX nucleic acid molecule  
XX  
XX Sequence 17 BP; 6 A; 9 C; 0 G; 0 T; 2 U; 0 Other;  
XX  
XX Query Match 0.8%; Score 13.8; DB 1; Length 17;

Best Local Similarity 82.4%; Pred. No. 1.9e+02;  
Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
QY 989 CACCAACACCCCTCCC 1005  
DB 1 CAACACACCCCUCC 17  
  
RESULT 348  
ACAO6298  
ID ACA06298 standard; RNA; 17 BP.  
XX ACA06298;  
XX  
XX 03-JUN-2003 (first entry)  
XX  
XX NFKB sub-unit modulating inozyme substrate #117.  
XX  
XX Enzymatic nucleic acid; nuclear factor kappa B; NFKB; inozyme; zinzyme;  
KW G-cleaver; amberzyme; cancer; REL-A activity; breast cancer; human;  
KW lung cancer; prostate cancer; colorectal cancer; brain cancer;  
KW oesophageal cancer; stomach cancer; bladder cancer; pancreatic cancer;  
KW cervical cancer; head and neck cancer; ovarian cancer; melanoma;  
KW lymphoma; glioma; multidrug resistant cancer; REL-A-specific inhibitor;  
KW chemotherapy; paclitaxel; docetaxel; cisplatin; methotrexate;  
KW cyclophosphamide; doxorubicin; fluorouracil carboplatin; edatrexate;  
KW gemcitabine; radiation therapy; inflammatory disease; asthma; diabetes;  
KW rheumatoid arthritis; restenosis; Crohn's disease; obesity; ischaemia;  
KW gene therapy; autoimmune disease; lupus; multiple sclerosis; sepsis;  
KW transplant/graft rejection; reperfusion injury; glomerulonephritis;  
KW allergic airway inflammation; inflammatory bowel disease; infection; ss.  
XX  
XX Homo sapiens.  
XX  
XX US2002177568-A1.  
XX  
XX 28-NOV-2002.  
XX  
XX 23-MAY-2001; 2001US-00864785.  
XX  
XX 07-DEC-1992; 92US-00987132.  
XX 18-MAY-1994; 94US-00245466.  
XX 15-AUG-1994; 94US-00291932.  
XX 23-DEC-1996; 96US-00777916.  
XX  
XX (STIN/) STINCHCOMB D T.  
XX (MCSW/) MCSWIGGEN J.  
XX (DRAP/) DRAPER K G.  
XX  
XX Stinchcomb DT, Mcswiggen J, Draper KG;  
XX WPI; 2003-340953/32.  
XX  
XX Novel enzymatic nucleic acid molecules which down regulates expression of  
XX a sequence encoding a subunit of nuclear factor kappa B useful for  
XX treating cancer, inflammatory disorders and autoimmune diseases.  
XX  
XX Claim 3; Page 29; 72pp; English.  
XX  
XX The invention describes an enzymatic nucleic acid molecule (I) which down  
XX regulates expression of a sequence encoding a subunit of nuclear factor  
XX kappa B (NFKB), where (I) is an inozyme, zinzyme, G-cleaver or amberzyme  
XX configuration. The enzymatic nucleic acid molecule is adapted to treat  
XX cancer and is useful for down-regulating REL-A activity in a cell, for  
XX treating a patient having a condition associated with the level of REL-A.  
XX (I) is useful for cleaving RNA comprising a sequence of REL-A gene, in  
XX the presence of a divalent cation, especially Mg<sup>2+</sup>. The enzymatic and  
XX antisense nucleic acid molecules are useful for treating breast, lung,  
XX prostate, colorectal, brain, oesophageal, stomach, bladder, pancreatic,  
XX cervical, head and neck, ovarian cancer, melanoma, lymphoma, glioma or  
XX multidrug resistant cancer. The method involves use of other drug  
XX therapies such as monoclonal antibodies, REL-A-specific inhibitors or  
XX chemotherapy including paclitaxel, docetaxel, cisplatin, methotrexate,  
XX cyclophosphamide, doxorubicin, fluorouracil carboplatin, edatrexate,  
XX gemcitabine or radiation therapy. The enzymatic and antisense nucleic  
XX acid molecules are also useful for treating inflammatory disease such as  
XX rheumatoid arthritis, restenosis, asthma, Crohn's disease, diabetes,  
XX obesity, autoimmune disease, lupus, multiple sclerosis, transplant/graft  
XX rejection, gene therapy applications, ischaemia/reperfusion injury  
XX (central nervous system (CNS) and myocardial), glomerulonephritis,  
XX sepsis, allergic airway inflammation, inflammatory bowel disease or  
XX infection. This sequence represents the substrate of a novel enzymatic  
XX nucleic acid molecule

CC cyclophosphamide, doxorubin, fluorouracil carboplatin, edatrexate,  
 CC gencitabine or radiation therapy. The enzymatic and antisense nucleic  
 CC acid molecules are also useful for treating inflammatory disease such as  
 CC rheumatoid arthritis, restenosis, asthma, Crohn's disease, diabetes,  
 CC obesity, autoimmune disease, lupus, multiple sclerosis, transplant/graft  
 CC rejection, gene therapy applications, ischaemia/reperfusion injury  
 CC (central nervous system (CNS) and myocardial), glomerulonephritis,  
 CC sepsis, allergic airway inflammation, inflammatory bowel disease or  
 CC nucleic acid molecule  
 XX  
 SQ Sequence 17 BP; 6 A; 8 C; 1 G; 0 T; 2 U; 0 Other;  
 Query Match 0.8%; Score 13.8; DB 1; Length 17;  
 Best Local Similarity 82.4%; Pred. No. 1.9e+02;  
 Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
 QY 992 CAACAACCCCTCCAGG 1008  
 Db 1 CAACAACCCCTCCAGG 17  
 RESULT 349  
 ID ACA06394 standard; RNA; 17 BP.  
 AC ACA06394;  
 XX  
 DT 03-JUN-2003 (first entry)  
 XX  
 DE NFkB sub-unit modulating inozyme substrate #213.  
 XX  
 KW Enzymatic nucleic acid; nuclear factor kappa B; NFkB; inozyme; zinzyme;  
 KW G-cleaver; amberzyme; cancer; REL-A activity; breast cancer; human;  
 KW lung cancer; prostate cancer; colorectal cancer; brain cancer;  
 KW oesophageal cancer; stomach cancer; bladder cancer; pancreatic cancer;  
 KW cervical cancer; head and neck cancer; ovarian cancer; melanoma;  
 KW lymphoma; glioma; multidrug resistant cancer; REL-A-specific inhibitor;  
 KW chemotheraphy; paclitaxel; docetaxel; cisplatin; methotrexate;  
 KW cyclophosphamide; doxorubin; fluorouracil carboplatin; edatrexate;  
 KW gencitabine; radiation therapy; inflammatory disease; asthma; diabetes;  
 KW rheumatoid arthritis; restenosis; Crohn's disease; obesity; ischaemia;  
 KW gene therapy; autoimmune disease; lupus; multiple sclerosis; sepsis;  
 KW transplant/graft rejection; reperfusion injury; glomerulonephritis;  
 KW allergic airway inflammation; inflammatory bowel disease; infection; ss.  
 OS  
 XX Homo sapiens.  
 XX  
 PN US2002177568-A1.  
 XX  
 XX 28-NOV-2002.  
 XX  
 XX 23-MAY-2001; 2001US-00864785.  
 XX  
 PR 07-DEC-1992; 92US-00987132.  
 PR 18-MAY-1994; 94US-00245466.  
 PR 15-AUG-1994; 94US-00291932.  
 PR 23-DEC-1996; 96US-00777916.  
 XX  
 XX (STIN/) STINCHOMB D T.  
 PA (MCSW/) MCSWIGGEN J.  
 PA (DRAP/) DRAPER K G.  
 XX  
 XX Stinchcomb DT, Mcswiggen J, Draper KG;  
 PI  
 DR  
 XX WPI; 2003-340953/32.  
 XX  
 XX Novel enzymatic nucleic acid molecules which down regulates expression of  
 PT a sequence encoding a subunit of nuclear factor kappa B useful for  
 PT treating cancer, inflammatory disorders and autoimmune diseases.  
 XX  
 XX Claim 3; Page 30; 72pp; English.  
 PS  
 XX

CC The invention describes an enzymatic nucleic acid molecule (I) which down  
 CC regulates expression of a sequence encoding a subunit of nuclear factor  
 CC kappa B (NFkB), where (I) is an inozyme, zinzyme, G-cleaver or amberzyme  
 CC configuration. The enzymatic nucleic acid molecule is adapted to treat  
 CC cancer and is useful for down-regulating REL-A activity in a cell, for  
 CC treating a patient having a condition associated with the level of REL-A.  
 CC (I) is useful for cleaving RNA comprising a sequence of REL-A gene, in  
 CC the presence of a divalent cation, especially Mg<sup>2+</sup>. The enzymatic and  
 CC antisense nucleic acid molecules are useful for treating breast, lung,  
 CC prostate, colorectal, brain, oesophageal, stomach, bladder, pancreatic,  
 CC cervical, head and neck, ovarian cancer, melanoma, lymphoma, glioma or  
 CC multidrug resistant cancer. The method involves use of other drug  
 CC therapies such as monoclonal antibodies, REL-A-specific inhibitors or  
 CC chemotheraphy including paclitaxel, docetaxel, cisplatin, methotrexate,  
 CC cyclophosphamide, doxorubin, fluorouracil carboplatin, edatrexate,  
 CC gencitabine or radiation therapy. The enzymatic and antisense nucleic  
 CC acid molecules are also useful for treating inflammatory disease such as  
 CC rheumatoid arthritis, restenosis, asthma, Crohn's disease, diabetes,  
 CC obesity, autoimmune disease, lupus, multiple sclerosis, transplant/graft  
 CC rejection, gene therapy applications, ischaemia/reperfusion injury  
 CC (central nervous system (CNS) and myocardial), glomerulonephritis,  
 CC sepsis, allergic airway inflammation, inflammatory bowel disease or  
 CC infection. This sequence represents the substrate of a novel enzymatic  
 CC nucleic acid molecule  
 XX  
 SQ Sequence 17 BP; 4 A; 8 C; 4 G; 0 T; 1 U; 0 Other;  
 Query Match 0.8%; Score 13.8; DB 1; Length 17;  
 Best Local Similarity 82.4%; Pred. No. 1.9e+02;  
 Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
 QY 1501 CAGCCCCCAGCTCCAG 1517  
 Db 1 CAGACCCCGCCGCGAG 17  
 RESULT 350  
 ID ACA06396 standard; RNA; 17 BP.  
 AC ACA06396;  
 XX  
 DT 03-JUN-2003 (first entry)  
 XX  
 DE NFkB sub-unit modulating inozyme substrate #215.  
 XX  
 KW Enzymatic nucleic acid; nuclear factor kappa B; NFkB; inozyme; zinzyme;  
 KW G-cleaver; amberzyme; cancer; REL-A activity; breast cancer; human;  
 KW lung cancer; prostate cancer; colorectal cancer; brain cancer;  
 KW oesophageal cancer; stomach cancer; bladder cancer; pancreatic cancer;  
 KW cervical cancer; head and neck cancer; ovarian cancer; melanoma;  
 KW lymphoma; glioma; multidrug resistant cancer; REL-A-specific inhibitor;  
 KW chemotheraphy; paclitaxel; docetaxel; cisplatin; methotrexate;  
 KW cyclophosphamide; doxorubin; fluorouracil carboplatin; edatrexate;  
 KW gencitabine; radiation therapy; inflammatory disease; asthma; diabetes;  
 KW rheumatoid arthritis; restenosis; Crohn's disease; obesity; ischaemia;  
 KW gene therapy; autoimmune disease; lupus; multiple sclerosis; sepsis;  
 KW transplant/graft rejection; reperfusion injury; glomerulonephritis;  
 KW allergic airway inflammation; inflammatory bowel disease; infection; ss.  
 OS  
 XX Homo sapiens.  
 XX  
 PN US2002177568-A1.  
 XX  
 XX 28-NOV-2002.  
 XX  
 XX 23-MAY-2001; 2001US-00864785.  
 XX  
 PR 07-DEC-1992; 92US-00987132.  
 PR 18-MAY-1994; 94US-00245466.  
 PR 15-AUG-1994; 94US-00291932.  
 PR 23-DEC-1996; 96US-00777916.  
 XX

PA (STIN/) STINCHOMB D T.  
 PA (MCSW/) MCSWIGGEN J.  
 PA (DRAP/) DRAPER K G.  
 XX  
 XX Stinchcomb DT, Mcswiggen J, Draper KG;  
 XX  
 XX WPI; 2003-340953/32.  
 XX  
 XX Novel enzymatic nucleic acid molecules which down regulates expression of  
 PT a sequence encoding a subunit of nuclear factor kappa B useful for  
 PT treating cancer, inflammatory disorders and autoimmune diseases.  
 PT  
 PT  
 XX Claim 3; Page 30; 72pp; English.  
 XX  
 XX The invention describes an enzymatic nucleic acid molecule (I) which down  
 CC regulates expression of a sequence encoding a subunit of nuclear factor  
 CC kappa B (NFKB), where (I) is an inozyme, zinzyme, G-cleaver or amberzyme  
 CC configuration. The enzymatic nucleic acid molecule is adapted to treat  
 CC cancer and is useful for down-regulating REL-A activity in a cell, for  
 CC treating a patient having a condition associated with the level of REL-A.  
 CC (I) is useful for cleaving RNA comprising a sequence of REL-A gene, in  
 CC the presence of a divalent cation, especially Mg<sup>2+</sup>. The enzymatic and  
 CC antisense nucleic acid molecules are useful for treating breast, lung,  
 CC prostate, colorectal, brain, oesophageal, stomach, bladder, pancreatic,  
 CC multidrug resistant cancer. The method involves use of other drug  
 CC therapies such as monoclonal antibodies, REL-A-specific inhibitors or  
 CC chemotherapy including paclitaxel, docetaxel, cisplatin, methotrexate,  
 CC cyclophosphamide, doxorubicin, fluorouracil carboplatin, edatrexate,  
 CC gemcitabine or radiation therapy. The enzymatic and antisense nucleic  
 CC acid molecules are also useful for treating inflammatory disease such as  
 CC rheumatoid arthritis, restenosis, asthma, Crohn's disease, diabetes,  
 CC obesity, autoimmune disease, lupus, multiple sclerosis, transplant/graft  
 CC rejection, gene therapy applications, ischaemia/reperfusion injury  
 CC (central nervous system (CNS) and myocardial), glomerulonephritis,  
 CC sepsis, allergic airway inflammation, inflammatory bowel disease or  
 CC infection. This sequence represents the substrate of a novel enzymatic  
 CC nucleic acid molecule  
 XX  
 XX Sequence 17 BP; 2 A; 9 C; 4 G; 0 T; 2 U; 0 Other;  
 SQ  
 Query Match 0.8%; Score 13.8; DB 1; Length 17;  
 Best Local Similarity 82.4%; Pred. No. 1.9e+02;  
 Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
 QY 1505 CCCAGCCTCCAGGCC 1521  
 Db 1 CCCAGCCGCGAGGCU 17  
 RESULT 351  
 ID ACA06517 standard; RNA; 17 BP.  
 XX  
 XX ACA06517;  
 XX  
 XX 03-JUN-2003 (first entry)  
 XX  
 XX NFKB sub-unit modulating inozyme substrate #336.  
 XX  
 XX Enzymatic nucleic acid; nuclear factor kappa B; NFKB; inozyme; zinzyme;  
 KW G-cleaver; amberzyme; cancer; REL-A activity; breast cancer; human;  
 KW lung cancer; prostate cancer; colorectal cancer; brain cancer;  
 KW oesophageal cancer; stomach cancer; bladder cancer; pancreatic cancer;  
 KW cervical cancer; head and neck cancer; ovarian cancer; melanoma;  
 KW lymphoma; glioma; multidrug resistant cancer; REL-A-specific inhibitor;  
 KW chemotherapy; paclitaxel; docetaxel; cisplatin; methotrexate;  
 KW cyclophosphamide; doxorubicin; fluorouracil carboplatin; edatrexate;  
 KW gemcitabine; radiation therapy; inflammatory disease; asthma; diabetes;  
 KW rheumatoid arthritis; restenosis; Crohn's disease; obesity; ischaemia;  
 KW gene therapy; autoimmune disease; lupus; multiple sclerosis; sepsis;  
 KW transplant/graft rejection; reperfusion injury; glomerulonephritis;  
 KW allergic airway inflammation; inflammatory bowel disease; infection; ss.

XX Homo sapiens.  
 XX US2002177568-A1.  
 XX 28-NOV-2002.  
 XX  
 XX 23-MAY-2001; 2001US-00864785.  
 XX  
 XX 07-DEC-1992; 92US-00987132.  
 XX 18-MAY-1994; 94US-00245466.  
 XX 15-AUG-1994; 94US-00291932.  
 XX 23-DEC-1996; 96US-00777916.  
 XX  
 XX (STIN/) STINCHOMB D T.  
 XX (MCSW/) MCSWIGGEN J.  
 XX (DRAP/) DRAPER K G.  
 XX  
 XX Stinchcomb DT, Mcswiggen J, Draper KG;  
 XX  
 XX WPI; 2003-340953/32.  
 XX  
 XX Novel enzymatic nucleic acid molecules which down regulates expression of  
 PT a sequence encoding a subunit of nuclear factor kappa B useful for  
 PT treating cancer, inflammatory disorders and autoimmune diseases.  
 PT  
 PT  
 XX Claim 3; Page 32; 72pp; English.  
 XX  
 XX The invention describes an enzymatic nucleic acid molecule (I) which down  
 CC regulates expression of a sequence encoding a subunit of nuclear factor  
 CC kappa B (NFKB), where (I) is an inozyme, zinzyme, G-cleaver or amberzyme  
 CC configuration. The enzymatic nucleic acid molecule is adapted to treat  
 CC cancer and is useful for down-regulating REL-A activity in a cell, for  
 CC treating a patient having a condition associated with the level of REL-A.  
 CC (I) is useful for cleaving RNA comprising a sequence of REL-A gene, in  
 CC the presence of a divalent cation, especially Mg<sup>2+</sup>. The enzymatic and  
 CC antisense nucleic acid molecules are useful for treating breast, lung,  
 CC prostate, colorectal, brain, oesophageal, stomach, bladder, pancreatic,  
 CC cervical, head and neck, ovarian cancer, melanoma, lymphoma, glioma or  
 CC multidrug resistant cancer. The method involves use of other drug  
 CC therapies such as monoclonal antibodies, REL-A-specific inhibitors or  
 CC chemotherapy including paclitaxel, docetaxel, cisplatin, methotrexate,  
 CC cyclophosphamide, doxorubicin, fluorouracil carboplatin, edatrexate,  
 CC gemcitabine or radiation therapy. The enzymatic and antisense nucleic  
 CC acid molecules are also useful for treating inflammatory disease such as  
 CC rheumatoid arthritis, restenosis, asthma, Crohn's disease, diabetes,  
 CC obesity, autoimmune disease, lupus, multiple sclerosis, transplant/graft  
 CC rejection, gene therapy applications, ischaemia/reperfusion injury  
 CC (central nervous system (CNS) and myocardial), glomerulonephritis,  
 CC sepsis, allergic airway inflammation, inflammatory bowel disease or  
 CC infection. This sequence represents the substrate of a novel enzymatic  
 CC nucleic acid molecule  
 XX  
 XX Sequence 17 BP; 2 A; 11 C; 3 G; 0 T; 1 U; 0 Other;  
 SQ  
 Query Match 0.8%; Score 13.8; DB 1; Length 17;  
 Best Local Similarity 82.4%; Pred. No. 1.9e+02;  
 Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
 QY 1505 CCCAGCCTCCAGGCC 1521  
 Db 1 CCCAGCCGCGAGGCU 17  
 RESULT 352  
 ID ADA99701 standard; DNA; 17 BP.  
 XX  
 XX ADA99701;  
 XX  
 XX 20-NOV-2003 (first entry)  
 XX  
 XX Human MD23 scanning oligonucleotide SEQ ID 690.

```
XX Cytostatic; immunostimulant; gene therapy; vaccine; human;
KW zinc finger protein; MD23; MD24; MD27; MD212; chromosome 7q22.1;
KW chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer;
KW developmental disorder; ss.
OS Homo sapiens.
XX
XX EP1281758-A2.
XX
XX 05-FEB-2003.
XX
XX 30-JUL-2002; 2002EP-00016874.
XX
XX 02-AUG-2001; 2001US-00922181.
XX
XX (AEOM-) AEOMICA INC.
XX
XX Shannon M, Gu Y, Nguyen C;
XX
XX WPI; 2003-423107/40.
XX
XX New zinc finger-containing proteins and nucleic acids, useful in
PT manufacturing a medicament for treating or preventing a disorder
PT associated with decreased or increased expression or activity of MD23,
PT MD24, MD27 or MD212, e.g. cancer.
XX
XX Example 8; SEQ ID NO 690; 103pp; English.
XX
XX The present invention relates to novel human zinc finger-containing
CC proteins and their coding sequences: MD23, MD24, MD27, MD212. MD23 is
CC encoded at chromosome 7q22.1, MD24 is encoded at chromosome 6p21.3-22.2,
CC MD27 is encoded at chromosome 16p11.2 and MD212 is encoded at chromosome
CC 15q26.1. The MD23, MD24, MD27, and MD212 sequences are useful in therapy,
CC or in manufacturing a medicament for treating or preventing a disorder
CC associated with decreased or increased expression or activity of MD23,
CC MD24, MD27, or MD212, e.g. cancer or developmental disorders. The nucleic
CC acids and proteins are also useful for diagnosing or monitoring a disease
CC caused by altered expression of MD23, MD24, MD27, or MD212. The nucleic
CC acids can also be used as probes to detect and characterize gross
CC alterations in MD23, MD24, MD27, or MD212 genetic locus. The probes are
CC useful in constructing microarrays for measuring gene expression. The
CC proteins are useful as therapeutic agents for gene therapy or as
CC vaccines. The present sequence was used to illustrate the invention.
XX
XX Sequence 17 BP; 5 A; 4 C; 6 G; 2 T; 0 U; 0 Other;
SQ
Query Match 0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.9e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 788 CCTTGAGATGATACACG 804
Db 1 CCTGGAGATGAGACG 17
RESULT 353
ADB00467/C
ID ADB00467 standard; DNA; 17 BP.
XX
XX ADB00467;
XX
XX 20-NOV-2003 (first entry)
XX
XX Human MD23 scanning oligonucleotide SEQ ID 1453.
XX
XX Cytostatic; immunostimulant; gene therapy; vaccine; human;
KW zinc finger protein; MD23; MD24; MD27; MD212; chromosome 7q22.1;
KW chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer;
KW developmental disorder; ss.
XX
XX Homo sapiens.
XX
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PN EP1281758-A2.
XX
XX 05-FEB-2003.
XX
XX 30-JUL-2002; 2002EP-00016874.
XX
XX 02-AUG-2001; 2001US-00922181.
XX
XX (AEOM-) AEOMICA INC.
XX
XX Shannon M, Gu Y, Nguyen C;
XX
XX WPI; 2003-423107/40.
XX
XX New zinc finger-containing proteins and nucleic acids, useful in
PT manufacturing a medicament for treating or preventing a disorder
PT associated with decreased or increased expression or activity of MD23,
PT MD24, MD27 or MD212, e.g. cancer.
XX
XX Example 8; SEQ ID NO 1453; 103pp; English.
XX
XX The present invention relates to novel human zinc finger-containing
CC proteins and their coding sequences: MD23, MD24, MD27, MD212. MD23 is
CC encoded at chromosome 7q22.1, MD24 is encoded at chromosome 6p21.3-22.2,
CC MD27 is encoded at chromosome 16p11.2 and MD212 is encoded at chromosome
CC 15q26.1. The MD23, MD24, MD27, and MD212 sequences are useful in therapy,
CC or in manufacturing a medicament for treating or preventing a disorder
CC associated with decreased or increased expression or activity of MD23,
CC MD24, MD27, or MD212, e.g. cancer or developmental disorders. The nucleic
CC acids and proteins are also useful for diagnosing or monitoring a disease
CC caused by altered expression of MD23, MD24, MD27, or MD212. The nucleic
CC acids can also be used as probes to detect and characterize gross
CC alterations in MD23, MD24, MD27, or MD212 genetic locus. The probes are
CC useful in constructing microarrays for measuring gene expression. The
CC proteins are useful as therapeutic agents for gene therapy or as
CC vaccines. The present sequence was used to illustrate the invention.
XX
XX Sequence 17 BP; 4 A; 7 C; 5 G; 1 T; 0 U; 0 Other;
SQ
Query Match 0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.9e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 926 GGGCTGCTGGCGATGA 942
Db 17 GTGCTGCTGGCGCTGA 1
RESULT 354
ADB02413
ID ADB02413 standard; DNA; 17 BP.
XX
XX ADB02413;
XX
XX 20-NOV-2003 (first entry)
XX
XX Human MD24 scanning oligonucleotide SEQ ID 3399.
XX
XX Cytostatic; immunostimulant; gene therapy; vaccine; human;
KW zinc finger protein; MD23; MD24; MD27; MD212; chromosome 7q22.1;
KW chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer;
KW developmental disorder; ss.
XX
XX Homo sapiens.
XX
XX EP1281758-A2.
XX
XX 05-FEB-2003.
XX
XX 30-JUL-2002; 2002EP-00016874.
XX
XX 02-AUG-2001; 2001US-00922181.
```

PA (ABOM-) AEOMICA INC.  
XX Shannon M, Gu Y, Nguyen C;  
XX WPI; 2003-423107/40.  
XX New zinc finger-containing proteins and nucleic acids, useful in  
PT manufacturing a medicament for treating or preventing a disorder  
PT associated with decreased or increased expression or activity of MD23,  
PT MD24, MD27 or MD212, e.g. cancer.  
XX Example 8; SEQ ID NO 3399; 103pp; English.  
XX  
CC The present invention relates to novel human zinc finger-containing  
CC proteins and their coding sequences: MD23, MD24, MD27, MD212. MD23 is  
CC encoded at chromosome 7q22.1. MD24 is encoded at chromosome 6p21.3-22.2.  
CC MD27 is encoded at chromosome 16p11.2 and MD212 is encoded at chromosome  
CC 15q26.1. The MD23, MD24, MD27, and MD212 sequences are useful in therapy,  
CC or in manufacturing a medicament for treating or preventing a disorder  
CC associated with decreased or increased expression or activity of MD23,  
CC MD24, MD27, or MD212, e.g. cancer or developmental disorders. The nucleic  
CC acids and proteins are also useful for diagnosing or monitoring a disease  
CC caused by altered expression of MD23, MD24, MD27, or MD212. The nucleic  
CC acids can also be used as probes to detect and characterize gross  
CC alterations in MD23, MD24, MD27, or MD212 genetic locus. The probes are  
CC useful in constructing microarrays for measuring gene expression. The  
CC proteins are useful as therapeutic agents for gene therapy or as  
CC vaccines. The present sequence was used to illustrate the invention.  
XX  
SQ Sequence 17 BP; 3 A; 4 C; 6 G; 4 T; 0 U; 0 Other;  
Query Match 0.8%; Score 13.8; DB 1; Length 17;  
Best Local Similarity 88.2%; Pred. No. 1.9e+02;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 464 GCTTGAGGAGTTCCTCA 480  
DB 1 GCTGGAGCAGTTCCTCA 17  
RESULT 355  
ACD58046  
ID ACD58046 standard; RNA; 17 BP.  
XX  
AC ACD58046;  
XX  
DT 23-SEP-2003 (first entry)  
XX  
DE HCV DNazyme substrate sequence #632.  
XX  
KW Nucleic acid molecule; Hepatitis C virus; HCV; Hepatitis B virus; HBV;  
KW RNA stability; RNA expression; RNA synthesis; antisense;  
KW enzymatic nucleic acid; hammerhead ribozyme; DNazyme; inozyme; zinzyme;  
KW amberzyme; G-cleaver ribozyme; decoy molecule; aptamer;  
KW HBV reverse transcriptase; Enhancer I region; viral replication;  
KW degenerative; disease state; HBV infection; HCV infection; cirrhosis;  
KW liver failure; hepatocellular carcinoma; hepatotropic; cytostatic;  
KW virucide; antiinflammatory; substrate; ss.  
XX  
OS Hepatitis C virus.  
XX  
PN WO200281494-A1.  
XX  
PD 17-OCT-2002.  
XX  
PF 26-MAR-2002; 2002WO-US009187.  
XX  
PR 26-MAR-2001; 2001US-00817879.  
PR 08-JUN-2001; 2001US-00877478.  
PR 08-JUN-2001; 2001US-0296876P.  
PR 24-OCT-2001; 2001US-0335059P.  
PR 05-DEC-2001; 2001US-0337055P.  
XX

PA (RIBO-) RIBOZYME PHARM INC.  
PA (BLAT/) BLATT L.  
PA (MACE/) MACEJAK D.  
PA (MCSW/) MCSWIGGEN J.  
PA (MORR/) MORRISSEY D.  
PA (PAVC/) PAVCO P.  
PA (LEBP/) LEE P.  
PA (DRAP/) DRAPER K.  
PA (ROBE/) ROBERTS E.  
XX  
PI Blatt L, Macejak D, Mcswiggen J, Morrissey D, Pavco P, Lee P;  
PI Draper K, Roberts E;  
XX  
XX WPI; 2003-229207/22.  
XX Novel compound useful for treating cirrhosis, liver failure,  
PT hepatocellular carcinoma, or condition associated with hepatitis C virus  
PT infection.  
XX  
XX Claim 1; Page 245; 387pp; English.  
XX  
CC The present invention relates to nucleic acid molecules which modulate  
CC the synthesis, expression and/or stability of Hepatitis C virus (HCV) or  
CC Hepatitis B virus (HBV) RNA. The nucleic acid molecules include antisense  
CC and enzymatic nucleic acids such as hammerhead ribozymes, DNazymes,  
CC inozymes, zinzymes, amberzymes, and G-cleaver ribozymes. Also disclosed  
CC are nucleic acid decoy molecules and aptamers that bind to HBV reverse  
CC transcriptase and/or HBV reverse transcriptase primer sequences, as well  
CC as oligonucleotides that specifically bind the Enhancer I region of HBV  
CC DNA. The nucleic acids may be used to modulate the expression of HBV  
CC genes and HBV viral replication. Also disclosed is a method for screening  
CC compounds and/or potential therapies directed against HBV, and compounds  
CC that modulate the expression and/or replication of HCV. The compounds and  
CC methods of the invention are useful for the treatment of degenerative and  
CC disease states related to HBV and HCV infection, replication and gene  
CC expression such as cirrhosis, liver failure, and hepatocellular  
CC carcinoma. The present sequence represents a substrate for one of the HCV  
CC DNazyme or minus strand DNazyme sequences disclosed in the present  
CC invention  
XX  
SQ Sequence 17 BP; 2 A; 1 C; 7 G; 0 T; 7 U; 0 Other;  
Query Match 0.8%; Score 13.8; DB 1; Length 17;  
Best Local Similarity 47.1%; Pred. No. 1.9e+02;  
Matches 8; Conservative 7; Mismatches 2; Indels 0; Gaps 0;  
QY 1400 TGTGATGTTGCTTTTG 1416  
DB 1 UGUGGAUGAUGCUGUUG 17  
RESULT 356  
ACD61087  
ID ACD61087 standard; RNA; 17 BP.  
XX  
AC ACD61087;  
XX  
DT 24-SEP-2003 (first entry)  
XX  
DE HCV DNazyme substrate sequence #2161.  
XX  
KW Nucleic acid molecule; Hepatitis C virus; HCV; Hepatitis B virus; HBV;  
KW RNA stability; RNA expression; RNA synthesis; antisense;  
KW enzymatic nucleic acid; hammerhead ribozyme; DNazyme; inozyme; zinzyme;  
KW amberzyme; G-cleaver ribozyme; decoy molecule; aptamer;  
KW HBV reverse transcriptase; Enhancer I region; viral replication;  
KW degenerative; disease state; HBV infection; HCV infection; cirrhosis;  
KW liver failure; hepatocellular carcinoma; hepatotropic; cytostatic;  
KW virucide; antiinflammatory; substrate; ss.  
XX  
OS Hepatitis C virus.  
XX  
PN WO200281494-A1.

XX RNA stability; RNA expression; RNA synthesis; antisense;  
PD enzymatic nucleic acid; hammerhead ribozyme; DNzyme; zinzyme;  
XX amberzyme; G-cleaver ribozyme; decoy molecule; aptamer;  
XX HBV reverse transcriptase; Enhancer I region; viral replication;  
PF degenerative; disease state; HBV infection; HCV infection; cirrhosis;  
XX liver failure; hepatocellular carcinoma; hepatotropic; cytostatic;  
XX virucide; antiinflammatory; substrate; ss.  
XX Hepatitis C virus.  
XX OS  
XX WO200281494-A1.  
PN 17-OCT-2002.  
XX  
XX 26-MAR-2002; 2002WO-US009187.  
XX  
XX 26-MAR-2001; 2001US-00817879.  
PR 08-JUN-2001; 2001US-00877478.  
PR 08-JUN-2001; 2001US-0296876P.  
PR 24-OCT-2001; 2001US-0335059P.  
PR 05-DEC-2001; 2001US-0337055P.  
XX  
XX (RIBO-) RIBOZYME PHARM INC.  
PA (BLAT/) BLATT L.  
PA (MACE/) MACEJAK D.  
PA (MCSW/) MCSWIGGEN J.  
PA (MORR/) MORRISSEY D.  
PA (PAVC/) PAVCO P.  
PA (LEEP/) LEE P.  
PA (DRAP/) DRAPER K.  
PA (ROBE/) ROBERTS E.  
XX  
PI Blatt L, Macejak D, Mcswiggen J, Morrissey D, Pavco P, Lee P;  
PI Draper K, Roberts E;  
XX WPI; 2003-229207/22.  
XX  
XX Novel compound useful for treating cirrhosis, liver failure,  
PT hepatocellular carcinoma, or condition associated with hepatitis C virus  
PT infection.  
XX  
XX Claim 1; Page 272; 387pp; English.  
XX  
XX The present invention relates to nucleic acid molecules which modulate  
CC the synthesis, expression and/or stability of Hepatitis C virus (HCV) or  
CC Hepatitis B virus (HBV) RNA. The nucleic acid molecules include antisense  
CC and enzymatic nucleic acids such as hammerhead ribozymes, DNzymes,  
CC inozymes, zinzymes, amberzymes, and G-cleaver ribozymes. Also disclosed  
CC are nucleic acid decoy molecules and aptamers that bind to HBV reverse  
CC transcriptase and/or HBV reverse transcriptase primer sequences, as well  
CC as oligonucleotides that specifically bind the Enhancer I region of HBV  
CC DNA. The nucleic acids may be used to modulate the expression of HBV  
CC genes and HBV viral replication. Also disclosed is a method for screening  
CC compounds and/or potential therapies directed against HBV, and compounds  
CC that modulate the expression and/or replication of HCV. The compounds and  
CC methods of the invention are useful for the treatment of degenerative and  
CC disease states related to HBV and HCV infection, replication and gene  
CC expression such as cirrhosis, liver failure, and hepatocellular  
CC carcinoma. The present sequence represents a substrate for one of the HCV  
CC DNzyme or minus strand DNzyme sequences disclosed in the present  
CC invention  
XX  
XX Sequence 17 BP; 3 A; 5 C; 2 G; 0 T; 7 U; 0 Other;  
SQ  
Query Match 0.8%; Score 13.8; DB 1; Length 17;  
Best Local Similarity 52.9%; Pred. No. 1.9e+02;  
Matches 9; Conservative 6; Mismatches 2; Indels 0; Gaps 0;  
QY 689 GAGGCCTCACTTCTTCT 705  
DB 1 GAUGACUCACUUCUUCU 17  
RESULT 357  
ACD62816/c  
ID ACD62816 standard; RNA; 17 BP.  
XX  
AC ACD62816;  
XX  
XX 24-SEP-2003 (first entry)  
DT  
XX HCV minus strand DNzyme substrate sequence #735.  
DE  
XX Nucleic acid molecule; Hepatitis C virus; HCV; Hepatitis B virus; HBV;  
KW

KW RNA stability; RNA expression; RNA synthesis; antisense;  
KW enzymatic nucleic acid; hammerhead ribozyme; DNzyme; zinzyme;  
KW amberzyme; G-cleaver ribozyme; decoy molecule; aptamer;  
KW HBV reverse transcriptase; Enhancer I region; viral replication;  
KW degenerative; disease state; HBV infection; HCV infection; cirrhosis;  
KW liver failure; hepatocellular carcinoma; hepatotropic; cytostatic;  
KW virucide; antiinflammatory; substrate; ss.  
XX  
XX Hepatitis C virus.  
XX OS  
XX WO200281494-A1.  
PN 17-OCT-2002.  
XX  
XX 26-MAR-2002; 2002WO-US009187.  
XX  
XX 26-MAR-2001; 2001US-00817879.  
PR 08-JUN-2001; 2001US-00877478.  
PR 08-JUN-2001; 2001US-0296876P.  
PR 24-OCT-2001; 2001US-0335059P.  
PR 05-DEC-2001; 2001US-0337055P.  
XX  
XX (RIBO-) RIBOZYME PHARM INC.  
PA (BLAT/) BLATT L.  
PA (MACE/) MACEJAK D.  
PA (MCSW/) MCSWIGGEN J.  
PA (MORR/) MORRISSEY D.  
PA (PAVC/) PAVCO P.  
PA (LEEP/) LEE P.  
PA (DRAP/) DRAPER K.  
PA (ROBE/) ROBERTS E.  
XX  
PI Blatt L, Macejak D, Mcswiggen J, Morrissey D, Pavco P, Lee P;  
PI Draper K, Roberts E;  
XX WPI; 2003-229207/22.  
XX  
XX Novel compound useful for treating cirrhosis, liver failure,  
PT hepatocellular carcinoma, or condition associated with hepatitis C virus  
PT infection.  
XX  
XX Claim 1; Page 288; 387pp; English.  
XX  
XX The present invention relates to nucleic acid molecules which modulate  
CC the synthesis, expression and/or stability of Hepatitis C virus (HCV) or  
CC Hepatitis B virus (HBV) RNA. The nucleic acid molecules include antisense  
CC and enzymatic nucleic acids such as hammerhead ribozymes, DNzymes,  
CC inozymes, zinzymes, amberzymes, and G-cleaver ribozymes. Also disclosed  
CC are nucleic acid decoy molecules and aptamers that bind to HBV reverse  
CC transcriptase and/or HBV reverse transcriptase primer sequences, as well  
CC as oligonucleotides that specifically bind the Enhancer I region of HBV  
CC DNA. The nucleic acids may be used to modulate the expression of HBV  
CC genes and HBV viral replication. Also disclosed is a method for screening  
CC compounds and/or potential therapies directed against HBV, and compounds  
CC that modulate the expression and/or replication of HCV. The compounds and  
CC methods of the invention are useful for the treatment of degenerative and  
CC disease states related to HBV and HCV infection, replication and gene  
CC expression such as cirrhosis, liver failure, and hepatocellular  
CC carcinoma. The present sequence represents a substrate for one of the HCV  
CC DNzyme or minus strand DNzyme sequences disclosed in the present  
CC invention  
XX  
XX Sequence 17 BP; 4 A; 4 C; 7 G; 0 T; 2 U; 0 Other;  
SQ  
Query Match 0.8%; Score 13.8; DB 1; Length 17;  
Best Local Similarity 88.2%; Pred. No. 1.9e+02;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 769 ACGCCATGTTCCAGCCC 785  
DB 17 ACGCCATGTTCCGGCTC 1



```

RESULT 358
ACC67637
ID ACC67637 standard; DNA; 17 BP.
XX
XX ACC67637;
AC
XX
XX 01-JUL-2003 (first entry)
DT
XX
XX Murine oligonucleotide associated with tumour suppression, SEQ ID 4884.
DE
XX
XX Cytostatic; virucide; neuroprotective; nootropic; neuroleptic; murine;
KW tumour suppression; tumour reversion; apoptosis; virus resistance;
KW viral disease; tumour; cell degeneration; cancer; Alzheimer's disease;
KW schizophrenia; ss.
XX
XX Mus musculus.
OS
XX
XX WO2003025176-A2.
PN
XX
XX 27-MAR-2003.
PD
XX
XX 17-SEP-2002; 2002WO-IB004210.
PF
XX
XX 17-SEP-2001; 2001FR-00011979.
PR
XX
XX (MOLE-) MOLECULAR ENGINES LAB.
PA
XX
XX Telerman A, Amson R, Tuijnder M;
PI
XX
XX WPI; 2003-333167/31.
DR
XX
XX New isolated nucleic acid, useful for treating viral diseases associated
PT with tumors and cell degeneration, also related polypeptides, antibodies
PT and transfected cells.
PT
XX
XX Disclosure; Page 602; 738pp; French.
PS
XX
XX The present invention relates to murine oligonucleotides (ACC62754-
CC ACC68806), which are associated with tumour suppression, tumour
CC reversion, apoptosis and virus resistance. The oligonucleotides are
CC useful as (1) as probes and primers for detecting, identifying,
CC quantifying and/or amplifying nucleic acid, e.g. as one component of a
CC gene chip; in vitro as (anti)sense reagents; and (2) for production of
CC recombinant polypeptides. The oligonucleotides are useful for preparation
CC of pharmaceuticals for prevention and/or treatment of viral diseases that
CC are characterised by development of tumours or cell degeneration.
CC specifically cancer but also Alzheimer's disease and schizophrenia
XX
XX Sequence 17 BP; 5 A; 4 C; 2 G; 6 T; 0 U; 0 Other;
SQ
    Query Match      0.8%; Score 13.8; DB 1; Length 17;
    Best Local Similarity 88.2%; Pred. No. 1.9e+02;
    Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1551 GATCCTGCACTCTAACA 1567
DB 1 GATCCTGTACTCTAATA 17

RESULT 359
ADB39727/c
ID ADB39727 standard; DNA; 17 BP.
XX
XX ADB39727;
AC
XX
XX 18-DEC-2003 (revised)
DT
XX 04-DEC-2003 (first entry)
DT
XX
XX Tumour suppression/reversion associated nucleotide #50.
DE
XX
XX cytostatic; antiviral; neuroprotective; nootropic; neuroleptic; ss;
KW primer; probe; tumour suppression; tumour reversion; apoptosis;
KW virus resistance; transgenic animals; Alzheimer's disease; schizophrenia;

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diagnosis.
KW
XX
XX Homo sapiens.
XX
XX WO2003040369-A2.
PN
XX
XX 15-MAY-2003.
PD
XX
XX 17-SEP-2002; 2002WO-IB004219.
PF
XX
XX 17-SEP-2001; 2001FR-00011981.
PR
XX
XX (MOLE-) MOLECULAR ENGINES LAB.
PA
XX
XX Telerman A, Amson R, Tuijnder M;
PI
XX
XX WPI; 2003-441574/41.
DR
XX
XX New nucleic acid encoding human prostate membrane-specific antigen,
PT useful e.g. for treatment of tumors and viral infection, also related
PT polypeptide and antibodies.
PT
XX
XX Disclosure; Page 37; 771pp; French.
PS
XX
XX The invention relates to the isolation of 6327 nucleotide sequences,
CC fragments of at least 15 consecutive nucleotides of these nucleotides, a
CC sequence having at least 80% identity, after optimal alignment, with the
CC nucleotides, a sequence that hybridizes under stringent conditions with
CC the nucleotides, or the complement, or corresponding RNA, of the
CC nucleotides. The nucleotides are used as probes or primers for detecting,
CC identifying, quantifying and/or amplifying nucleic acids, as in vitro
CC sense and antisense sequences, of nucleotides involved in tumour
CC suppression or reversion, apoptosis and or viral resistance, to produce
CC recombinant polypeptides, and to prepare transgenic animals, as
CC experimental models. The nucleotides (also vectors containing them and
CC cells containing the vectors), the encoded polypeptides and antibodies
CC (Ab) against the polypeptide are useful for prevention and/or treatment
CC of viral infections or diseases characterized by development of tumours
CC or cell degeneration (e.g. Alzheimer's disease or schizophrenia).
CC Analysis of the expression of the nucleotides can be used for diagnosis
CC and/or prognosis of these diseases. The nucleotides and polypeptides can
CC also be used to screen for their specific interactive molecules,
CC potentially useful for treating diseases associated with abnormal
CC expression of the nucleotides.
XX
XX Sequence 17 BP; 2 A; 10 C; 2 G; 3 T; 0 U; 0 Other;
SQ
    Query Match      0.8%; Score 13.8; DB 1; Length 17;
    Best Local Similarity 88.2%; Pred. No. 1.9e+02;
    Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 91 GGGAGAGTGGGCAGGTC 107
DB 17 GGGAGGGTGGGCAGATC 1

RESULT 360
ADI47981
ID ADI47981 standard; DNA; 17 BP.
XX
XX ADI47981;
AC
XX
XX 15-APR-2004 (first entry)
DT
XX
XX Human tumour suppression/reversion-related DNA sequence SeqID484.
DE
XX
XX tumour suppression; tumour reversion; apoptosis; virus resistance;
KW cytostatic; virucide; neuroprotective; nootropic; neuroleptic; probe;
KW primer; PCR; gene chip; antisense; viral disease; tumour;
KW cell degeneration; cancer; Alzheimer's disease; schizophrenia; ds; human.
XX
XX Homo sapiens.
XX

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PN WO2003025177-A2.
XX
PD 27-MAR-2003.
XX
XX 17-SEP-2002; 2002WO-IB004523.
XX PF
XX 17-SEP-2001; 2001FR-00011980.
PR
XX (MOLE-) MOLECULAR ENGINES LAB.
XX
XX Telferman A, Amson R, Tuijnder M;
XX WPI; 2003-313354/30.
XX
PT New isolated nucleic acid, useful for treating viral diseases associated
PT with tumors and cell degeneration, also related polypeptides, antibodies
PT and transfected cells.
XX
PS Disclosure; SEQ ID NO 484; 30pp; French.
XX
CC This invention relates to novel isolated nucleic acid sequences involved
CC in the phenomena of tumour suppression, tumour reversion, apoptosis
CC and/or resistance to viruses. The invention may be useful for the
CC development of compounds with a cytostatic, virucide, neuroprotective,
CC neurotropic or neuroleptic activity. The DNA sequences may be useful as
CC probes and primers for detecting, identifying, quantifying and/or
CC amplifying nucleic acid, for example as one component of a gene chip, in
CC vitro as antisense reagents and for production of recombinant
CC polypeptides. The invention may therefore be useful for preparation of
CC pharmaceuticals for prevention and/or treatment of viral diseases that
CC are characterised by development of tumours or cell degeneration.
CC specifically cancer but also Alzheimer's disease and schizophrenia. The
CC present sequence is that of a nucleic acid sequence of the invention.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/publishedpct_sequences
XX
SQ Sequence 17 BP; 5 A; 4 C; 2 G; 6 T; 0 U; 0 Other;

Query Match 0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. NO. 1.9e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1551 GATCCTGCACCTCAACA 1567
Db 1 GATCCTGTACTCTAATA 17

RESULT 361
ABZ94171/C
ID ABZ94171 standard; DNA; 17 BP.
XX
XX AC ABZ94171;
XX
XX 17-OCT-2003 (first entry)
XX
XX Human adenosine A1 receptor antisense fragment no.34.
XX
XX Human; antisense; lung dysfunction; nasal airway dysfunction;
XX antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
XX antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
XX antisense gene therapy; respiratory; lung; adenosine sensitivity;
XX adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
XX lung inflammation; respiratory disease; ds.
XX
XX Homo sapiens.
XX OS
XX WO200285308-A2.
XX PN
XX 31-OCT-2002.
XX PD
XX 23-APR-2002; 2002WO-US013135.
XX PF
XX

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PR 24-APR-2001; 2001US-0286137P.
XX
XX (EPIG-) EPIGENESIS PHARM INC.
XX
XX NYce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
XX PI Miller S, Tang L, Shahabuddin S;
XX
XX WPI; 2003-229219/22.
XX
XX Pharmaceutical composition for treating ailments associated with impaired
XX respiration, has oligo(s) antisense to specific gene(s) or its
XX corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
XX ubiquinone.
XX
XX Disclosure; SEQ ID NO 9413; 872pp; English.
XX
XX The invention relates to a novel pharmacological composition, which has a
XX first active agent comprising an oligonucleotide antisense to the
XX initiation codon, coding region, 5' or 3' end genomic flanking regions,
XX 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
XX junctions of genes encoding a polypeptide associated with lung and/or
XX nasal airway dysfunction and a second active agent comprising an
XX antiinflammatory steroid and ubiquinone. A composition of the invention
XX has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
XX immunosuppressive, and cytostatic activity. The composition may have a
XX use in antisense gene therapy. The composition is useful for treating or
XX preventing a respiratory, lung or malignant disease or condition, also
XX for enhancing the prophylactic or therapeutic respiratory effect of an
XX antiinflammatory steroid in a subject, for reducing or depleting levels
XX of, or reducing sensitivity to adenosine, reducing levels of adenosine
XX receptor, producing bronchodilation, increasing levels of ubiquinone or
XX lung surfactant in a subject's tissue, or treating bronchoconstriction,
XX lung inflammation, lung allergies, or a respiratory disease or condition.
XX Note: The sequence data for this patent is not represented in the printed
XX specification, but was obtained in electronic format directly from WIPO
XX at ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 17 BP; 2 A; 5 C; 9 G; 1 T; 0 U; 0 Other;

Query Match 0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.9e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1530 GCCCAGCCTCTCCCGC 1546
Db 17 GCCCAGCCTGTGCCCCG 1

RESULT 362
ABZ95047/C
ID ABZ95047 standard; DNA; 17 BP.
XX
XX AC ABZ95047;
XX
XX 17-OCT-2003 (first entry)
XX
XX Human adenosine A1 receptor antisense fragment no.910.
XX
XX Human; antisense; lung dysfunction; nasal airway dysfunction;
XX antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
XX antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
XX antisense gene therapy; respiratory; lung; adenosine sensitivity;
XX adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
XX lung inflammation; respiratory disease; ds.
XX
XX Homo sapiens.
XX OS
XX WO200285308-A2.
XX PN
XX 31-OCT-2002.
XX PD
XX 23-APR-2002; 2002WO-US013135.
XX PF
XX

```

PR 24-APR-2001; 2001US-0286137P.  
XX (EPIC-) EPIGENESIS PHARM INC.  
XX  
PI Nyce JW, Li Y, Sandraagra A, Katz E, Pabalan J, Aguilar D;  
PI Miller S, Tang L, Shanabuddin S;  
XX  
DR WPI; 2003-229219/22.  
XX  
XX Pharmaceutical composition for treating ailments associated with impaired  
PT respiration, has oligo(s) antisense to specific gene(s) or its  
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or  
PT ubiquinone.  
XX  
PS Disclosure; SEQ ID NO 10289; 872pp; English.  
XX  
XX The invention relates to a novel pharmaceutical composition, which has a  
CC first active agent comprising an oligonucleotide antisense to the  
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,  
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of  
CC junctions of genes encoding a polypeptide associated with lung and/or  
CC nasal airway dysfunction and a second active agent comprising an  
CC antiinflammatory steroid and ubiquinone. A composition of the invention  
CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,  
CC immunosuppressive, and cytostatic activity. The composition may have a  
CC use in antisense gene therapy. The composition is useful for treating or  
CC preventing a respiratory, lung or malignant disease or condition, also  
CC for enhancing the prophylactic or therapeutic respiratory effect of an  
CC antiinflammatory steroid in a subject, for reducing or depleting levels  
CC of, or reducing sensitivity to adenosine, reducing levels of adenosine or  
CC receptor, producing bronchodilation, increasing levels of ubiquinone or  
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,  
CC lung inflammation, lung allergies, or a respiratory disease or condition.  
CC Note: The sequence data for this patent is not represented in the printed  
CC specification, but was obtained in electronic format directly from WIPO  
CC at ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 17 BP; 2 A; 5 C; 9 G; 1 T; 0 U; 0 Other;  
Query Match 0.8%; Score 13.8; DB 1; Length 17;  
Best Local Similarity 88.2%; Pred. No. 1.9e+02;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
OY 1530 GCCAGCCTCTCCCGC 1546  
DB 17 GCCAGCCTGTCCCGC 1  
RESULT 363  
ADL48005  
ID ADL48005 standard; RNA; 17 BP.  
XX  
AC ADL48005;  
XX  
DT 20-MAY-2004 (first entry)  
XX  
DE Human IKK-gamma substrate sequence #515.  
XX  
KW antisense oligonucleotide; neurite growth inhibitor; NOGO;  
KW prostaglandin D2 receptor; PTGDR; IkappaB kinase; IKK;  
KW protein kinase PKR; cerebrovascular accident;  
KW central nervous system injury; CNS injury; spinal cord injury; cancer;  
KW melanoma; lymphoma; glioma; inflammatory disease; rheumatoid arthritis;  
KW restenosis; asthma; Crohn's disease; diabetes; obesity;  
KW autoimmune disease; lupus; multiple sclerosis; transplant rejection;  
KW graft rejection; ischaemia; reperfusion; glomerulonephritis; sepsis;  
KW allergy; asthma; allergic rhinitis; atopic dermatitis; Human IKK-gamma;  
KW substrate; ds.  
XX  
OS Unidentified.  
XX  
PN WO200281628-A2.  
XX

PD 17-OCT-2002.  
XX  
PF 03-APR-2002; 2002WO-US010512.  
XX  
PR 05-APR-2001; 2001US-00827395.  
PR 29-MAY-2001; 2001US-0294412P.  
PR 28-AUG-2001; 2001US-0315315P.  
XX  
PA (RIBO-) RIBOZYME PHARM INC.  
XX  
PI Blatt L, Chowrira B, Haeblerli P, Mcswiggen J, Fosnaugh K;  
XX WPI; 2003-058513/05.  
DR  
XX  
PT Novel enzymatic nucleic acid that down-regulates expression of neurite  
PT growth inhibitor receptor, prostaglandin D2 receptor, IkappaB kinase or  
PT protein kinase PKR genes, for treating cancer and inflammatory disease.  
XX  
PS Claim 59; SEQ ID NO 1538; 317pp; English.  
XX  
CC The invention comprises nucleic acids (e.g. antisense oligonucleotides)  
CC that down regulate the expression or inhibit the function of a receptor  
CC for a neurite growth inhibitor, NOGO, prostaglandin D2 receptor (PTGDR),  
CC IkappaB kinase (IKK), or protein kinase PKR. The nucleic acids of the  
CC invention are useful for treating: cerebrovascular accident, central  
CC nervous system (CNS) injury, spinal cord injury, cancer (e.g. melanoma,  
CC lymphoma or glioma), inflammatory disease (e.g. rheumatoid arthritis,  
CC restenosis or asthma), Crohn's disease, diabetes, obesity, autoimmune  
CC disease, lupus, multiple sclerosis, transplant/graft rejection, allergic  
CC ischaemia/reperfusion injury, glomerulonephritis, sepsis, and allergic  
CC conditions (e.g. asthma, allergic rhinitis or atopic dermatitis). The  
CC nucleic acids of the invention are also useful for down-regulating the  
CC expression of a target gene and as a diagnostic tool to examine genetic  
CC drifts and mutations within diseased cells or to detect the presence of a  
CC target RNA in a cell. The present RNA sequence represents a human IKK-  
CC gamma substrate sequence.  
XX  
SQ Sequence 17 BP; 3 A; 6 C; 3 G; 0 T; 5 U; 0 Other;  
Query Match 0.8%; Score 13.8; DB 1; Length 17;  
Best Local Similarity 58.8%; Pred. No. 1.9e+02;  
Matches 10; Conservative 5; Mismatches 2; Indels 0; Gaps 0;  
OY 697 ACTTCTTCTTTCCCAAG 713  
DB 1 ACUCUCGUGUCCCAAG 17  
RESULT 364  
ADL50256/c  
ID ADL50256 standard; RNA; 17 BP.  
XX  
AC ADL50256;  
XX  
DT 20-MAY-2004 (first entry)  
XX  
DE Human PKR substrate sequence #1370.  
XX  
KW antisense oligonucleotide; neurite growth inhibitor; NOGO;  
KW prostaglandin D2 receptor; PTGDR; IkappaB kinase; IKK;  
KW protein kinase PKR; cerebrovascular accident;  
KW central nervous system injury; CNS injury; spinal cord injury; cancer;  
KW melanoma; lymphoma; glioma; inflammatory disease; rheumatoid arthritis;  
KW restenosis; asthma; Crohn's disease; diabetes; obesity;  
KW autoimmune disease; lupus; multiple sclerosis; transplant rejection;  
KW graft rejection; ischaemia; reperfusion; glomerulonephritis; sepsis;  
KW allergy; asthma; allergic rhinitis; atopic dermatitis; human PKR;  
KW substrate; ds.  
XX  
OS Unidentified.  
XX  
PN WO200281628-A2.  
XX



PD 17-OCT-2002.  
 XX  
 PF 03-APR-2002; 2002WO-US010512.  
 XX  
 XX  
 PR 05-APR-2001; 2001US-00827395.  
 PR 29-MAY-2001; 2001US-0294412P.  
 PR 28-AUG-2001; 2001US-0315315P.  
 XX  
 XX (RIBO-) RIBOZYME PHARM INC.  
 PA  
 XX  
 XX Blatt L, Chowrira B, Haerberli P, Mcswiggen J, Fosnaugh K;  
 XX WPI; 2003-058513/05.  
 DR  
 XX  
 PT Novel enzymatic nucleic acid that down-regulates expression of neurite  
 PT growth inhibitor receptor, prostaglandin D2 receptor, IkappaB kinase or  
 PT protein kinase PKR genes, for treating cancer and inflammatory disease.  
 XX  
 XX Claim 9; SEQ ID NO 880; 317pp; English.  
 XX  
 CC The invention comprises nucleic acids (e.g. antisense oligonucleotides)  
 CC that down regulate the expression or inhibit the function of a receptor  
 CC for a neurite growth inhibitor, NOGO, prostaglandin D2 receptor (PTGDR),  
 CC IkappaB kinase (IKK) or protein kinase PKR. The nucleic acids of the  
 CC invention are useful for treating: cerebrovascular accident, central  
 CC nervous system (CNS) injury, spinal cord injury, cancer (e.g. melanoma,  
 CC lymphoma or glioma), inflammatory disease (e.g. rheumatoid arthritis,  
 CC restenosis or asthma), Crohn's disease, diabetes, obesity, autoimmune  
 CC disease, lupus, multiple sclerosis, transplant/graft rejection,  
 CC ischaemia/reperfusion injury, glomerulonephritis, sepsis, and allergic  
 CC conditions (e.g. asthma, allergic rhinitis or atopic dermatitis). The  
 CC nucleic acids of the invention are also useful for down-regulating the  
 CC expression of a target gene and as a diagnostic tool to examine genetic  
 CC drifts and mutations within diseased cells or to detect the presence of a  
 CC target RNA in a cell. The present RNA sequence represents a human NOGO  
 CC receptor amberzyme substrate sequence.  
 XX  
 SQ Sequence 17 BP; 2 A; 7 C; 5 G; 0 T; 3 U; 0 Other;  
 Query Match 0.8%; Score 13.8; DB 1; Length 17;  
 Best Local Similarity 70.6%; Pred. No. 1.9e+02;  
 Matches 12; Conservative 3; Mismatches 2; Indels 0; Gaps 0;  
 QY 1117 CCTGCTGGAGCAGCTG 1133  
 || : ||:|||||:  
 Db 1 CCUCUCGAGCAGCUG 17  
 RESULT 367  
 ADM54165/c  
 ID ADM54165 standard; mRNA; 17 BP.  
 XX  
 AC ADM54165;  
 XX  
 XX 03-JUN-2004 (first entry)  
 XX  
 DE Human GRID mRNA substrate sequence #440.  
 XX  
 KW Human; ss; GRID; Grb2-related with insert domain; hammerhead ribozyme;  
 KW NCH ribozyme; G-cleaver ribozyme; Zinzyme; DNzyme; amberzyme; inozyme;  
 KW hairpin ribozyme; tissue rejection; graft rejection; leukaemia.  
 XX  
 OS Homo sapiens.  
 XX  
 XX US2003134806-A1.  
 PN  
 XX  
 PD 17-JUL-2003.  
 XX  
 XX 23-FEB-2001; 2001US-00792818.  
 PF  
 XX 10-FEB-2000; 2000US-0181594P.  
 PR  
 XX (JARV/) JARVIS T.

PA (CARL/) CARLOWITZ I V.  
 PA (MCSW/) MCSWIGGEN J.  
 PA (HAMB/) HAWBLIN P A.  
 PA (ELLI/) ELLIS J H.  
 XX  
 PI Jarvis T, Carlowitz IV, Mcswiggen J, Hamblin PA, Ellis JH;  
 XX WPI; 2003-829646/77.  
 DR  
 XX  
 PT New nucleic acid molecule that down-regulates expression of Grb2-related  
 PT with insert domain (GRID) gene, useful for treating a condition  
 PT associated with the level of GRID, e.g. tissue/graft rejection and  
 PT leukemia.  
 XX  
 XX Claim 4; SEQ ID NO 440; 74pp; English.  
 PS  
 CC The invention relates to a nucleic acid molecule that down-regulates  
 CC expression of Grb2-related with insert domain (GRID) gene, e.g. a  
 CC hammerhead ribozyme, NCH ribozyme, G-cleaver ribozyme, Zinzyme, DNzyme,  
 CC amberzyme, inozyme or hairpin ribozyme. Also include are a mammalian cell  
 CC including the novel nucleic acid molecule, reducing GRID activity in a  
 CC cell by contacting the cell with the novel nucleic acid molecule,  
 CC treating a patient having a condition associated with the level of GRID  
 CC (e.g. tissue/graft rejection or leukaemia) by contacting the cell with  
 CC the novel nucleic acid molecule, cleaving RNA of a GRID gene by  
 CC contacting the cell with the novel nucleic acid molecule, an expression  
 CC vector comprising a nucleic acid sequences (encoding at least the novel  
 CC nucleic acid molecule in a manner that allows its expression), a  
 CC mammalian cell including the expression vector and an enzymatic nucleic  
 CC acid molecule that cleaves RNA derived from a GRID gene. The nucleic acid  
 CC molecule is useful for treating a condition associated with the level of  
 CC GRID, e.g. tissue/graft rejection and leukaemia. The present sequence is  
 CC a target region for the enzymatic nucleic acids of the invention.  
 XX  
 SQ Sequence 17 BP; 3 A; 4 C; 8 G; 0 T; 2 U; 0 Other;  
 Query Match 0.8%; Score 13.8; DB 1; Length 17;  
 Best Local Similarity 88.2%; Pred. No. 1.9e+02;  
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 1539 CTCGCCGCTCTGGATCC 1555  
 |||||:|||||:  
 Db 17 CTCGCCGCTGTGAACC 1  
 RESULT 368  
 ABD18019/c  
 ID ABD18019 standard; DNA; 17 BP.  
 XX  
 XX ABD18019;  
 AC  
 XX 29-JUL-2004 (first entry)  
 DT  
 XX Human adenosine A1 receptor oligonucleotide fragment 34.  
 DE  
 XX  
 KW Human; antisense; bronchoconstriction; allergy; hyposecretion; pain;  
 KW respiratory tract inflammation; adenosine sensitivity; lung; cancer;  
 KW surfactant depletion; antiallergic; antiinflammatory; antiasthmatic;  
 KW analgesic; hypotensive; immunosuppressive; cytostatic; cystic fibrosis;  
 KW beta-adrenergic agonist; respiratory disease; pulmonary vasoconstriction;  
 KW respiratory distress syndrome; allergic rhinitis; pulmonary hypertension;  
 KW emphysema; chronic obstructive pulmonary disease; cancer; bronchitis;  
 KW pulmonary transplantation rejection; ds.  
 XX  
 OS Homo sapiens.  
 XX  
 XX WO200285309-A2.  
 PN  
 XX 31-OCT-2002.  
 PD  
 XX 23-APR-2002; 2002WO-US013143.  
 PF  
 XX 24-APR-2001; 2001US-0286036P.  
 PR

```

XX PA (EPIG-) EPIGENESIS PHARM INC.
XX PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
XX PI Miller S, Tang L, Shahabuddin S;
XX DR WPI; 2003-093058/08.
XX PT
XX PT Pharmaceutical composition for treating asthma, has antisense
XX PT oligonucleotide containing less percentage of adenosine, targeted to
XX PT nucleic acids associated with lung airway or lung dysfunction, and
XX PT bronchodilating agent.
XX PS Claim 15; SEQ ID NO 9413; 763pp; English.
XX CC
XX CC This invention describes a novel composition (a) a first active agent,
XX CC comprising oligonucleotides, effective for alleviating
XX CC bronchoconstriction, respiratory tract inflammation, allergies and
XX CC bronchodilation, respiratory tract inflammation, allergies and
XX CC reducing adenosine sensitivity, levels of adenosine (A) or (A) receptors,
XX CC surfactant depletion or hyposcretion, when administered to a mammal. The
XX CC oligonucleotides are derived from a gene encoding or regulating
XX CC expression of a target polypeptide associated with lung airway or lung
XX CC dysfunction or cancer and can be anti-sense to the corresponding mRNA.
XX CC The invention also describes (a) that comprises: (a) a delivery
XX CC device, in separate containers, (b) the oligonucleotides, (c)
XX CC instructions for adding a carrier and for use of the kit. The composition
XX CC of the invention has anti-allergic, anti-inflammatory, antiasthmatic,
XX CC analgesic, hypotensive, immunosuppressive and cytostatic activity, is a
XX CC beta-adrenergic agonist. The composition is useful for preventing or
XX CC treating a respiratory, lung or malignant disease. The administered
XX CC composition comprises oligo and is administered to reduce the production
XX CC or availability, or to increase the degradation of the target mRNA or to
XX CC reduce the amount of target polypeptide present in the lungs. The
XX CC pulmonary obstruction, and/or bronchoconstriction and/or lung
XX CC inflammation, allergies and/or surfactant hypoproduction are associated
XX CC with a disease or condition such as pulmonary vasoconstriction,
XX CC inflammation, allergies, asthma, impeded respiration, respiratory
XX CC distress syndrome, pain, cystic fibrosis, allergic rhinitis, pulmonary
XX CC hypertension, emphysema, chronic obstructive pulmonary disease, pulmonary
XX CC transplantation rejection, pulmonary infections, bronchitis or cancer.
XX CC The reduced adenosine content of the anti-sense oligos corresponding to
XX CC thymidines present in the target RNA serves to prevent the breakdown of
XX CC the oligonucleotides into products that free adenosine into the system
XX CC e.g., lung, brain, heart, kidney, etc, tissue environment and thereby, to
XX CC prevent any unwanted effects due to it
XX SQ Sequence 17 BP; 2 A; 5 C; 9 G; 1 T; 0 U; 0 Other;

Query Match 0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.9e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1530 GCCCAGCCTCTCCCGC 1546
Db 17 GCCCAGCCTGTGCCGC 1

RESULT 369
ID ABD18895/c
XX ABD18895 standard; DNA; 17 BP.
XX AC ABD18895;
XX DT 29-JUL-2004 (first entry)
XX DE Human adenosine A1 receptor oligonucleotide fragment 910.
XX KW Human; antisense; bronchoconstriction; allergy; hyposcretion; pain;
XX KW respiratory tract inflammation; adenosine sensitivity; lung; cancer;
XX KW surfactant depletion; anti-allergic; anti-inflammatory; antiasthmatic;
XX KW analgesic; hypotensive; immunosuppressive; cytostatic; cystic fibrosis;
XX KW beta-adrenergic agonist; respiratory disease; pulmonary vasoconstriction;
XX KW respiratory distress syndrome; allergic rhinitis; pulmonary hypertension;
emphysema; chronic obstructive pulmonary disease; cancer; bronchitis;
pulmonary transplantation rejection; ds.
Homo sapiens.
WO200285309-A2.
31-OCT-2002.
23-APR-2002; 2002WO-US013143.
24-APR-2001; 2001US-0286036P.
(EPIG-) EPIGENESIS PHARM INC.
Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
Miller S, Tang L, Shahabuddin S;
WPI; 2003-093058/08.
Pharmaceutical composition for treating asthma, has antisense
oligonucleotide containing less percentage of adenosine, targeted to
nucleic acids associated with lung airway or lung dysfunction, and
bronchodilating agent.
Claim 15; SEQ ID NO 10289; 763pp; English.
This invention describes a novel composition (a) a first active agent,
comprising oligonucleotides, effective for alleviating
bronchoconstriction, respiratory tract inflammation, allergies and
reducing adenosine sensitivity, levels of adenosine (A) or (A) receptors,
surfactant depletion or hyposcretion, when administered to a mammal. The
oligonucleotides are derived from a gene encoding or regulating
expression of a target polypeptide associated with lung airway or lung
dysfunction or cancer and can be anti-sense to the corresponding mRNA.
The invention also describes (a) that comprises: (a) a delivery
device, in separate containers, (b) the oligonucleotides, (c)
instructions for adding a carrier and for use of the kit. The composition
of the invention has anti-allergic, anti-inflammatory, antiasthmatic,
analgesic, hypotensive, immunosuppressive and cytostatic activity, is a
beta-adrenergic agonist. The composition is useful for preventing or
treating a respiratory, lung or malignant disease. The administered
composition comprises oligo and is administered to reduce the production
or availability, or to increase the degradation of the target mRNA or to
reduce the amount of target polypeptide present in the lungs. The
pulmonary obstruction, and/or bronchoconstriction and/or lung
inflammation, allergies and/or surfactant hypoproduction are associated
with a disease or condition such as pulmonary vasoconstriction,
inflammation, allergies, asthma, impeded respiration, respiratory
distress syndrome, pain, cystic fibrosis, allergic rhinitis, pulmonary
hypertension, emphysema, chronic obstructive pulmonary disease, pulmonary
transplantation rejection, pulmonary infections, bronchitis or cancer.
The reduced adenosine content of the anti-sense oligos corresponding to
thymidines present in the target RNA serves to prevent the breakdown of
the oligonucleotides into products that free adenosine into the system
e.g., lung, brain, heart, kidney, etc, tissue environment and thereby, to
prevent any unwanted effects due to it
Sequence 17 BP; 2 A; 5 C; 9 G; 1 T; 0 U; 0 Other;

Query Match 0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.9e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1530 GCCCAGCCTCTCCCGC 1546
Db 17 GCCCAGCCTGTGCCGC 1

RESULT 370
ADG63002
ID ADG63002 standard; DNA; 17 BP.
XX

```



```
PR 08-MAR-2002; 2002JP-00064373.
XX (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.
XX WPI; 2004-093977/10.
XX Novel polynucleotide useful for PCR amplification along with two DNA
PT fragment from another set of sequences, or for detecting single
PT nucleotide polymorphism in human gene.
XX
XX Claim 2; SEQ ID NO 7308; 2627pp; Japanese.
XX
XX The present invention relates to a polynucleotide isolated from a human
CC gene and is useful for detecting a single nucleotide polymorphism in a
CC human gene or for diagnosing of disease. The invention enables the
CC detection of a single nucleotide polymorphism in a human gene. The
CC present sequence represents a primer of the invention.
XX
XX Sequence 17 BP; 4 A; 4 C; 7 G; 2 T; 0 U; 0 Other;
SQ
    Query Match      0.8%; Score 13.8; DB 1; Length 17;
    Best Local Similarity 88.2%; Pred. No. 1.9e+02;
    Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 666 CTGCCCTTCAGCTGCC 682
DB 17 CTGGCATTGAGCTGCC 1
RESULT 373
ADI84915
ID ADI84915 standard; RNA; 17 BP.
XX
XX AC ADI84915;
XX
XX 03-JUN-2004 (first entry)
XX
XX HCV DNazyme substrate sequence #2161.
DE
XX ss; enzymatic nucleic acid; RNA cleavage; hepatitis C virus; HCV;
KW HCV infection; type I interferon; DNazyme.
KW
XX Hepatitis C virus.
OS
XX US2003125270-A1.
FN
XX
XX 03-JUL-2003.
PD
XX
XX 18-DEC-2000; 2000US-00740332.
PF
XX
XX 18-DEC-2000; 2000US-00740332.
PR
XX (BLAT/) BLATT L.
PA (MCSW/) MCSWIGGEN J.
PA (ROBE/) ROBERTS E.
PA (PAVC/) PAVCO P A.
PA (MACE/) MACEJACK D.
XX
XX Blatt L, Mcswiggen J, Roberts E, Pavco PA, Macejack D;
PI
XX WPI; 2004-031273/03.
DR
XX
XX 18-DEC-2000; 2000US-00740332.
PF
XX
XX 18-DEC-2000; 2000US-00740332.
PR
XX (BLAT/) BLATT L.
PA (MCSW/) MCSWIGGEN J.
PA (ROBE/) ROBERTS E.
PA (PAVC/) PAVCO P A.
PA (MACE/) MACEJACK D.
XX
XX Blatt L, Mcswiggen J, Roberts E, Pavco PA, Macejack D;
PI
XX WPI; 2004-031273/03.
DR
XX
XX Enzymatic nucleic acid molecules which specifically cleave RNA derived
PT from hepatitis C virus (HCV), useful for the treatment of HCV infections,
PT especially in combination with type I interferon therapy.
XX
XX Claim 1; SEQ ID NO 2161; 198pp; English.
PS
XX The invention relates to an enzymatic nucleic acid molecule which
CC specifically cleaves RNA derived from hepatitis C virus (HCV), in which
CC the binding arms of the enzymatic nucleic acid molecule comprises
CC sequences complementary to any of the defined substrate sequences given
CC in the specification. The nucleic acid molecule may be administered for
CC in the specification. The nucleic acid molecule may be administered for
CC
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CC the treatment of HCV infections, especially in combination with type I
CC interferons. The present sequence represents a HCV DNazyme substrate
CC sequence.
XX
XX Sequence 17 BP; 3 A; 5 C; 2 G; 0 T; 7 U; 0 Other;
SQ
    Query Match      0.8%; Score 13.8; DB 1; Length 17;
    Best Local Similarity 52.9%; Pred. No. 1.9e+02;
    Matches 9; Conservative 6; Mismatches 2; Indels 0; Gaps 0;
QY 689 GAGGCCTCACCTCTCT 705
DB 1 GAUGACUCACUUCUCU 17
RESULT 374
ADI83386
ID ADI83386 standard; RNA; 17 BP.
XX
XX AC ADI83386;
XX
XX 03-JUN-2004 (first entry)
XX
XX HCV DNazyme substrate sequence #632.
DE
XX ss; enzymatic nucleic acid; RNA cleavage; hepatitis C virus; HCV;
KW HCV infection; type I interferon; DNazyme.
KW
XX Hepatitis C virus.
OS
XX US2003125270-A1.
FN
XX
XX 03-JUL-2003.
PD
XX
XX 18-DEC-2000; 2000US-00740332.
PF
XX
XX 18-DEC-2000; 2000US-00740332.
PR
XX (BLAT/) BLATT L.
PA (MCSW/) MCSWIGGEN J.
PA (ROBE/) ROBERTS E.
PA (PAVC/) PAVCO P A.
PA (MACE/) MACEJACK D.
XX
XX Blatt L, Mcswiggen J, Roberts E, Pavco PA, Macejack D;
PI
XX WPI; 2004-031273/03.
DR
XX
XX Enzymatic nucleic acid molecules which specifically cleave RNA derived
PT from hepatitis C virus (HCV), useful for the treatment of HCV infections,
PT especially in combination with type I interferon therapy.
XX
XX Claim 1; SEQ ID NO 632; 198pp; English.
PS
XX The invention relates to an enzymatic nucleic acid molecule which
CC specifically cleaves RNA derived from hepatitis C virus (HCV), in which
CC the binding arms of the enzymatic nucleic acid molecule comprises
CC sequences complementary to any of the defined substrate sequences given
CC in the specification. The nucleic acid molecule may be administered for
CC the treatment of HCV infections, especially in combination with type I
CC interferons. The present sequence represents a HCV DNazyme substrate
CC sequence.
XX
XX Sequence 17 BP; 2 A; 1 C; 7 G; 1 T; 6 U; 0 Other;
SQ
    Query Match      0.8%; Score 13.8; DB 1; Length 17;
    Best Local Similarity 52.9%; Pred. No. 1.9e+02;
    Matches 9; Conservative 6; Mismatches 2; Indels 0; Gaps 0;
QY 1400 TGTGGATGTGCTTTTG 1416
DB 1 UGUGGAUGATGCUUGU 17
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RESULT 375
ACN64993/C
ID ACN64993 standard; DNA; 17 BP.
XX AC ACN64993;
XX DT 02-DEC-2004 (first entry)
XX DE Human GDMLP-1 probe SEQ ID NO:1895.
XX KW Human; ss; probe; myosin-like protein-1; hGDMLP-1;
XX KW hGDMLP-1 agonist hGDMLP antagonist; hGDMLP inhibitor; heart disorder;
XX KW skeletal muscle function.
XX OS Homo sapiens.
XX PN US2004137589-A1.
XX PD 15-JUL-2004.
XX PF 26-NOV-2003; 2003US-00723361.
XX PR 26-MAY-2000; 2000US-0207456P.
XX PR 21-SEP-2000; 2000US-0234687P.
XX PR 27-SEP-2000; 2000US-0236359P.
XX PR 04-OCT-2000; 2000GB-00024263.
XX PR 30-JAN-2001; 2001WO-US000661.
XX PR 30-JAN-2001; 2001WO-US000662.
XX PR 30-JAN-2001; 2001WO-US000663.
XX PR 30-JAN-2001; 2001WO-US000664.
XX PR 30-JAN-2001; 2001WO-US000665.
XX PR 30-JAN-2001; 2001WO-US000666.
XX PR 30-JAN-2001; 2001WO-US000667.
XX PR 30-JAN-2001; 2001WO-US000668.
XX PR 30-JAN-2001; 2001WO-US000669.
XX PR 30-JAN-2001; 2001WO-US000670.
XX PR 05-FEB-2001; 2001US-0266860P.
XX PR 25-MAY-2001; 2001US-00866108.
XX PA (GUY/) GU Y.
XX PA (JITY/) JI Y.
XX PA (PENN/) PENN S G.
XX PA (HANZ/) HANZEL D K.
XX PA (RANK/) RANK D.
XX PA (CHEN/) CHEN W.
XX PA (SHAN/) SHANNON M E.
XX PI Gu Y, Ji Y, Penn SG, Hanzel DK, Rank D, Chen W, Shannon ME;
XX WPI; 2004-533378/51.
XX PT Novel myosin-like protein-1, useful for treating or preventing disorder
XX PT associated with decreased expression or activity of human genome-derived
XX PT myosin-like protein-1 such as disorder of heart and/or skeletal muscle
XX PT function.
XX PS Disclosure; SEQ ID NO 1895; Opp; English.
XX CC The invention relates to a novel polypeptide (I) comprising a sequence
XX CC (S1) of myosin-like protein-1 (hGDMLP-1) having 2568 amino acids fully
XX CC defined in the specification, a fragment of at least 8 amino acids of
XX CC (S1), 95% deviation from (S1) which are conservative substitutions, and
XX CC 65% identity to (S1). A polypeptide of the invention acts as an agonist or
XX CC antagonist of hGDMLP-1, or as an inhibitor of hGDMLP-1 activity. A
XX CC pharmaceutical composition of the invention is useful for treating or
XX CC preventing a disorder associated with decreased expression or activity of
XX CC hGDMLP-1, such as a disorder of heart and/or skeletal muscle function.
XX CC The present sequence represents a 17-mer nucleotide, used in the
XX CC invention for scanning the sequence represented in ACN63102
XX SQ Sequence 17 BP; 2 A; 7 C; 4 G; 4 T; 0 U; 0 Other;
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Query Match 0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. NO. 1.9e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 93 GAGAGTGGGCGAGTCCT 109
DB 17 GAGAGAGCCAGGTCCT 1

RESULT 376
ACN71759
ID ACN71759 standard; DNA; 17 BP.
XX AC ACN71759;
XX DT 02-DEC-2004 (first entry)
XX DE Human GDMLP-1 probe SEQ ID NO:8661.
XX KW Human; ss; probe; myosin-like protein-1; hGDMLP-1;
XX KW hGDMLP-1 agonist hGDMLP antagonist; hGDMLP inhibitor; heart disorder;
XX KW skeletal muscle function.
XX OS Homo sapiens.
XX PN US2004137589-A1.
XX PD 15-JUL-2004.
XX PF 26-NOV-2003; 2003US-00723361.
XX PR 26-MAY-2000; 2000US-0207456P.
XX PR 21-SEP-2000; 2000US-0234687P.
XX PR 27-SEP-2000; 2000US-0236359P.
XX PR 04-OCT-2000; 2000GB-00024263.
XX PR 30-JAN-2001; 2001WO-US000661.
XX PR 30-JAN-2001; 2001WO-US000662.
XX PR 30-JAN-2001; 2001WO-US000663.
XX PR 30-JAN-2001; 2001WO-US000664.
XX PR 30-JAN-2001; 2001WO-US000665.
XX PR 30-JAN-2001; 2001WO-US000666.
XX PR 30-JAN-2001; 2001WO-US000667.
XX PR 30-JAN-2001; 2001WO-US000668.
XX PR 30-JAN-2001; 2001WO-US000669.
XX PR 30-JAN-2001; 2001WO-US000670.
XX PR 05-FEB-2001; 2001US-0266860P.
XX PR 25-MAY-2001; 2001US-00866108.
XX PA (GUY/) GU Y.
XX PA (JITY/) JI Y.
XX PA (PENN/) PENN S G.
XX PA (HANZ/) HANZEL D K.
XX PA (RANK/) RANK D.
XX PA (CHEN/) CHEN W.
XX PA (SHAN/) SHANNON M E.
XX PI Gu Y, Ji Y, Penn SG, Hanzel DK, Rank D, Chen W, Shannon ME;
XX WPI; 2004-533378/51.
XX PT Novel myosin-like protein-1, useful for treating or preventing disorder
XX PT associated with decreased expression or activity of human genome-derived
XX PT myosin-like protein-1 such as disorder of heart and/or skeletal muscle
XX PT function.
XX PS Disclosure; SEQ ID NO 8661; Opp; English.
XX CC The invention relates to a novel polypeptide (I) comprising a sequence
XX CC (S1) of myosin-like protein-1 (hGDMLP-1) having 2568 amino acids fully
XX CC defined in the specification, a fragment of at least 8 amino acids of
XX CC (S1), 95% deviation from (S1) which are conservative substitutions, and
XX CC 65% identity to (S1). A polypeptide of the invention acts as an agonist or
XX CC antagonist of hGDMLP-1, or as an inhibitor of hGDMLP-1 activity. A
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XX WPI; 2004-533378/51.  
XX Novel myosin-like protein-1, useful for treating or preventing disorder  
PT associated with decreased expression or activity of human genome-derived  
PT myosin-like protein-1 such as disorder of heart and/or skeletal muscle  
PT function.  
XX  
XX Disclosure; SEQ ID NO 9689; Opp; English.  
PS  
XX  
XX The invention relates to a novel polypeptide (I) comprising a sequence  
CC (S1) of myosin-like protein-1 (hGDMPLP-1) having 2568 amino acids fully  
CC defined in the specification, a fragment of at least 8 amino acids of  
CC (S1), 95% deviation from (S1) which are conservative substitutions, and  
CC 65% identity to (S1). A polypeptide of the invention acts as an agonist or  
CC antagonist of hGDMPLP-1, or as an inhibitor of hGDMPLP-1 activity. A  
CC pharmaceutical composition of the invention is useful for treating or  
CC preventing a disorder associated with decreased expression or activity of  
CC hGDMPLP-1, such as a disorder of heart and/or skeletal muscle function.  
CC The present sequence represents a 17-mer nucleotide, used in the  
CC invention for scanning the sequence represented in ACN63103  
XX  
XX Sequence 17 BP; 2 A; 9 C; 3 G; 3 T; 0 U; 0 Other;  
SQ  
Query Match 0.8%; Score 13.8; DB 1; Length 17;  
Best Local Similarity 88.2%; Pred. No. 1.9e+02;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 91 GGGAGAGTGGCAGGTC 107  
DB 17 GGGAGAGTGGCAGGTC 1  
RESULT 379  
ACN71758  
ID ACN71758 standard; DNA; 17 BP.  
XX  
XX ACN71758;  
XX  
XX 02-DEC-2004 (first entry)  
XX  
XX Human GDMPLP-1 probe SEQ ID NO:8660.  
XX  
XX Human; ss; probe; myosin-like protein-1; hGDMPLP-1;  
KW hGDMPLP-1 agonist hGDMPLP antagonist; hGDMPLP inhibitor; heart disorder;  
KW skeletal muscle function.  
XX  
XX Homo sapiens.  
XX  
XX US2004137589-A1.  
XX  
XX 15-JUL-2004.  
XX  
XX 26-NOV-2003; 2003US-00723361.  
XX  
XX 26-MAY-2000; 2000US-0207456P.  
XX 21-SEP-2000; 2000US-0234687P.  
XX 27-SEP-2000; 2000US-0236359P.  
XX 04-OCT-2000; 2000GB-00024263.  
XX 30-JAN-2001; 2001WO-US000661.  
XX 30-JAN-2001; 2001WO-US000662.  
XX 30-JAN-2001; 2001WO-US000664.  
XX 30-JAN-2001; 2001WO-US000665.  
XX 30-JAN-2001; 2001WO-US000666.  
XX 30-JAN-2001; 2001WO-US000667.  
XX 30-JAN-2001; 2001WO-US000668.  
XX 30-JAN-2001; 2001WO-US000669.  
XX 30-JAN-2001; 2001WO-US000670.  
XX 05-FEB-2001; 2001US-0266860P.  
XX 25-MAY-2001; 2001US-00866108.  
XX  
XX (GUY/) GU Y.

PA (JIY/) JI Y.  
PA (PENN/) PENN S G.  
PA (HANZ/) HANZEL D K.  
PA (RANK/) RANK D.  
PA (CHEN/) CHEN W.  
PA (SHAN/) SHANNON M E.  
XX  
PI Gu Y, Ji Y, Penn SG, Hanzel DK, Rank D, Chen W, Shannon ME;  
XX  
XX WPI; 2004-533378/51.  
XX  
XX Novel myosin-like protein-1, useful for treating or preventing disorder  
PT associated with decreased expression or activity of human genome-derived  
PT myosin-like protein-1 such as disorder of heart and/or skeletal muscle  
PT function.  
XX  
XX Disclosure; SEQ ID NO 8660; Opp; English.  
XX  
XX The invention relates to a novel polypeptide (I) comprising a sequence  
CC (S1) of myosin-like protein-1 (hGDMPLP-1) having 2568 amino acids fully  
CC defined in the specification, a fragment of at least 8 amino acids of  
CC (S1), 95% deviation from (S1) which are conservative substitutions, and  
CC 65% identity to (S1). A polypeptide of the invention acts as an agonist or  
CC antagonist of hGDMPLP-1, or as an inhibitor of hGDMPLP-1 activity. A  
CC pharmaceutical composition of the invention is useful for treating or  
CC preventing a disorder associated with decreased expression or activity of  
CC hGDMPLP-1, such as a disorder of heart and/or skeletal muscle function.  
CC The present sequence represents a 17-mer nucleotide, used in the  
CC invention for scanning the sequence represented in ACN63103  
XX  
XX Sequence 17 BP; 7 A; 3 C; 6 G; 1 T; 0 U; 0 Other;  
SQ  
Query Match 0.8%; Score 13.8; DB 1; Length 17;  
Best Local Similarity 88.2%; Pred. No. 1.9e+02;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 267 CTAGAGAGGCCAGAA 283  
DB 1 CTGGAGAGGCCAGAA 17  
RESULT 380  
ACN71761  
ID ACN71761 standard; DNA; 17 BP.  
XX  
XX ACN71761;  
XX  
XX 02-DEC-2004 (first entry)  
XX  
XX Human GDMPLP-1 probe SEQ ID NO:8663.  
XX  
XX Human; ss; probe; myosin-like protein-1; hGDMPLP-1;  
KW hGDMPLP-1 agonist hGDMPLP antagonist; hGDMPLP inhibitor; heart disorder;  
KW skeletal muscle function.  
XX  
XX Homo sapiens.  
XX  
XX US2004137589-A1.  
XX  
XX 15-JUL-2004.  
XX  
XX 26-NOV-2003; 2003US-00723361.  
XX  
XX 26-MAY-2000; 2000US-0207456P.  
XX 21-SEP-2000; 2000US-0234687P.  
XX 27-SEP-2000; 2000US-0236359P.  
XX 04-OCT-2000; 2000GB-00024263.  
XX 30-JAN-2001; 2001WO-US000661.  
XX 30-JAN-2001; 2001WO-US000662.  
XX 30-JAN-2001; 2001WO-US000664.  
XX 30-JAN-2001; 2001WO-US000665.  
XX 30-JAN-2001; 2001WO-US000666.  
XX 30-JAN-2001; 2001WO-US000667.  
XX 30-JAN-2001; 2001WO-US000668.  
XX 30-JAN-2001; 2001WO-US000669.  
XX 05-FEB-2001; 2001US-0266860P.  
XX 25-MAY-2001; 2001US-00866108.  
XX  
XX (GUY/) GU Y.

```

PR 30-JAN-2001; 2001WO-US000667.
PR 30-JAN-2001; 2001WO-US000668.
PR 30-JAN-2001; 2001WO-US000669.
PR 30-JAN-2001; 2001WO-US000670.
PR 05-FEB-2001; 2001US-0266860P.
PR 25-MAY-2001; 2001US-00866108.
XX
PA (GUY/) GU Y.
PA (JIY/) JI Y.
PA (PENN/) PENN S G.
PA (HANZ/) HANZEL D K.
PA (RANK/) RANK D.
PA (CHEN/) CHEN W.
PA (SHAN/) SHANNON M E.
XX
PI Gu Y, Ji Y, Penn SG, Hanzel DK, Rank D, Chen W, Shannon ME;
XX WPI; 2004-533378/51.
XX
XX Novel myosin-like protein-1, useful for treating or preventing disorder
PT associated with decreased expression or activity of human genome-derived
PT myosin-like protein-1 such as disorder of heart and/or skeletal muscle
PT function.
XX
XX Disclosure; SEQ ID NO 8663; Opp; English.
XX
XX The invention relates to a novel polypeptide (I) comprising a sequence
CC (S1) of myosin-like protein-1 (hGDMPLP-1) having 2568 amino acids fully
CC defined in the specification, a fragment of at least 8 amino acids of
CC (S1), 95% deviation from (S1) which are conservative substitutions, and
CC 65% identity to (S1). A polypeptide of the invention acts as an agonist or
CC antagonist of hGDMPLP-1, or as an inhibitor of hGDMPLP-1 activity. A
CC pharmaceutical composition of the invention is useful for treating or
CC preventing a disorder associated with decreased expression or activity of
CC hGDMPLP-1, such as a disorder of heart and/or skeletal muscle function.
CC The present sequence represents a 17-mer nucleotide, used in the
CC invention for scanning the sequence represented in ACN63103
XX
XX Sequence 17 BP; 8 A; 2 C; 7 G; 0 T; 0 U; 0 Other;
SQ
Query Match 0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.9e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 270 GAAGAAGCCAGAGAA 286
DB 1 GAGGAAGCCAGAGGA 17
XX
RESULT 381
ACN65741/c
ID ACN65741 standard; DNA; 17 BP.
XX
AC ACN65741;
XX
XX 02-DEC-2004 (first entry)
XX
XX Human GDMPLP-1 probe SEQ ID NO:2643.
XX
XX Human; ss; probe; myosin-like protein-1; hGDMPLP-1;
KW hGDMPLP-1 agonist hGDMPLP antagonist; hGDMPLP inhibitor; heart disorder;
KW skeletal muscle function.
XX
XX Homo sapiens.
XX
XX US2004137589-A1.
XX
XX 15-JUL-2004.
XX
XX 26-NOV-2003; 2003US-00723361.
XX
XX 26-MAY-2000; 2000US-0207456P.
PR
XX 21-SEP-2000; 2000US-0234687P.

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PR 27-SEP-2000; 2000US-0236359P.
PR 04-OCT-2000; 2000GB-00024263.
PR 30-JAN-2001; 2001WO-US000661.
PR 30-JAN-2001; 2001WO-US000662.
PR 30-JAN-2001; 2001WO-US000663.
PR 30-JAN-2001; 2001WO-US000664.
PR 30-JAN-2001; 2001WO-US000665.
PR 30-JAN-2001; 2001WO-US000666.
PR 30-JAN-2001; 2001WO-US000667.
PR 30-JAN-2001; 2001WO-US000668.
PR 30-JAN-2001; 2001WO-US000669.
PR 30-JAN-2001; 2001WO-US000670.
PR 05-FEB-2001; 2001US-0266860P.
PR 25-MAY-2001; 2001US-00866108.
XX
XX (GUY/) GU Y.
XX (JIY/) JI Y.
XX (PENN/) PENN S G.
XX (HANZ/) HANZEL D K.
XX (RANK/) RANK D.
XX (CHEN/) CHEN W.
XX (SHAN/) SHANNON M E.
XX
PI Gu Y, Ji Y, Penn SG, Hanzel DK, Rank D, Chen W, Shannon ME;
XX WPI; 2004-533378/51.
XX
XX Novel myosin-like protein-1, useful for treating or preventing disorder
PT associated with decreased expression or activity of human genome-derived
PT myosin-like protein-1 such as disorder of heart and/or skeletal muscle
PT function.
XX
XX Disclosure; SEQ ID NO 2643; Opp; English.
XX
XX The invention relates to a novel polypeptide (I) comprising a sequence
CC (S1) of myosin-like protein-1 (hGDMPLP-1) having 2568 amino acids fully
CC defined in the specification, a fragment of at least 8 amino acids of
CC (S1), 95% deviation from (S1) which are conservative substitutions, and
CC 65% identity to (S1). A polypeptide of the invention acts as an agonist or
CC antagonist of hGDMPLP-1, or as an inhibitor of hGDMPLP-1 activity. A
CC pharmaceutical composition of the invention is useful for treating or
CC preventing a disorder associated with decreased expression or activity of
CC hGDMPLP-1, such as a disorder of heart and/or skeletal muscle function.
CC The present sequence represents a 17-mer nucleotide, used in the
CC invention for scanning the sequence represented in ACN63102
XX
XX Sequence 17 BP; 1 A; 4 C; 8 G; 4 T; 0 U; 0 Other;
SQ
Query Match 0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.9e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 845 CTTCCAGACCCGCCAA 861
DB 17 CTGCCAGACCCGCCAA 1
XX
RESULT 382
ACN70453
ID ACN70453 standard; DNA; 17 BP.
XX
XX ACN70453;
XX
XX 02-DEC-2004 (first entry)
XX
XX Human GDMPLP-1 probe SEQ ID NO:7355.
XX
XX Human; ss; probe; myosin-like protein-1; hGDMPLP-1;
KW hGDMPLP-1 agonist hGDMPLP antagonist; hGDMPLP inhibitor; heart disorder;
KW skeletal muscle function.
XX
XX Homo sapiens.
XX

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RESULT 384		Best Local Similarity	88.2%;	Pred. No. 1.9e+02;			
ID	ACN71762	ACN71762 standard; DNA; 17 BP.	Matches	15;	Conservative	0;	Mismatches
XX	AC	ACN71762;				2;	Indels
XX	AC	ACN71762;				0;	Gaps
XX	AC	ACN71762;				0;	Gaps
DT	DT	02-DEC-2004 (first entry)					
XX	XX	Human GDMPLP-1 probe SEQ ID NO:8664.					
XX	XX	Human; ss; probe; myosin-like protein-1; hGDMPLP-1;					
KW	KW	hGDMPLP-1 agonist hGDMPLP antagonist; hGDMPLP inhibitor; heart disorder;					
KW	KW	skeletal muscle function.					
XX	OS	Homo sapiens.					
XX	FN	US2004137589-A1.					
XX	PD	15-JUL-2004.					
XX	PF	26-NOV-2003; 2003US-00723361.					
XX	XX	26-MAY-2000; 2000US-0207456P.					
PR	PR	21-SEP-2000; 2000US-0234687P.					
PR	PR	27-SEP-2000; 2000US-0236359P.					
PR	PR	04-OCT-2000; 2000GB-00024263.					
PR	PR	30-JAN-2001; 2001WO-US000661.					
PR	PR	30-JAN-2001; 2001WO-US000662.					
PR	PR	30-JAN-2001; 2001WO-US000663.					
PR	PR	30-JAN-2001; 2001WO-US000664.					
PR	PR	30-JAN-2001; 2001WO-US000665.					
PR	PR	30-JAN-2001; 2001WO-US000666.					
PR	PR	30-JAN-2001; 2001WO-US000667.					
PR	PR	30-JAN-2001; 2001WO-US000668.					
PR	PR	30-JAN-2001; 2001WO-US000669.					
PR	PR	30-JAN-2001; 2001WO-US000670.					
PR	PR	05-FEB-2001; 2001US-0266860P.					
PR	PR	25-MAY-2001; 2001US-00866108.					
XX	XX	(GUY/) GU Y.					
PA	PA	(JIY/) JI Y.					
PA	PA	(PENN/) PENN S G.					
PA	PA	(HANZ/) HANZEL D K.					
PA	PA	(RANK/) RANK D.					
PA	PA	(CHEN/) CHEN W.					
PA	PA	(SHAN/) SHANNON M E.					
XX	XX	Gu Y, Ji Y, Penn SG, Hanzel DK, Rank D, Chen W, Shannon ME;					
PI	PI	WPI; 2004-533378/51.					
XX	XX						
XX	XX	Novel myosin-like protein-1, useful for treating or preventing disorder					
PT	PT	associated with decreased expression or activity of human genome-derived					
PT	PT	myosin-like protein-1 such as disorder of heart and/or skeletal muscle					
PT	PT	function.					
XX	XX	Disclosure; SEQ ID NO 8664; Opp; English.					
XX	XX	The invention relates to a novel polypeptide (I) comprising a sequence					
CC	CC	(S1) of myosin-like protein-1 (hGDMPLP-1) having 2568 amino acids fully					
CC	CC	defined in the specification, a fragment of at least 8 amino acids of					
CC	CC	(S1), 95% deviation from (S1) which are conservative substitutions, and					
CC	CC	65% identity to (S1). A polypeptide of the invention acts as an agonist or					
CC	CC	antagonist of hGDMPLP-1, or as an inhibitor of hGDMPLP-1 activity. A					
CC	CC	pharmaceutical composition of the invention is useful for treating or					
CC	CC	hGDMPLP-1, such as a disorder of heart and/or skeletal muscle function.					
CC	CC	The present sequence represents a 17-mer nucleotide, used in the					
CC	CC	invention for scanning the sequence represented in ACN63103					
XX	XX	Sequence 17 BP; 8 A; 2 C; 7 G; 0 T; 0 U; 0 Other;					
SQ	SQ	Query Match	0.8%;	Score	13.8;	DB	1;
						Length	17;

CC preventing a disorder associated with decreased expression or activity of  
 CC hGDMLP-1, such as a disorder of heart and/or skeletal muscle function.  
 CC The present sequence represents a 17-mer nucleotide, used in the  
 CC invention for scanning the sequence represented in ACN63103

XX SQ Sequence 17 BP; 6 A; 2 C; 6 G; 3 T; 0 U; 0 Other;

Query Match 0.8%; Score 13.8; DB 1; Length 17;

Best Local Similarity 88.2%; Pred. No. 1.9e+02;

Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 292 AGGATGCCCTAAATGAG 308

||||| ||| |||||

DB 1 AGGATGACCTGAATGAG 17

RESULT 386

ACN72786/c

ID ACN72786 standard; DNA; 17 BP.

XX ACN72786;

XX ACN72786;

XX ACN72786;

DT 02-DEC-2004 (first entry)

XX Human GDMLP-1 probe SEQ ID NO:9688.

DE Human; ss; probe; myosin-like protein-1; hGDMLP-1;

XX hGDMLP-1 agonist hGDMLP antagonist; hGDMLP inhibitor; heart disorder;

KW skeletal muscle function.

XX Homo sapiens.

OS US2004137589-A1.

PN 15-JUL-2004.

XX 26-NOV-2003; 2003US-00723361.

XX 26-MAY-2000; 2000US-0207456P.

XX 21-SEP-2000; 2000US-0234687P.

XX 27-SEP-2000; 2000US-0236359P.

XX 04-OCT-2000; 2000GB-00024263.

XX 30-JAN-2001; 2001WO-US000661.

XX 30-JAN-2001; 2001WO-US000662.

XX 30-JAN-2001; 2001WO-US000663.

XX 30-JAN-2001; 2001WO-US000664.

XX 30-JAN-2001; 2001WO-US000665.

XX 30-JAN-2001; 2001WO-US000666.

XX 30-JAN-2001; 2001WO-US000667.

XX 30-JAN-2001; 2001WO-US000668.

XX 30-JAN-2001; 2001WO-US000669.

XX 05-FEB-2001; 2001WO-US000670.

XX 25-MAY-2001; 2001US-0268660P.

XX (GUY/) GU Y.

PA (JIV/) JI Y.

PA (PENN/) PENN S G.

PA (HANZ/) HANZEL D K.

PA (RANK/) RANK D.

PA (CHEN/) CHEN W.

PA (SHAN/) SHANNON M E.

XX Gu Y, Ji Y, Penn SG, Hanzel DK, Rank D, Chen W, Shannon ME;

PI WPI; 2004-533378/51.

XX Novel myosin-like protein-1, useful for treating or preventing disorder

PT associated with decreased expression or activity of human genome-derived

PT myosin-like protein-1 such as disorder of heart and/or skeletal muscle

PT function.

XX Disclosure; SEQ ID NO 9688; 0pp; English.

XX The invention relates to a novel polypeptide (I) comprising a sequence  
 CC (S1) of myosin-like protein-1 (hGDMLP-1) having 2568 amino acids fully  
 CC defined in the specification, a fragment of at least 8 amino acids of  
 CC (S1), 95% deviation from (S1) which are conservative substitutions, and  
 CC 65% identity to (S1). A polypeptide of the invention acts as an agonist or  
 CC antagonist of hGDMLP-1, or as an inhibitor of hGDMLP-1 activity. A  
 CC pharmaceutical composition of the invention is useful for treating or  
 CC preventing a disorder associated with decreased expression or activity of  
 CC hGDMLP-1, such as a disorder of heart and/or skeletal muscle function.  
 CC The present sequence represents a 17-mer nucleotide, used in the  
 CC invention for scanning the sequence represented in ACN63103

XX SQ Sequence 17 BP; 2 A; 8 C; 4 G; 3 T; 0 U; 0 Other;

Query Match 0.8%; Score 13.8; DB 1; Length 17;

Best Local Similarity 88.2%; Pred. No. 1.9e+02;

Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 92 GGAGAGTGGCGAGGTCC 108

||||| ||| |||||

DB 17 GGAGAGTGGCGAGGTCC 1

RESULT 387

ABL52123/c

ID ABL52123 standard; DNA; 15 BP.

XX ABL52123;

XX ABL52123;

XX 12-JUL-2002 (first entry)

XX Human PER1 allele specific oligonucleotide primer SEQ ID NO:48.

DE Human; period (Drosophila) homologue 1; PER1; polymorphic variant;

KW polymorphic site; genotyping; haplotyping; circadian rhythm regulation;

KW single nucleotide polymorphism; SNP; gene; primer; ss.

XX Homo sapiens.

XX Key Location/Qualifiers

FT misc\_feature 14

FT /tag= a

FT /note= "polymorphic site indicated by an ambiguity base"

XX WO200222650-A2.

XX 21-MAR-2002.

XX 13-SEP-2001; 2001WO-US028780.

XX 13-SEP-2000; 2000US-0232468P.

XX (GENA-) GENAISSANCE PHARM INC.

XX Duda A, Kliem SE, Koshiy B;

XX WPI; 2002-393941/42.

XX Novel isolated human period Drosophila homolog 1 polynucleotide, useful

PT for therapeutic purposes, for studying the expression and function of the

PT polynucleotide, and for expressing the homolog.

XX Claim 17; Page 15; 162pp; English.

XX The present invention describes an isolated human period (Drosophila)

CC homologue 1, (PER1) polynucleotide (I) comprising a sequence which is a

CC polymorphic variant for a reference sequence (ABL52077) for the PER1 gene

CC or its fragment, or a polymorphic variant of a reference sequence

CC (ABL52078) for a PER1 cDNA or its fragment. The present invention also

CC describes methods for genotyping and haplotyping the PER1 gene of an

CC individual. (I) is useful in studying the expression and function of

CC PER1, and in expressing PER1 protein for use in screening for candidate

CC drugs to treat diseases related to PER1 activity. (I) is useful for  
 CC therapeutic purposes. A recombinant non-human organism transformed or  
 CC transfected with (I) can be used for studying expression of the PER1  
 CC isogenes in vivo, for in vivo screening and testing of drugs targeted  
 CC against PER1 protein, and for testing the efficacy of therapeutic agents  
 CC and compounds for disorders associated with circadian rhythm regulation.  
 CC The present sequence represents an allele specific oligonucleotide primer  
 CC for human PER1, which is used in the exemplification of the present  
 CC invention  
 XX  
 XX Sequence 15 BP; 1 A; 3 C; 8 G; 2 T; 0 U; 1 Other;  
 SQ  
 Query Match 0.8%; Score 13.6; DB 1; Length 15;  
 Best Local Similarity 92.9%; Pred. No. 1.3e+02;  
 Matches 13; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1500 CCAGGCCCGCCT 1513  
 Db :|||||||  
 14 YCAGGCCCGCCT 1  
 RESULT 388  
 AAS95535  
 ID AAS95535 standard; DNA; 15 BP.  
 XX  
 AC AAS95535;  
 XX  
 DT 14-FEB-2002 (first entry)  
 XX  
 DE Human IL8RB gene allele-specific oligonucleotide probe #11.  
 XX  
 KW Human; interleukin 8 receptor beta; IL8RB; ss; antiinflammatory; probe;  
 KW haplotyping; haplotype pair; single nucleotide polymorphism; genotyping;  
 KW gene therapy; drug screening; chronic obstructive pulmonary disease;  
 KW inflammatory disease; sequencing primer; PCR primer.  
 XX  
 OS Homo sapiens.  
 XX  
 XX WO200179221-A2.  
 XX  
 PD 25-OCT-2001.  
 XX  
 PF 12-APR-2001; 2001WO-US011942.  
 XX  
 PR 12-APR-2000; 2000US-0196734P.  
 XX  
 PA (GENA-) GENAISSANCE PHARM INC.  
 XX  
 PI Bentivegna SC, Chew A, Choi JY, Denton RR, Nandabalan K;  
 XX  
 XX WPI; 2002-055250/07.  
 XX  
 CC New polymorphic variants comprising interleukin-8 receptor beta (IL8RB)  
 CC isogene, useful in expressing IL8RB protein for use in screening for  
 CC candidate drugs to treat diseases related to IL8RB activity, e.g.  
 CC inflammatory disorders.  
 XX  
 XX Claim 16; Page 13; 74pp; English.  
 XX  
 CC The invention relates to single nucleotide polymorphisms in the human  
 CC interleukin 8 receptor beta (IL8RB) gene. A method for haplotyping the  
 CC IL8RB gene in an individual comprises identifying the nucleotide at one  
 CC or more polymorphic sites and determining whether one of the copies of  
 CC the gene is defined by one of the IL8RB haplotypes given in the  
 CC specification or whether both copies are defined by a haplotype pair.  
 CC This method is useful in genotyping, whereby all possible haplotype pairs  
 CC can be assigned to specific genotypes. An association between a trait and  
 CC a haplotype or haplotype pair of the IL8RB gene can be identified by  
 CC comparing the frequency of the haplotype or haplotype pair in a  
 CC population exhibiting the trait with the frequency of the haplotype or  
 CC haplotype pair in a reference population, where a higher haplotype  
 CC frequency in the trait population indicates the trait is associated with  
 CC the haplotype or haplotype pair. IL8RB and its corresponding DNA are used

CC for studying the expression and function of IL8RB, for use in screening  
 CC for candidate drugs to treat diseases related to IL8RB activity, such as  
 CC chronic obstructive pulmonary disease and other inflammatory disorders.  
 CC The sequences are also useful for studying the effect of variation on the  
 CC biological activity of IL8RB as well as on the binding affinity of  
 CC candidate drugs targeting IL8RB. Sequences AAS95525-AAS95579 represent  
 CC allele-specific oligonucleotide probes, sequencing primers and PCR  
 CC primers used to detect IL8RB gene polymorphisms  
 XX  
 XX Sequence 15 BP; 5 A; 4 C; 4 G; 1 T; 0 U; 1 Other;  
 SQ

Query Match 0.8%; Score 13.6; DB 1; Length 15;  
 Best Local Similarity 92.9%; Pred. No. 1.3e+02;  
 Matches 13; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 197 CAACGGGGTGAAC 210  
 Db :|||||||  
 1 CAACGGGGTGAAC 14  
 RESULT 389  
 AAT54903  
 ID AAT54903 standard; RNA; 15 BP.  
 XX  
 AC AAT54903;  
 XX  
 DT 25-MAR-2003 (revised)  
 DT 07-APR-1997 (first entry)  
 XX  
 DE Mouse relA hammerhead ribozyme target sequence (nt. position 1250).  
 XX  
 KW Enzymatic nucleic acid; ribozyme; trans cleavage; inhibition;  
 KW gene expression; downregulation; interleukin-5; IL-5; ICAM-1;  
 KW intercellular adhesion molecule; rel A; tumour necrosis factor;  
 KW TNF-alpha; respiratory syncytial virus; RSV; bcr-abl; oncogene;  
 KW translocation; chronic myelogenous leukaemia; CML; cancer;  
 KW Philadelphia chromosome; inflammation; autoimmune disease;  
 KW atherosclerosis; myocardial infarction; stroke; restenosis;  
 KW transplant rejection; rheumatoid arthritis; psoriasis;  
 KW myocardial ischaemia; Kawasaki disease; septic shock; HIV;  
 KW human immunodeficiency virus; acquired immune deficiency syndrome; AIDS;  
 KW ss.  
 XX  
 OS Mus musculus.  
 XX  
 XX WO9523225-A2.  
 XX  
 PD 31-AUG-1995.  
 XX  
 XX 23-FEB-1995; 95WO-IB000156.  
 XX  
 XX 23-FEB-1994; 94US-00201109.  
 XX 29-MAR-1994; 94US-00218934.  
 XX 04-APR-1994; 94US-00222795.  
 XX 07-APR-1994; 94US-00224483.  
 XX 15-APR-1994; 94US-00227958.  
 XX 15-APR-1994; 94US-00228041.  
 XX 18-MAY-1994; 94US-00245736.  
 XX 06-JUL-1994; 94US-00271280.  
 XX 15-AUG-1994; 94US-00291932.  
 XX 17-AUG-1994; 94US-00291433.  
 XX 19-AUG-1994; 94US-00292620.  
 XX 02-SEP-1994; 94US-00293520.  
 XX 08-SEP-1994; 94US-00300000.  
 XX 23-SEP-1994; 94US-00311486.  
 XX 28-SEP-1994; 94US-00311749.  
 XX 03-OCT-1994; 94US-00314397.  
 XX 07-OCT-1994; 94US-00316771.  
 XX 11-OCT-1994; 94US-00319492.  
 XX 04-NOV-1994; 94US-00321993.  
 XX 10-NOV-1994; 94US-00334847.  
 XX 10-NOV-1994; 94US-00337608.



PR 28-NOV-1994; 94US-00345516.  
 PR 16-DEC-1994; 94US-00357577.  
 PR 23-DEC-1994; 94US-00363233.  
 PR 30-JAN-1995; 95US-00380734.  
 XX (RIBO-) RIBOZYME PHARM INC.  
 XX Stinchcomb DT, Chowkira B, Dorenzo A, Draper KG, Dudycz LM;  
 PI Grimm S, Karpaisky A, Kislich K, Matulic-Adamic J, Mcswiggen JA;  
 PI Modak A, Pavco P, Beigleman L, Sullivan SM, Sweedler D, Thompson JD;  
 PI Tracz D, Usman N, Wincott FE, Woolf T;  
 XX WPI; 1995-351090/45.  
 DR Ribozymes having modified bases and methods for producing them - for use  
 XX in inhibiting disease related genes.  
 XX Claim 2; Page 226; 407pp; English.  
 XX The present sequence represents a preferred target sequence for an  
 CC enzymatic nucleic acid (i.e. a ribozyme) which cleaves relA mRNA at the  
 CC nucleotide base position indicated in the DE line. The relA gene product  
 CC is a subunit of the transcriptional regulator NF-kappaB and is implicated  
 CC specifically in the induction of inflammatory responses. Regions of the  
 CC mRNA that do not form secondary folding structures and that contain  
 CC potential hammerhead and hairpin ribozyme cleavage sites were identified  
 CC by computer analysis. Ribozymes directed against these mRNA sequences  
 CC were designed and synthesised with modifications that improve their  
 CC nuclease resistance. The ribozymes are designed to cleave the target  
 CC sequences and thereby inhibit relA expression, making them potentially  
 CC useful for treating rheumatoid arthritis, restenosis and asthma as well  
 CC as for increasing tolerance to transplanted tissues. The potential  
 CC immunosuppressive properties of a ribozyme that cleaves relA mRNA means  
 CC that uses are limited to local delivery, acute indications or ex vivo  
 CC treatment. (Updated on 25-MAR-2003 to correct PI field.)  
 XX Sequence 15 BP; 2 A; 8 C; 3 G; 0 T; 2 U; 0 Other;  
 SQ Query Match 0.8%; Score 13.4; DB 1; Length 15;  
 Best Local Similarity 86.7%; Pred. No. 1.4e+02;  
 Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
 QY 1507 CCAGCCTCCAGGCC 1521  
 Db 1 CCAGCCUCCAGGCUC 15  
 RESULT 390  
 AAV31969/c  
 ID AAV31969 standard; DNA; 15 BP.  
 XX AAV31969;  
 AC AAV31969;  
 XX 21-AUG-1998 (first entry)  
 DT Peptide nucleic acid probe 112.  
 DE Peptide nucleic acid; PNA; probe; hybridisation; mycobacteria;  
 KW ribosomal nucleic acid; rRNA; drug-resistant strain; mutation; ss.  
 XX Synthetic.  
 OS Mycobacterium sp.  
 XX Key Location/Qualifiers  
 FH modified\_base 1..15  
 FT /\*tag= a  
 FT /note= "This sequence contains a polyamide backbone  
 instead of a deoxyribose backbone"  
 XX WO9815648-A1.  
 PN 16-APR-1998.  
 XX Stender H, Lund K, Mollerup TA;

PF 03-OCT-1997; 97WO-DK000425.  
 XX 04-OCT-1996; 96DK-00001096.  
 PR 18-OCT-1996; 96DK-00001156.  
 PR 05-MAY-1997; 97DK-00000512.  
 XX (DAKO-) DAKO AS.  
 XX Stender H, Lund K, Mollerup TA;  
 XX WPI; 1998-240831/21.  
 DR Peptide nucleic acid probes for detection of ribosomal nucleic acid of  
 XX mycobacteria - allow differentiation between species of tuberculosis  
 XX complex and others and can penetrate cell membranes without pretreatment.  
 XX Claim 22; Page 67; 106pp; English.  
 XX This is the nucleotide sequence of the peptide nucleic acid (PNA) probe  
 CC used in the method of the invention, to detect ribosomal nucleic acid of  
 CC mycobacteria. The probes are used, in situ or in vitro, for detection of  
 CC the Mycobacterium tuberculosis complex (MTC), specifically M.  
 CC tuberculosis, and especially in sputum samples, but also in other body  
 CC fluids, biopsy specimens, foods, soil, air and water. Particularly, they  
 CC are used to diagnose, stage or monitor infection, or for identification  
 CC of drug-resistant strains (which generally have mutations in rRNA)  
 XX Sequence 15 BP; 2 A; 3 C; 1 G; 9 T; 0 U; 0 Other;  
 SQ Query Match 0.8%; Score 13.4; DB 1; Length 15;  
 Best Local Similarity 93.3%; Pred. No. 1.4e+02;  
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 177 AAGGAATTCAAAT 191  
 Db 15 AAGGAATGTCAAAT 1  
 RESULT 391  
 AAV31970/c  
 ID AAV31970 standard; DNA; 15 BP.  
 XX AAV31970;  
 AC AAV31970;  
 XX 21-AUG-1998 (first entry)  
 DT Peptide nucleic acid probe 113.  
 DE Peptide nucleic acid; PNA; probe; hybridisation; mycobacteria;  
 KW ribosomal nucleic acid; rRNA; drug-resistant strain; mutation; ss.  
 XX Synthetic.  
 OS Mycobacterium sp.  
 XX Key Location/Qualifiers  
 FH modified\_base 1..15  
 FT /\*tag= a  
 FT /note= "This sequence contains a polyamide backbone  
 instead of a deoxyribose backbone"  
 XX WO9815648-A1.  
 PN 16-APR-1998.  
 XX Stender H, Lund K, Mollerup TA;

```

XX DR WPI; 1998-240831/21.
XX
XX PT Peptide nucleic acid probes for detection of ribosomal nucleic acid of
XX mycobacteria - allow differentiation between species of tuberculosis
XX complex and others and can penetrate cell membranes without pretreatment.
XX
XX PS Claim 22; Page 67; 106pp; English.
XX
XX CC This is the nucleotide sequence of the peptide nucleic acid (PNA) probe
XX used in the method of the invention, to detect ribosomal nucleic acid of
XX mycobacteria. The probes are used, in situ or in vitro, for detection of
XX the Mycobacterium tuberculosis complex (MTC), specifically M.
XX tuberculosis, and especially in sputum samples, but also in other body
XX fluids, biopsy specimens, foods, soil, air and water. Particularly, they
XX are used to diagnose, stage or monitor infection, or for identification
XX of drug-resistant strains (which generally have mutations in rRNA)
XX
XX SQ Sequence 15 BP; 2 A; 2 C; 1 G; 10 T; 0 U; 0 Other;
XX
XX Query Match 0.8%; Score 13.4; DB 1; Length 15;
XX Best Local Similarity 93.3%; Pred. No. 1.4e+02;
XX Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
QY 177 AAGGAAATTCAAAAT 191
DB 15 AAGGAAATTCAAAAT 1
XX
RESULT 392
AAV31967/c
ID AAV31967 standard; DNA; 15 BP.
XX
XX AC AAV31967;
XX
XX DT 21-AUG-1998 (first entry)
XX
XX DE Peptide nucleic acid probe 110.
XX
XX KW Peptide nucleic acid; PNA; probe; hybridisation; mycobacteria;
XX ribosomal nucleic acid; rRNA; drug-resistant strain; mutation; ss.
XX
XX OS Synthetic.
XX OS Mycobacterium sp.
XX
XX FH Key Location/Qualifiers
XX modified_base 1..15
XX /tag= a
XX /note= "This sequence contains a polyamide backbone
XX instead of a deoxyribose backbone"
XX
XX PN W09815648-A1.
XX
XX PD 16-APR-1998.
XX
XX PF 03-OCT-1997; 97WO-DK000425.
XX
XX PR 04-OCT-1996; 96DK-00001096.
XX PR 18-OCT-1996; 96DK-00001156.
XX PR 05-MAY-1997; 97DK-00000512.
XX
XX (DAKO-) DAKO AS.
XX
XX Stender H, Lund K, Mollerup TA;
XX
XX WPI; 1998-240831/21.
XX
XX PT Peptide nucleic acid probes for detection of ribosomal nucleic acid of
XX mycobacteria - allow differentiation between species of tuberculosis
XX complex and others and can penetrate cell membranes without pretreatment.
XX
XX PS Claim 22; Page 67; 106pp; English.
XX
XX CC This is the nucleotide sequence of the peptide nucleic acid (PNA) probe
XX used in the method of the invention, to detect ribosomal nucleic acid of
XX mycobacteria. The probes are used, in situ or in vitro, for detection of
XX the Mycobacterium tuberculosis complex (MTC), specifically M.
XX tuberculosis, and especially in sputum samples, but also in other body
XX fluids, biopsy specimens, foods, soil, air and water. Particularly, they
XX are used to diagnose, stage or monitor infection, or for identification
XX of drug-resistant strains (which generally have mutations in rRNA)
XX
XX SQ Sequence 15 BP; 2 A; 2 C; 2 G; 9 T; 0 U; 0 Other;
XX
XX Query Match 0.8%; Score 13.4; DB 1; Length 15;
XX Best Local Similarity 93.3%; Pred. No. 1.4e+02;
XX Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
QY 177 AAGGAAATTCAAAAT 191
DB 15 AAGGAAATTCAAAAT 1
XX
RESULT 393
AAAX31120/c
ID AAAX31120 standard; DNA; 15 BP.
XX
XX AC AAAX31120;
XX
XX DT 21-MAY-1999 (first entry)
XX
XX DE Tag sequence of a transcript increased in colorectal cancer.
XX
XX KW Tag sequence; colorectal cancer; pancreatic cancer; colon cancer;
XX diagnosis; prognosis; treatment; ss.
XX
XX OS Homo sapiens.
XX
XX PN W09853319-A2.
XX
XX PD 26-NOV-1998.
XX
XX PF 20-MAY-1998; 98WO-US010277.
XX
XX PR 21-MAY-1997; 97US-0047352P.
XX
XX (UYJO ) UNIV JOHNS HOPKINS.
XX
XX Vogelstein B, Kinzler KW;
XX WPI; 1999-070161/06.
XX
XX Use of isolated gene transcripts - useful for developing products for the
XX diagnosis, prognosis and treatment of cancers, particularly colon and
XX pancreatic cancer.
XX
XX Claim 2; Page 31; 120pp; English.
XX
XX AAAX30947-31815 represent tag sequences of transcripts that are
XX differentially expressed in colorectal cancer, in pancreatic cancer, or
XX in both. The tag sequences can be used to identify genes by matching the
XX tag to a gen data base member, or by using the tag sequences as probes to
XX isolate unidentified genes from cDNA libraries. The tag sequences can
XX also be used in a method for diagnosing colon or pancreatic cancer in a
XX sample suspected of being neoplastic. The method comprises comparing the
XX level of at least one transcript in a first sample of a tissue to a
XX second sample, where the first sample is a colonic tissue suspected of
XX being neoplastic and the second sample is a normal human colonic tissue.
XX The transcript is identified by a tag selected from AAAX30947-31815. The
XX methods of the invention can be used in the diagnosis, prognosis and
XX treatment of cancer
XX
XX SQ Sequence 15 BP; 1 A; 5 C; 6 G; 3 T; 0 U; 0 Other;
XX
XX Query Match 0.8%; Score 13.4; DB 1; Length 15;
XX Best Local Similarity 93.3%; Pred. No. 1.4e+02;

```

Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 807 GCTCAGCAGGCCATG 821  
 |||||  
 Db 15 GCCCAGCAGGCCATG 1

RESULT 394  
 AAX31728/C  
 ID AAX31728 standard; DNA; 15 BP.  
 XX  
 AC AAX31728;  
 XX  
 DT 21-MAY-1999 (first entry)  
 XX  
 DE Transcript tag sequence increased in pancreatic and colorectal cancer.  
 XX  
 KW Tag sequence; colorectal cancer; pancreatic cancer; colon cancer;  
 KW diagnosis; prognosis; treatment; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO9853319-A2.  
 XX  
 PD 26-NOV-1998.  
 XX  
 PF 20-MAY-1998; 98WO-US010277.  
 XX  
 PR 21-MAY-1997; 97US-0047352P.  
 XX  
 PA (UYJO ) UNIV JOHNS HOPKINS.  
 XX  
 PI Vogelstein B, Kinzler KW;  
 XX  
 DR WPI; 1999-070161/06.  
 XX

Use of isolated gene transcripts - useful for developing products for the diagnosis, prognosis and treatment of cancers, particularly colon and pancreatic cancer.

Disclosure; Page 73; 120pp; English.

CC AAX30947-31815 represent tag sequences of transcripts that are  
 CC differentially expressed in colorectal cancer, in pancreatic cancer, or  
 CC in both. The tag sequences can be used to identify genes by matching the  
 CC tag to a gen data base member, or by using the tag sequences as probes to  
 CC isolate unidentified genes from cDNA libraries. The tag sequences can  
 CC also be used in a method for diagnosing colon or pancreatic cancer in a  
 CC sample suspected of being neoplastic. The method comprises comparing the  
 CC level of at least one transcript in a first sample of a tissue to a  
 CC second sample, where the first sample is a colonic tissue suspected of  
 CC being neoplastic and the second sample is a normal human colonic tissue.  
 CC The transcript is identified by a tag selected from AAX30947-31815. The  
 CC methods of the invention can be used in the diagnosis, prognosis and  
 CC treatment of cancer  
 XX  
 SQ Sequence 15 BP; 1 A; 5 C; 6 G; 3 T; 0 U; 0 Other;

Query Match 0.8%; Score 13.4; DB 1; Length 15;  
 Best Local Similarity 93.3%; Pred. No. 1.4e+02;  
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 807 GCTCAGCAGGCCATG 821  
 |||||  
 Db 15 GCCCAGCAGGCCATG 1

RESULT 395  
 AAF50848  
 ID AAF50848 standard; DNA; 15 BP.  
 XX  
 AC AAF50848;  
 XX

DT 30-MAR-2001 (first entry)  
 XX  
 DE IGF-I oligonucleotide #1808.  
 XX  
 KW Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;  
 KW cytostatic; dermatological; cardiant; virucide; ophthalmological; keloid;  
 KW skin disorder; insulin-like Growth Factor 1 receptor; IGF-1; pityriasis;  
 KW IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;  
 KW growth factor mediated cell proliferation; ichthyosis; serborrhea; ruba;  
 KW keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;  
 KW hyperneovascular condition; hyperplasia; kidney disease;  
 KW neovascular condition of the retina; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200078341-A1.  
 XX  
 PD 28-DEC-2000.  
 XX  
 PF 21-JUN-2000; 2000WO-AU000693.  
 XX  
 PR 21-JUN-1999; 99US-0140345P.  
 XX  
 PA (MURD-) MURDOCH CHILDRENS RES INST.  
 XX  
 PI Wraight CJ, Werther GA, Edmondson SR;  
 XX  
 DR WPI; 2001-041421/05.  
 XX

Ameliorating the effects of a disorder, e.g. psoriasis, by administering UV (ultra-violet) treatment (optional) and an antisense nucleic acid that inhibits or reduces growth factor mediated cell proliferation and/or inflammation.

Example 8; Page 72; 201pp; English.

CC The present invention relates to a method for ameliorating the effects of skin disorders. The method comprises contacting the skin with an antisense oligonucleotide, (for Insulin-like Growth Factor [IGF]-1 receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of inhibiting or reducing growth factor mediated cell proliferation, CC inflammation and/or other disorders. The present sequence is an oligonucleotide which can be used to design the antisense CC oligonucleotides of the present invention (see AAF45151 and AAF45153-F45161). The method is useful for ameliorating the effects of psoriasis, CC ichthyosis, pityriasis, ruba, pilaris, serborrhea, keloids, keratosis, CC neoplasias, scleroderma, warts, benign growths, cancers of the skin, a CC hyperneovascular condition such as a neovascular condition of the retina, CC brain or skin, growth factor-mediated malignancies, other sclerotic CC disease, kidney disease, hyperproliferation of the inside of blood vessels or any other hyperplasia  
 XX  
 SQ Sequence 15 BP; 4 A; 3 C; 6 G; 2 T; 0 U; 0 Other;

Query Match 0.8%; Score 13.4; DB 1; Length 15;  
 Best Local Similarity 93.3%; Pred. No. 1.4e+02;  
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 532 TGCTGGAGACGACC 546  
 |||||  
 Db 1 TGGTGGAGACGACC 15

RESULT 396  
 ABK32682/C  
 ID ABK32682 standard; DNA; 15 BP.  
 XX  
 AC ABK32682;  
 XX  
 DT 23-APR-2002 (first entry)  
 XX  
 XX Human colorectal and pancreatic cancer SAGE tag #49.  
 DE

KW Human; colon cancer; colorectal cancer; pancreatic cancer; SAGE tag;  
 KW serial analysis of gene expression; diagnostic; prognostic; probe;  
 KW cancer marker; ss.  
 XX  
 XX Homo sapiens.  
 OS  
 XX US6333152-B1.  
 PN  
 XX 25-DEC-2001.  
 PD  
 XX 20-MAY-1998; 98US-00081646.  
 PF  
 XX 20-MAY-1998; 98US-00081646.  
 PR  
 XX (UYJO ) UNIV JOHNS HOPKINS.  
 PA  
 XX Vogelstein B, Kinzler KW, Zhang L, Zhou W;  
 PI WPI; 2002-153821/20.  
 XX  
 XX New human nucleic acid containing specific SAGE tags, useful as  
 PT diagnostic markers for cancer, also derived probes.  
 PT  
 XX Disclosure; Col 87; 161pp; English.  
 PS  
 XX The invention relates to an isolated, purified human nucleic acid (I)  
 CC that has the same sequence as a mRNA found in humans and is a SAGE  
 CC (serial analysis of gene expression) tag comprising a single stranded  
 CC probe containing at least 10 consecutive nucleotides. SAGE tags, are  
 CC diagnostic and prognostic markers of cancer, especially of the colon and  
 CC pancreas. ABK31900-ABK32770 represent human colon and pancreatic cancer  
 CC SAGE tags of the invention  
 CC  
 XX Sequence 15 BP; 1 A; 5 C; 6 G; 3 T; 0 U; 0 Other;  
 SQ  
 Query Match 0.8%; Score 13.4; DB 1; Length 15;  
 Best Local Similarity 93.3%; Pred. No. 1.4e+02;  
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 807 GCTCAGCAGGCCATG 821  
 DB 15 GCCCAGCAGGCCATG 1  
 RESULT 397  
 ABK32073/c  
 ID ABK32073 standard; DNA; 15 BP.  
 XX  
 AC ABK32073;  
 XX  
 DT 23-APR-2002 (first entry)  
 XX  
 DE Human colon cancer SAGE tag #174.  
 XX  
 KW Human; colon cancer; colorectal cancer; pancreatic cancer; SAGE tag;  
 KW serial analysis of gene expression; diagnostic; prognostic; probe;  
 KW cancer marker; ss.  
 XX  
 XX Homo sapiens.  
 OS  
 XX US6333152-B1.  
 PN  
 XX 25-DEC-2001.  
 PD  
 XX 20-MAY-1998; 98US-00081646.  
 PF  
 XX 20-MAY-1998; 98US-00081646.  
 PR  
 XX (UYJO ) UNIV JOHNS HOPKINS.  
 PA  
 XX Vogelstein B, Kinzler KW, Zhang L, Zhou W;  
 PI WPI; 2002-153821/20.  
 XX

XX  
 PT New human nucleic acid containing specific SAGE tags, useful as  
 PT diagnostic markers for cancer, also derived probes.  
 XX  
 XX Disclosure; Col 25; 161pp; English.  
 XX  
 CC The invention relates to an isolated, purified human nucleic acid (I)  
 CC that has the same sequence as a mRNA found in humans and is a SAGE  
 CC (serial analysis of gene expression) tag comprising a single stranded  
 CC probe containing at least 10 consecutive nucleotides. SAGE tags, are  
 CC diagnostic and prognostic markers of cancer, especially of the colon and  
 CC pancreas. ABK31900-ABK32770 represent human colon and pancreatic cancer  
 CC SAGE tags of the invention  
 XX  
 SQ Sequence 15 BP; 1 A; 5 C; 6 G; 3 T; 0 U; 0 Other;  
 Query Match 0.8%; Score 13.4; DB 1; Length 15;  
 Best Local Similarity 93.3%; Pred. No. 1.4e+02;  
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 807 GCTCAGCAGGCCATG 821  
 DB 15 GCCCAGCAGGCCATG 1  
 RESULT 398  
 ABK01805  
 ID ABK01805 standard; RNA; 15 BP.  
 XX  
 AC ABK01805;  
 XX  
 DT 23-DEC-2002 (first entry)  
 XX  
 DE Hepatitis C virus (HCV) ribozyme related RNA sequence #74.  
 XX  
 KW Enzymatic nucleic acid; RNA cleavage; Hepatitis C virus infection;  
 KW ribozyme; HCV expression; HCV replication; cirrhosis; virucide;  
 KW liver failure; hepatocellular carcinoma; HCV infection; drug therapy;  
 KW type I interferon; interferon alpha; interferon beta; cytostatic; ss;  
 KW interferon gamma; consensus interferon; hepatotropic; antiinflammatory.  
 XX  
 OS Unidentified.  
 OS  
 XX US2002082225-A1.  
 PN  
 XX 27-JUN-2002.  
 PD  
 XX 23-MAR-1999; 99US-00274553.  
 PF  
 XX 23-MAR-1999; 99US-00274553.  
 PR  
 XX (BLAT/) BLATT L.  
 PA (MCSW/) MCSWIGGEN J A.  
 PA (ROBE/) ROBERTS B.  
 PA (PAVC/) PAVCO P A.  
 PA (MACE/) MACEJACK D.  
 XX  
 XX Blatt L, Mcswiggen JA, Roberts B, Pavco PA, Macejack D;  
 PI WPI; 2002-617759/66.  
 XX  
 XX New ribozymes targeting RNA derived from hepatitis C virus inhibit viral  
 PT replication and are useful to treat hepatitis C virus infections and  
 PT cirrhosis, liver failure or hepatocellular carcinoma.  
 XX  
 PS Disclosure; SEQ ID NO 1587; 80pp; English.  
 XX  
 CC The present invention relates to enzymatic nucleic acids which  
 CC specifically cleave RNA derived from Hepatitis C virus (HCV). The  
 CC enzymatic nucleic acid or ribozyme is in a hammerhead (HH) or hairpin  
 CC (HP) motif where the binding arms comprise sequences complementary to one  
 CC of the substrate sequences defined in the specification. The HCV  
 CC ribozymes are useful for modulating the expression and/or replication of

CC HCV. They can be used to treat cirrhosis, liver failure and/or  
 CC hepatocellular carcinoma. The HCV ribozymes are also useful for treating  
 CC a condition associated with HCV infection in conjunction with one or more  
 CC other drug therapies, particularly type I interferon, especially  
 CC interferon alpha, beta or gamma or consensus interferon. The present  
 CC sequence represents a RNA sequence of unknown function. Note: The present  
 CC sequence is given in the sequence data but is not mentioned elsewhere in  
 CC the specification. The complete sequence data for this patent was  
 CC obtained in electronic format directly from the USPTO web site at  
 CC seqdata.uspto.gov/psipdsIDEntry.html  
 XX  
 SQ Sequence 15 BP; 3 A; 8 C; 3 G; 0 T; 1 U; 0 Other;  
 Query Match 0.8%; Score 13.4; DB 1; Length 15;  
 Best Local Similarity 86.7%; Pred. No. 1.4e+02;  
 Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
 QY 1509 AGCCTCCAGGCCCC 1523  
 Db 1 AGCCUCCAGGCCCC 15  
 RESULT 399  
 ABX01804  
 ID ABX01804 standard; RNA; 15 BP.  
 AC  
 XX ABX01804;  
 DT 23-DEC-2002 (first entry)  
 DE Hepatitis C virus (HCV) ribozyme related RNA sequence #73.  
 KW Enzymatic nucleic acid; RNA cleavage; Hepatitis C virus infection;  
 KW HCV ribozyme; HCV expression; HCV replication; cirrhosis; virucide;  
 KW liver failure; hepatocellular carcinoma; HCV infection; drug therapy;  
 KW type I interferon; interferon alpha; interferon beta; cytostatic; 86;  
 KW interferon gamma; consensus interferon; hepatotropic; antiinflammatory.  
 XX  
 OS Unidentified.  
 XX  
 PN US2002082225-A1.  
 XX 27-JUN-2002.  
 PD  
 XX 23-MAR-1999; 99US-00274553.  
 XX 23-MAR-1999; 99US-00274553.  
 XX (BLAT/) BLATT L.  
 PA (MCSW/) MCSWIGGEN J A.  
 PA (ROBE/) ROBERTS B.  
 PA (PVC/) PAVCO P A.  
 PA (MACE/) MACEJACK D.  
 XX  
 PI Blatt L, Mcswiggen JA, Roberts B, Pavco PA, Macejack D;  
 XX  
 WPI; 2002-617759/66.  
 XX  
 PT New ribozymes targeting RNA derived from hepatitis C virus inhibit viral  
 PT replication and are useful to treat hepatitis C virus infections and  
 PT cirrhosis, liver failure or hepatocellular carcinoma.  
 XX  
 PS Disclosure; SEQ ID NO 1586; 80pp; English.  
 XX  
 CC The present invention relates to enzymatic nucleic acids which  
 CC specifically cleave RNA derived from Hepatitis C virus (HCV). The  
 CC enzymatic nucleic acid or ribozyme is in a hammerhead (HH) or hairpin  
 CC (HP) motif where the binding arms comprise sequences complementary to one  
 CC of the substrate sequences defined in the specification. The HCV  
 CC ribozymes are useful for modulating the expression and/or replication of  
 CC HCV. They can be used to treat cirrhosis, liver failure and/or  
 CC hepatocellular carcinoma. The HCV ribozymes are also useful for treating  
 CC a condition associated with HCV infection in conjunction with one or more

CC other drug therapies, particularly type I interferon, especially  
 CC interferon alpha, beta or gamma or consensus interferon. The present  
 CC sequence represents a RNA sequence of unknown function. Note: The present  
 CC sequence is given in the sequence data but is not mentioned elsewhere in  
 CC the specification. The complete sequence data for this patent was  
 CC obtained in electronic format directly from the USPTO web site at  
 CC seqdata.uspto.gov/psipdsIDEntry.html  
 XX  
 SQ Sequence 15 BP; 3 A; 8 C; 3 G; 0 T; 1 U; 0 Other;  
 Query Match 0.8%; Score 13.4; DB 1; Length 15;  
 Best Local Similarity 86.7%; Pred. No. 1.4e+02;  
 Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
 QY 1508 CAGCCTCCAGGCCCC 1522  
 Db 1 CAGCCUCCAGGCCCC 15  
 RESULT 400  
 AAV70490  
 ID AAV70490 standard; DNA; 16 BP.  
 AC  
 XX AAV70490;  
 DT 08-APR-1999 (first entry)  
 DE Sequence ID# 68 from patent specification WO9850403.  
 KW Nucleic acid detection; nucleic acid characterisation; hybridisation;  
 KW infection; disease; cancer; forensic; paternity; multiplexing; ss.  
 XX  
 OS Unidentified.  
 XX  
 PN WO9850403-A1.  
 XX 12-NOV-1998.  
 PD  
 XX 05-MAY-1998; 98WO-US003194.  
 XX 05-MAY-1997; 97US-00851588.  
 PR 19-SEP-1997; 97US-00934097.  
 PR 03-MAR-1998; 98US-00034205.  
 XX  
 PA (THIR-) THIRD WAVE TECHNOLOGIES INC.  
 XX  
 PI Dong F, Lyamichev VI, Prudent JR, Fors L, Neri BP, Brow MAD;  
 PI Anderson TA, Dahlberg JE;  
 XX  
 WPI; 1998-610317/51.  
 XX  
 PT Detection and characterisation of nucleic acid sequences - by mixing a  
 PT folded target and one or more probes to form a probe/folded target  
 PT complex and detecting and characterising the complexes.  
 XX  
 PS Disclosure; Page 180; 279pp; English.  
 XX  
 CC The invention relates to methods and compositions of detection and  
 CC characterisation of nucleic acid sequences and sequence changes. One  
 CC method of detection and characterisation comprises: (a) providing: (i) a  
 CC folded target having a DNA sequence comprising at least 1 double stranded  
 CC region and at least 1 single stranded region; and (ii) at least 1 probe  
 CC complementary to at least a portion of the folded target; and (b) mixing  
 CC the target and probes so that the probe hybridises to form a probe  
 CC /folded target complex. Also provided are methods for determination of  
 CC structure formation in nucleic acid targets; for analysing folded nucleic  
 CC acids targets; and for analysis of nucleic acid structures. The methods  
 CC can be used for the detection and characterisation of nucleic acid  
 CC sequences to detect the presence of pathogenic nucleic acid sequences  
 CC indicative of an infection, the presence of variants or alleles of  
 CC mammalian genes associated with disease and cancers, and the  
 CC identification of the source of nucleic acids found in forensic samples,  
 CC as well as in paternity determinations. The methods allow simultaneous

CC analysis of both strands (e.g. the sense and antisense strands) and are  
CC ideal for high-level multiplexing. The products produced are amenable to  
CC qualitative, quantitative and positional analysis. The methods may be  
CC performed in solution or in the solid phase (e.g. on a solid support).  
CC The methods are powerful in that they allow for analysis of longer  
CC fragments of nucleic acid than current methodologies. The present  
CC sequence represents the sequence no:68 in the specification for which no  
CC information is provided  
XX  
SQ Sequence 16 BP; 3 A; 8 C; 4 G; 1 T; 0 U; 0 Other;  
Query Match 0.8%; Score 13.4; DB 1; Length 16;  
Best Local Similarity 93.3%; Pred. NO. 1.7e+02;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1508 CAGCCTCCAGGCC 1522  
Db 2 CAGCCTCCAGGCC 16  
RESULT 401  
AAV70489  
ID AAV70489 standard; DNA; 16 BP.  
XX  
AC AAV70489;  
XX  
DT 08-APR-1999 (first entry)  
XX  
DE Sequence ID# 67 from patent specification WO9850403.  
XX  
KW Nucleic acid detection; nucleic acid characterisation; hybridisation;  
KW infection; disease; cancer; forensic; paternity; multiplexing; ss.  
XX  
OS Unidentified.  
XX  
PN WO9850403-A1.  
XX  
PD 12-NOV-1998.  
XX  
PF 05-MAY-1998; 98WO-US003194.  
XX  
PR 05-MAY-1997; 97US-00851588.  
PR 19-SEP-1997; 97US-00934097.  
PR 03-MAR-1998; 98US-00034205.  
XX  
PA (THIR-) THIRD WAVE TECHNOLOGIES INC.  
XX  
PI Dong F, Lyamichev VI, Prudent JR, Fors L, Neri BP, Brow MAD;  
PI Anderson TA, Dahlberg JE;  
XX  
WPI; 1998-610317/51.  
XX  
PT Detection and characterisation of nucleic acid sequences - by mixing a  
PT folded target and one or more probes to form a probe/folded target  
PT complex and detecting and characterising the complexes.  
XX  
PS Disclosure; Page 180; 279pp; English.  
XX  
CC The invention relates to methods and compositions of detection and  
CC characterisation of nucleic acid sequences and sequence changes. One  
CC method of detection and characterisation comprises: (a) providing: (i) a  
CC folded target having a DNA sequence comprising at least 1 double stranded  
CC region and at least 1 single stranded region; and (ii) at least 1 probe  
CC complementary to at least a portion of the folded target; and (b) mixing  
CC the target and probes so that the probe hybridises to form a probe  
CC /folded target complex. Also provided are methods for determination of  
CC structure formation in nucleic acid targets; for analysing folded nucleic  
CC acids targets; and for analysis of nucleic acid structures. The methods  
CC can be used for the detection and characterisation of nucleic acid  
CC sequences to detect the presence of pathogenic nucleic acid sequences  
CC indicative of an infection, the presence of variants or alleles of  
CC mammalian genes associated with disease and cancers, and the  
CC identification of the source of nucleic acids found in forensic samples,  
CC

CC as well as in paternity determinations. The methods allow simultaneous  
CC analysis of both strands (e.g. the sense and antisense strands) and are  
CC ideal for high-level multiplexing. The products produced are amenable to  
CC qualitative, quantitative and positional analysis. The methods may be  
CC performed in solution or in the solid phase (e.g. on a solid support).  
CC The methods are powerful in that they allow for analysis of longer  
CC fragments of nucleic acid than current methodologies. The present  
CC sequence represents the sequence no:67 in the specification for which no  
CC information is provided  
XX  
SQ Sequence 16 BP; 4 A; 8 C; 3 G; 1 T; 0 U; 0 Other;  
Query Match 0.8%; Score 13.4; DB 1; Length 16;  
Best Local Similarity 93.3%; Pred. NO. 1.7e+02;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1508 CAGCCTCCAGGCC 1522  
Db 2 CAGCCTCCAGGCC 16  
RESULT 402  
AAV70489  
ID AAV70489 standard; DNA; 16 BP.  
XX  
AC AAV70489;  
XX  
DT 24-MAR-1999 (first entry)  
XX  
DE Triple helix third strand of dystrophin gene nucleotides 4480-4495.  
XX  
KW Triple helix formation; DNA detection; triple helix; identification; bacteria;  
KW oncogene; virus; ss.  
XX  
OS Synthetic.  
OS Homo sapiens.  
XX  
PN US5861244-A.  
XX  
PD 19-JAN-1999.  
XX  
PF 22-DEC-1993; 93US-00173489.  
XX  
PR 29-OCT-1992; 92US-00968436.  
XX  
PA (PROF-) PROFILE DIAGNOSTIC SCI INC.  
XX  
PI Hepburn AG, Wang C;  
XX  
WPI; 1999-130384/11.  
XX  
PT Assay of genetic sequences based on triplex formation from double  
PT stranded analyte - and hybrid of anchor and reporter sequences, with  
PT reporter released if triplex formation occurs, used e.g. to identify  
PT bacteria.  
XX  
PS Disclosure; Col 15-16; 168pp; English.  
XX  
CC The present sequence represents a polynucleotide that is able to form a  
CC triple helix with a double stranded sequence. Cytosine bases in the  
CC present can be replaced with 5-methylcytosine for increased triplex  
CC stability. The present sequence is used in the assay of the invention,  
CC where it can be part of the anchor DNA or reporter DNA sequence. The  
CC assay comprises adding a sample containing double-stranded DNA test  
CC sequences to an aqueous medium containing at least one complex of anchor  
CC DNA, attached to a solid support, and reporter DNA, where either a part  
CC of the anchor DNA or reporter DNA is designed to form a triple-strand  
CC structure with part of the test sequence. Triplex formation results in  
CC displacement of the reporter DNA which is detected as an indication of  
CC the presence of the DNA test sequence. The method is used to detect DNA  
CC sequences, particularly for identification of bacteria (by detecting  
CC genes for ribosomal RNA) in clinical samples, but also detection of  
CC oncogenes and Hepatitis B virus  
CC

```
XX
SQ Sequence 16 BP; 0 A; 4 C; 1 G; 11 T; 0 U; 0 Other;
  Query Match      0.8%; Score 13.4; DB 1; Length 16;
  Best Local Similarity 93.3%; Pred. NO. 1.7e+02;
  Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 271 AAGAGCCCAAGAAGA 285
Db 15 AAGAGCCCAAGAAGA 1

RESULT 403
ABL46101
ID ABL46101 standard; DNA; 16 BP.
XX
AC ABL46101;
XX
DT 26-APR-2002 (first entry)
XX
DE Hepatitis C virus PCR primer SEQ ID NO:68.
XX
KW Nucleic acid accessible hybridisation site; detection; hybridisation;
KW characterisation; identification; nucleic acid structure; diagnosis;
KW PCR primer; probe; ss.
XX
OS Hepatitis C virus.
OS Synthetic.
XX
PN WO200198537-A2.
XX
PD 27-DEC-2001.
XX
PF 15-JUN-2001; 2001WO-US019401.
XX
PR 17-JUN-2000; 2000US-0212308P.
PR 15-JUN-2001; 2001US-00212308.
XX
PA (THIR-) THIRD WAVE TECHNOLOGIES INC.
XX
PI Lyamichev V, Allawi H, Dong F, Neri BP, Vener IT;
XX
DR WPI; 2002-049698/06.
XX
PT Identifying oligonucleotides hybridizing to nucleic acids containing
PT secondary structure, useful in clinical diagnosis, comprises identifying
PT primers that interact with the target to form an extension product under
PT amplification conditions.
XX
PS Example 8; Page 370; 409pp; English.
XX
CC The present invention describes a method for identifying oligonucleotides
CC with desired hybridisation properties to nucleic acid targets containing
CC secondary structure. The method comprises amplifying a target nucleic
CC acid having at least one accessible and one inaccessible site. Primers
CC that form an extension product are identified as the oligonucleotides
CC which can interact with the folded target nucleic acid. Oligonucleotides
CC from the present invention can be used in novel detection methods for
CC clinical diagnostic purposes, including the detection and identification
CC of pathogenic organisms (e.g. HIV). The method allows the ability to
CC rapidly analyse nucleic acid structures. ABL46034 to ABL46367 represent
CC sequences used in the exemplification of the present invention
XX
SQ Sequence 16 BP; 3 A; 8 C; 4 G; 1 T; 0 U; 0 Other;
  Query Match      0.8%; Score 13.4; DB 1; Length 16;
  Best Local Similarity 93.3%; Pred. NO. 1.7e+02;
  Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1508 CAGCCTCCAGGCCCC 1522
Db 2 CAGCCTCCAGGCCCC 16

RESULT 404
ABL46100
ID ABL46100 standard; DNA; 16 BP.
XX
AC ABL46100;
XX
DT 26-APR-2002 (first entry)
XX
DE Hepatitis C virus PCR primer SEQ ID NO:67.
XX
KW Nucleic acid accessible hybridisation site; detection; hybridisation;
KW characterisation; identification; nucleic acid structure; diagnosis;
KW PCR primer; probe; ss.
XX
OS Hepatitis C virus.
OS Synthetic.
XX
PN WO200198537-A2.
XX
PD 27-DEC-2001.
XX
PF 15-JUN-2001; 2001WO-US019401.
XX
PR 17-JUN-2000; 2000US-0212308P.
PR 15-JUN-2001; 2001US-00212308.
XX
PA (THIR-) THIRD WAVE TECHNOLOGIES INC.
XX
PI Lyamichev V, Allawi H, Dong F, Neri BP, Vener IT;
XX
DR WPI; 2002-049698/06.
XX
PT Identifying oligonucleotides hybridizing to nucleic acids containing
PT secondary structure, useful in clinical diagnosis, comprises identifying
PT primers that interact with the target to form an extension product under
PT amplification conditions.
XX
PS Example 8; Page 370; 409pp; English.
XX
CC The present invention describes a method for identifying oligonucleotides
CC with desired hybridisation properties to nucleic acid targets containing
CC secondary structure. The method comprises amplifying a target nucleic
CC acid having at least one accessible and one inaccessible site. Primers
CC that form an extension product are identified as the oligonucleotides
CC which can interact with the folded target nucleic acid. Oligonucleotides
CC from the present invention can be used in novel detection methods for
CC clinical diagnostic purposes, including the detection and identification
CC of pathogenic organisms (e.g. HIV). The method allows the ability to
CC rapidly analyse nucleic acid structures. ABL46034 to ABL46367 represent
CC sequences used in the exemplification of the present invention
XX
SQ Sequence 16 BP; 4 A; 8 C; 3 G; 1 T; 0 U; 0 Other;
  Query Match      0.8%; Score 13.4; DB 1; Length 16;
  Best Local Similarity 93.3%; Pred. NO. 1.7e+02;
  Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1508 CAGCCTCCAGGCCCC 1522
Db 2 CAGCCTCCAGGCCCC 16

RESULT 405
ADR82290
ID ADR82290 standard; DNA; 16 BP.
XX
AC ADR82290;
XX
DT 03-JUN-2004 (first entry)
XX
DE Nucleic acid analysis method associated oligonucleotide seqid 67.
XX
```

```
KW nucleic acid analysis; hepatitis C virus;
KW non-contiguous single-stranded region; NCSR; cleavage structure;
KW clinical; diagnostic; microorganism detection;
KW microorganism identification; ss.
XX Synthetic.
XX
XX US6709815-B1.
XX
XX PD 23-MAR-2004.
XX
XX PF 18-JUL-2000; 2000US-00402618.
XX
XX PR 05-MAY-1997; 97US-00851588.
XX PR 19-SEP-1997; 97US-00934097.
XX PR 03-MAR-1998; 98US-00034205.
XX
XX PA (THIR-) THIRD WAVE TECHNOLOGIES INC.
XX
XX PI Dong F, Lyamichiev VI, Prudent JR, Fors L, Neri BP, Brow MAD;
PI Anderson TA, Dahlberg JE;
XX
XX DR WPI; 2004-256067/24.
XX
XX XX Analyzing nucleic acids, comprises mixing target nucleic acid such as
XX PT hepatitis C virus nucleic acid, bridging oligonucleotide, second
XX PT oligonucleotide and cleavage agent to form cleavage structure.
XX
XX PS Disclosure; SEQ ID NO 67; 143pp; English.
XX
XX CC The invention describes a method of analysing nucleic acids comprising
XX CC providing a target nucleic acid, e.g. hepatitis C virus nucleic acid
XX CC having non-contiguous single-stranded regions (NCSR) separated by an
XX CC intervening region, a bridging oligonucleotide capable of binding to the
XX CC first and second NCSR; a second oligonucleotide binding to a portion of
XX CC the first NCSR and a cleavage agent, and mixing the contents to form a
XX CC cleavage structure. The method is useful for analysing nucleic acids,
XX CC e.g. hepatitis C virus nucleic acid useful for clinical diagnostic
XX CC purposes and detection and identification of pathogenic microorganisms
XX CC such as hepatitis C virus. This sequence represents an oligonucleotide
XX CC associated with the nucleic acid analysis method of the invention.
XX
XX SQ Sequence 16 BP; 4 A; 8 C; 3 G; 1 T; 0 U; 0 Other;
XX
XX Query Match 0.8%; Score 13.4; DB 1; Length 16;
XX Best Local Similarity 93.3%; Pred. No. 1.7e+02;
XX Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX QY 1508 CAGCCTCCAGGCCCC 1522
XX
XX DB |||||
XX 2 CAGCCTCCAGGACCC 16
XX
XX RESULT 406
XX ADK82291
XX ID ADK82291 standard; DNA; 16 BP.
XX
XX AC ADK82291;
XX
XX DT 03-JUN-2004 (first entry)
XX
XX DE Nucleic acid analysis method associated oligonucleotide seqid 68.
XX
XX KW nucleic acid analysis; hepatitis C virus;
XX KW non-contiguous single-stranded region; NCSR; cleavage structure;
XX KW clinical; diagnostic; microorganism detection;
XX KW microorganism identification; ss.
XX
XX OS Synthetic.
XX
XX PN US6709815-B1.
XX
XX PD 23-MAR-2004.
```

```
XX
XX PF 18-JUL-2000; 2000US-00402618.
XX
XX PR 05-MAY-1997; 97US-00851588.
XX PR 19-SEP-1997; 97US-00934097.
XX PR 03-MAR-1998; 98US-00034205.
XX
XX PA (THIR-) THIRD WAVE TECHNOLOGIES INC.
XX
XX PI Dong F, Lyamichiev VI, Prudent JR, Fors L, Neri BP, Brow MAD;
PI Anderson TA, Dahlberg JE;
XX
XX DR WPI; 2004-256067/24.
XX
XX XX Analyzing nucleic acids, comprises mixing target nucleic acid such as
XX PT hepatitis C virus nucleic acid, bridging oligonucleotide, second
XX PT oligonucleotide and cleavage agent to form cleavage structure.
XX
XX PS Disclosure; SEQ ID NO 68; 143pp; English.
XX
XX CC The invention describes a method of analysing nucleic acids comprising
XX CC providing a target nucleic acid, e.g. hepatitis C virus nucleic acid
XX CC having non-contiguous single-stranded regions (NCSR) separated by an
XX CC intervening region, a bridging oligonucleotide capable of binding to the
XX CC first and second NCSR; a second oligonucleotide binding to a portion of
XX CC the first NCSR and a cleavage agent, and mixing the contents to form a
XX CC cleavage structure. The method is useful for analysing nucleic acids,
XX CC e.g. hepatitis C virus nucleic acid useful for clinical diagnostic
XX CC purposes and detection and identification of pathogenic microorganisms
XX CC such as hepatitis C virus. This sequence represents an oligonucleotide
XX CC associated with the nucleic acid analysis method of the invention.
XX
XX SQ Sequence 16 BP; 3 A; 8 C; 4 G; 1 T; 0 U; 0 Other;
XX
XX Query Match 0.8%; Score 13.4; DB 1; Length 16;
XX Best Local Similarity 93.3%; Pred. No. 1.7e+02;
XX Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX QY 1508 CAGCCTCCAGGCCCC 1522
XX
XX DB |||||
XX 2 CAGCCTCCAGGACCC 16
XX
XX RESULT 407
XX ADM80152/c
XX ID ADM80152 standard; DNA; 16 BP.
XX
XX AC ADM80152;
XX
XX DT 03-JUN-2004 (first entry)
XX
XX DE Linker peptide encoding DNA SEQ ID NO:11.
XX
XX KW ds; gene; in vitro diagnosis; virus-related disease; HIV-1; HIV-2;
XX KW linker.
XX
XX OS Synthetic.
XX
XX FH Key Location/Qualifiers
XX FT CDS 2..16
XX FT /*tag= a
XX FT /partial
XX FT /note= "No start/stop codon given"
XX
XX PN FR2844519-A1.
XX
XX PD 19-MAR-2004.
XX
XX PF 17-SEP-2002; 2002FR-00011485.
XX PR 17-SEP-2002; 2002FR-00011485.
XX
XX PA (INMR ) BIO MERIEUX.
```



XX Letourneur O;  
PI WPI: 2004-259482/25.  
DR P-PSDB; ADM80153.  
XX  
PT New recombinant DNA encoding chimeric protein, useful for in vitro  
PT diagnosis of viral infections, comprises sequences encoding epitopic  
PT regions, a linker and a binding region.  
XX  
XX Claim 5; SEQ ID NO 11; 33pp; French.  
PS  
CC The invention relates to a novel recombinant DNA (I) encoding a  
CC recombinant chimeric protein (II). The protein consists of at least two  
CC nucleotide fragments, each encoding an epitopic region of at least one  
CC microorganism; at least one sequence encoding a linker, and at least one  
CC sequence encoding a binding region. The DNA and/or protein are used for  
CC in vitro diagnosis, especially of virus-related diseases, specifically  
CC HIV-1 or -2 infections. The protein is easy to purify and synthesize, and  
CC has strong immunoreactivity with sera from virus-infected subjects. The  
CC present sequence encodes a linker of the recombinant chimeric peptide of  
CC the invention.  
XX  
SQ Sequence 16 BP; 2 A; 5 C; 6 G; 3 T; 0 U; 0 Other;  
Query Match 0.8%; Score 13.4; DB 1; Length 16;  
Best Local Similarity 93.3%; Pred. No. 1.7e+02;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 476 CCTGAACACGAGCTC 490  
DB 15 CCTGAACCGAGCTC 1  
RESULT 408  
ADR32381  
ID ADR32381 standard; DNA; 16 BP.  
XX  
AC ADR32381;  
XX  
DT 04-NOV-2004 (first entry)  
XX  
DE E. coli nicking agent target DNA #26.  
XX  
DE ss; nicking agent; assay panel; diagnosis; expression pattern;  
KW DNA fingerprinting; nosocomial infection; microbiological assay;  
KW bacterial contamination; genome mapping; bioremediation.  
XX  
OS Escherichia coli.  
XX  
XX WO2004067765-A2.  
XX  
PD 12-AUG-2004.  
XX  
XX 29-JAN-2004; 2004WO-US002720.  
XX  
XX 29-JAN-2003; 2003US-0443811P.  
XX  
XX (KECK-) KECK GRADUATE INST.  
XX  
XX Van Ness J, Galas DJ, Van Ness LK;  
XX  
XX WPI: 2004-581010/56.  
XX  
PT Identifying nucleic acid sample source, useful for identifying bacterial  
PT strains involved in nosocomial infections, comprises treating the nucleic  
PT acid sample with components comprising a nicking agent under nicking  
PT conditions.  
XX  
PS Example 1; Page 65; 238pp; English.  
XX  
CC The invention relates to a method of treating a nucleic acid sample with  
CC components under nicking conditions, where the components comprise a

CC nicking agent, and the conditions cause the nicking agent to nick the  
CC nucleic acid sample to thus produce a family of initiating  
CC oligonucleotide fragments, and subjecting one or more members of the  
CC family of initiating oligonucleotide fragments to a characterization  
CC process to thus provide results. The method is useful for creating an  
CC assay panel of diagnostic oligonucleotides that can identify any organism  
CC or individual. The method is useful for characterizing other DNA  
CC molecules e.g., cDNA, and for characterizing cDNA expression patterns.  
CC The method, kit or composition is useful for identifying the source  
CC organism of a nucleic acid sample e.g., bacterium, fungus, virus, plant,  
CC non-human animal or human. The method is particularly useful for rapidly  
CC fingerprinting DNA to identifying prokaryotic and eukaryotic species, it  
CC subpecies, and especially strains or individuals of the subpecies. It  
CC is especially useful for identifying different bacterial strains involved  
CC in e.g., nosocomial infections. Furthermore, the method is useful for  
CC diagnosing bacterial disease in plants and humans, monitoring for  
CC bacterial content and/or contamination in the environment, monitoring  
CC food for bacterial contamination, monitoring manufacturing processes for  
CC bacterial contamination, monitoring quality assurance/quality control of  
CC laboratory tests involving microbiological assays, tracing bacterial  
CC contamination and/or outbreaks of bacterial infections, genome mapping,  
CC monitoring bioremediation sites, and for monitoring agricultural sites  
CC for test crops, bacteria and recombinant molecules. This sequence  
CC corresponds to nucleic acid used in the method of the invention.  
XX  
SQ Sequence 16 BP; 4 A; 1 C; 4 G; 7 T; 0 U; 0 Other;  
Query Match 0.8%; Score 13.4; DB 1; Length 16;  
Best Local Similarity 93.3%; Pred. No. 1.7e+02;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 501 TTCTGGATGAATGGT 515  
DB 1 TTCTGGATGAATGTT 15  
RESULT 409  
ADR32430  
ID ADR32430 standard; DNA; 16 BP.  
XX  
AC ADR32430;  
XX  
DT 04-NOV-2004 (first entry)  
XX  
DE E. coli fingerprint oligonucleotide #12.  
XX  
DE ss; nicking agent; assay panel; diagnosis; expression pattern;  
KW DNA fingerprinting; nosocomial infection; microbiological assay;  
KW bacterial contamination; genome mapping; bioremediation.  
XX  
OS Escherichia coli.  
XX  
XX WO2004067765-A2.  
XX  
PD 12-AUG-2004.  
XX  
XX 29-JAN-2004; 2004WO-US002720.  
XX  
XX 29-JAN-2003; 2003US-0443811P.  
XX  
XX (KECK-) KECK GRADUATE INST.  
XX  
XX Van Ness J, Galas DJ, Van Ness LK;  
XX  
XX WPI: 2004-581010/56.  
XX  
PT Identifying nucleic acid sample source, useful for identifying bacterial  
PT strains involved in nosocomial infections, comprises treating the nucleic  
PT acid sample with components comprising a nicking agent under nicking  
PT conditions.  
XX  
PS Example 1; Page 70; 238pp; English.  
XX

The invention relates to a method of treating a nucleic acid sample with components under nicking conditions, where the components comprise a nicking agent, and the conditions cause the nicking agent to nick the nucleic acid sample to thus produce a family of initiating oligonucleotide fragments, and subjecting one or more members of the oligonucleotide fragments, to thus produce a family of initiating oligonucleotide fragments to a characterization process to thus provide results. The method is useful for creating an assay panel of diagnostic oligonucleotides that can identify any organism or individual. The method is useful for characterizing other DNA molecules e.g., cDNA, and for characterizing cDNA expression patterns. The method, kit or composition is useful for identifying the source organism of a nucleic acid sample e.g., bacterium, fungus, virus, plant, non-human animal or human. The method is particularly useful for rapidly fingerprinting DNA to identifying prokaryotic and eukaryotic species, subspecies, and especially strains or individuals of the subspecies. It is especially useful for identifying different bacterial strains involved in e.g., nosocomial infections. Furthermore, the method is useful for diagnosing bacterial disease in plants and humans, monitoring for bacterial content and/or contamination in the environment, monitoring food for bacterial contamination, monitoring manufacturing processes for bacterial contamination, monitoring quality assurance/quality control of laboratory tests involving microbiological assays, tracing bacterial contamination and/or outbreaks of bacterial infections, genome mapping, monitoring bioremediation sites, and for monitoring agricultural sites for test crops, bacteria and recombinant molecules. This sequence corresponds to nucleic acid used in the method of the invention.

```

Query Match          0.8%;   Score 13.4;   DB 1;   Length 16;
Best Local Similarity 93.3%;   Pred. No. 1.7e+02;
Matches 14;   Conservative 0;   Mismatches 1;   Indels 0;   Gaps 0
Qy      501  TTCTGGATGAATGGT 515
          |||||
Db      1  TTCTGGATGAATGT 15

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RESULT 410
ADR33575
ID  ADR33575 standard; DNA; 16 BP.
XX
AC  ADR33575;

```

XX	04-NOV-2004	(first entry)
DT		
XX		
XX		
DE		
XX		
XX	E. coli strain K12	detection oligonucleotide K12-558515.
KW	ss;	nicking agent; assay panel; diagnosis; expression pattern;
KW	DNA fingerprinting;	nosocomial infection; microbiological assay;
XX	bacterial contamination;	genome mapping; bioremediation.
XX		
OS	Escherichia coli.	
XX		
PN	WO2004067765-A2.	
XX		
XX	12-AUG-2004.	
XX		
PF	29-JAN-2004;	2004WO-US002720.
XX		
XX	29-JAN-2003;	2003US-0443811P.
PR		
XX	(KECK-)	KECK GRADUATE INST.
PA		
XX		
XX	Van Ness J,	Galas DJ, Van Ness LK;
PI		
XX		
XX	WPI;	2004-581010/56.
DR		
XX		
XX	Identifying nucleic acid	sample source, useful for identifying bacterial
PT	strains involved in	nosocomial infections, comprises treating the nucleic
PT	acid sample with	components comprising a nicking agent under nicking
PT	conditions.	
PT		

FT modified\_base methyl cytosine residues"  
FT 1..4  
FT /\*tag= a  
FT /mod\_base= OTHER  
FT /note= "OTHER = beta-D-oxy-locked nucleic acid but  
FT optionally DNA nucleotides, optionally phosphate  
FT internucleotide linkages"  
FT 13..16  
FT modified\_base  
FT /\*tag= c  
FT /mod\_base= OTHER  
FT /note= "OTHER = beta-D-oxy-locked nucleic acid but  
FT optionally DNA nucleotides, optionally phosphate  
FT internucleotide linkages"  
XX  
PN WO2004069991-A2.  
XX  
XX 19-AUG-2004.  
XX  
XX 10-FEB-2004; 2004WO-DK0000096.  
XX  
XX 10-FEB-2003; 2003DK-00000183.  
PR 18-NOV-2003; 2003DK-00001708.  
XX  
XX (SANT-) SANTARIS PHARMA AS.  
XX  
XX Hansen B, Thru CA, Petersen KD, Westergaard M, Wissenbach M;  
PI WPI; 2004-625494/60.  
XX  
XX New locked nucleic acid containing oligomeric compound capable of  
PT modulating survivin expression, useful for treating cancer such as breast  
PT carcinoma, lung carcinoma, etc.  
XX  
XX Claim 1; SEQ ID NO 8; 122pp; English.  
XX  
XX The invention relates to an oligomeric compound (I) capable of modulating  
CC survivin expression, having 8-50 nucleotides and/or nucleotide analogues,  
CC where the compound comprises a subsequence of at least 8 nucleotides or  
CC nucleotide analogues, where the subsequence is located within a sequence  
CC chosen from one of 143 sequences given in the specification. (I) is  
CC useful for treating a mammal suffering from or susceptible from a disease  
CC caused by abnormal angiogenesis, by administering (I) containing one or  
CC more LNA units that are targeted to survivin. (I) is useful as a  
CC medicament and for the manufacture of a medicament for the treatment of  
CC cancer, in combination with chemotherapeutic agent such as busulfan  
CC (myleran), carboplatin (paraplatin), Taxol, doxorubicin (adriamycin),  
CC etc. (I) or a conjugate (II) containing (I) is useful in the preparation  
CC of a medicament for the treatment of atherosclerosis, psoriasis, diabetic  
CC retinopathy, rheumatoid arthritis, asthma, warts and allergic dermatitis.  
CC (I), (II) or a pharmaceutical (III) containing (I) is useful for treating  
CC cancer in the form of a solid tumour, sarcoma, glioma or carcinoma chosen  
CC from malignant melanoma, basal cell carcinoma, ovarian carcinoma, breast  
CC carcinoma, non-small cell lung cancer, renal cell carcinoma, bladder  
CC carcinoma, recurrent superficial bladder cancer, stomach carcinoma,  
CC prostatic carcinoma, pancreatic carcinoma, lung carcinoma, cervical  
CC carcinoma, cervical dysplasia, laryngeal papillomatosis, colon carcinoma,  
CC colorectal carcinoma and carcinoid tumours. The malignant melanoma is  
CC chosen from superficial spreading melanoma, nodular melanoma, lentigo  
CC maligna melanoma, acral melanoma, amelanotic melanoma, and desmoplastic  
CC melanoma. The sarcoma is chosen from osteosarcoma, Ewing's sarcoma,  
CC chondrosarcoma, malignant fibrous histiocytoma, fibrosarcoma and Kaposi's  
CC sarcoma. The treatment further involves administration of a  
CC chemotherapeutic agent such as taxanes, preferably Taxol, Paclitaxel or  
CC Docetaxel. (I), (II) or (III) is also useful for preventing or limiting  
CC apoptosis or for preventing cellular proliferation. This sequence  
CC corresponds to an antisense oligonucleotide targeted to the human  
CC survivin gene.  
XX  
SQ Sequence 16 BP; 1 A; 3 C; 1 G; 11 T; 0 U; 0 Other;

QY 278 CAAGAAGAAGAAGA 292  
||| ||||| |||||  
Db 16 CAATAAGAAGAAGA 2

Search completed: September 13, 2005, 10:42:46  
Job time : 10 secs

Query Match 0.8%; Score 13.4; DB 1; Length 16;  
Best Local Similarity 93.3%; Pred. No. 1.7e+02;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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RESULT 1	H93557	48 bp	mRNA	linear	EST 01-DEC-1995
LOCUS	H93557				
DEFINITION	yy14dl1.r1 Soares fetal liver spleen INFLS Homo sapiens cDNA clone IMAGE:24709 5' similar to gb:X14723 CLUSTERIN PRECURSOR (HUMAN); mRNA sequence.				
ACCESSION	H93557				
VERSION	H93557.1	GI:1099885			
KEYWORDS	EST.				
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
	Eukaryota: Metazoa: Chordata: Vertebrata: Euteleostomi:				

and Marra, M.  
 Generation and analysis of 280,000 human expressed sequence tags  
 Genome Res. 6 (9), 807-828 (1996)  
 97044478  
 MEDLINE  
 PUBMED  
 COMMENT  
 Contact: Wilson RK  
 Washington University School of Medicine  
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
 Tel: 314 286 1800  
 Fax: 314 286 1810  
 Email: est@watson.wustl.edu  
 High quality sequence starts: 1  
 High quality sequence stops: 1  
 Source: IMAGE Consortium, LLNL  
 This clone is available royalty-free through LLNL; contact the  
 IMAGE Consortium (info@image.llnl.gov) for further information.  
 Trace considered overall poor quality  
 Seq primer: -21m13  
 High quality sequence stop: 1.  
 Location/Qualifiers  
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 /mol\_type="mRNA"  
 /db\_xref="GDB:502112"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:85055"  
 /sex="male"  
 /dev\_stage="49 years old"  
 /lab\_host="SOLR cells (kanamycin resistant)"  
 /clone\_lib="Stratagene liver (#937224)"  
 /note="Organ: liver; Vector: pBluescript SK; Site 1:  
 EcoRI; Site 2: XhoI; Cloned unidirectionally. Primer:  
 Oligo dT. Hepatectomy, from normal male caucasian. Average  
 insert size: 1.1 kb; Uni-ZAP XR Vector; ~5' adaptor  
 sequence: 5' GAATTCGGCAGAG 3' ~3' adaptor sequence: 5'  
 CTCGAGTTTTTTTTTTTTTTT 3'"

Query Match 2.4%; Score 40.2; DB 1; Length 46;  
 Best Local Similarity 91.3%; Pred. No. 1.1;  
 Matches 42; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1553 TCCTGCACCTTAACACTCGACTCTGCTGCTCATGGGAAGACAGAA 1598  
 |||||  
 Db 46 TCCTGNACGTTAAACCGACTCTGCTGCTCATGGGAAGACAGAA 1

RESULT 3  
 BF339449  
 LOCUS  
 DEFINITION BF339449 39 bp mRNA linear EST 22-NOV-2000  
 5', mRNA sequence.  
 ACCESSION BF339449  
 VERSION BF339449.1 GI:11285904  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 1 (bases 1 to 39)  
 NIH-MGC http://mgc.nci.nih.gov/.  
 National Institutes of Health, Mammalian Gene Collection (MGC)  
 Unpublished (1999)  
 Contact: Robert Straubeberg, Ph.D.  
 Email: cgabbs-remail.nih.gov  
 Tissue Procurement: David N. Louis, M.D.  
 cDNA Library Preparation: Life Technologies, Inc.  
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
 DNA Sequencing by: Incyte Genomics, Inc.  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
 http://image.llnl.gov  
 Plate: LLAM9508 row: f column: 01  
 High quality sequence stop: 38.

and Marra, M.  
 Generation and analysis of 280,000 human expressed sequence tags  
 Genome Res. 6 (9), 807-828 (1996)  
 97044478  
 MEDLINE  
 PUBMED  
 COMMENT  
 Contact: Wilson RK  
 Washington University School of Medicine  
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
 Tel: 314 286 1800  
 Fax: 314 286 1810  
 Email: est@watson.wustl.edu  
 High quality sequence starts: 1  
 High quality sequence stops: 1  
 Source: IMAGE Consortium, LLNL  
 This clone is available royalty-free through LLNL; contact the  
 IMAGE Consortium (info@image.llnl.gov) for further information.  
 Trace considered overall poor quality  
 Seq primer: -21m13  
 High quality sequence stop: 1.  
 Location/Qualifiers  
 1..46  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="GDB:502112"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:85055"  
 /sex="male"  
 /dev\_stage="49 years old"  
 /lab\_host="SOLR cells (kanamycin resistant)"  
 /clone\_lib="Stratagene liver (#937224)"  
 /note="Organ: liver; Vector: pBluescript SK; Site 1:  
 EcoRI; Site 2: XhoI; Cloned unidirectionally. Primer:  
 Oligo dT. Hepatectomy, from normal male caucasian. Average  
 insert size: 1.1 kb; Uni-ZAP XR Vector; ~5' adaptor  
 sequence: 5' GAATTCGGCAGAG 3' ~3' adaptor sequence: 5'  
 CTCGAGTTTTTTTTTTTTTTT 3'"

Query Match 2.4%; Score 40.2; DB 1; Length 46;  
 Best Local Similarity 91.3%; Pred. No. 1.1;  
 Matches 42; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1553 TCCTGCACCTTAACACTCGACTCTGCTGCTCATGGGAAGACAGAA 1598  
 |||||  
 Db 46 TCCTGNACGTTAAACCGACTCTGCTGCTCATGGGAAGACAGAA 1

RESULT 3  
 BF339449  
 LOCUS  
 DEFINITION BF339449 39 bp mRNA linear EST 22-NOV-2000  
 5', mRNA sequence.  
 ACCESSION BF339449  
 VERSION BF339449.1 GI:11285904  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 1 (bases 1 to 39)  
 NIH-MGC http://mgc.nci.nih.gov/.  
 National Institutes of Health, Mammalian Gene Collection (MGC)  
 Unpublished (1999)  
 Contact: Robert Straubeberg, Ph.D.  
 Email: cgabbs-remail.nih.gov  
 Tissue Procurement: David N. Louis, M.D.  
 cDNA Library Preparation: Life Technologies, Inc.  
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
 DNA Sequencing by: Incyte Genomics, Inc.  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
 http://image.llnl.gov  
 Plate: LLAM9508 row: f column: 01  
 High quality sequence stop: 38.

FEATURES  
 source  
 1..39  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:4186752"  
 /tissue\_type="glioblastoma with EGFR amplification"  
 /lab\_host="DH10B (T1 phage-resistant)"  
 /clone\_lib="NCI\_CGAP\_Brn64"  
 /note="Organ: brain; Vector: pCMV-SPORT6; Site 1: NotI;  
 Site 2: SalI; Cloned unidirectionally. Primer: Oligo dT.  
 Average insert size 1.57 kb. Constructed by Life  
 Technologies. Note: this is a NCI\_CGAP Library."

Query Match 2.4%; Score 39; DB 1; Length 39;  
 Best Local Similarity 100.0%; Pred. No. 1.2;  
 Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 416 GTTCTACGCACGGCTCTGCAGAGTGGCTCAGGCCTGGT 454  
 |||||  
 Db 1 GTTCTACGCACGGCTCTGCAGAGTGGCTCAGGCCTGGT 39

RESULT 4  
 BF342092  
 LOCUS  
 DEFINITION BF342092 39 bp mRNA linear EST 22-NOV-2000  
 5', mRNA sequence.  
 ACCESSION BF342092  
 VERSION BF342092.1 GI:11288842  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 1 (bases 1 to 39)  
 NIH-MGC http://mgc.nci.nih.gov/.  
 National Institutes of Health, Mammalian Gene Collection (MGC)  
 Unpublished (1999)  
 Contact: Robert Straubeberg, Ph.D.  
 Email: cgabbs-remail.nih.gov  
 Tissue Procurement: David N. Louis, M.D.  
 cDNA Library Preparation: Life Technologies, Inc.  
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
 DNA Sequencing by: Incyte Genomics, Inc.  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
 http://image.llnl.gov  
 Plate: LLAM9409 row: o column: 11  
 High quality sequence stop: 37.

FEATURES  
 source  
 1..39  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:4148962"  
 /tissue\_type="glioblastoma with EGFR amplification"  
 /lab\_host="DH10B (T1 phage-resistant)"  
 /clone\_lib="NCI\_CGAP\_Brn64"  
 /note="Organ: brain; Vector: pCMV-SPORT6; Site 1: NotI;  
 Site 2: SalI; Cloned unidirectionally. Primer: Oligo dT.  
 Average insert size 1.57 kb. Constructed by Life  
 Technologies. Note: this is a NCI\_CGAP Library."

Query Match 2.4%; Score 39; DB 1; Length 39;  
 Best Local Similarity 100.0%; Pred. No. 1.2;  
 Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 416 GTTCTACGCACGGCTCTGCAGAGTGGCTCAGGCCTGGT 454  
 |||||  
 Db 1 GTTCTACGCACGGCTCTGCAGAGTGGCTCAGGCCTGGT 39

```

RESULT 5
LOCUS       T71848
DEFINITION  y64e06.sl Stragatene liver (#937224) Homo sapiens cDNA clone
            IMAGE:85474 3' similar to gb:xl14723 CLUSTERIN PRECURSOR (HUMAN);
            mRNA sequence.
ACCESSION   T71848
VERSION     T71848.1 GI:686369
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
            1 (bases 1 to 40)
REFERENCE   1 (bases 1 to 40)
AUTHORS    Hillier,L., Lennon,G., Becker,M., Bonaldo,M.F., Chiapelli,B.,
            Chisoso,S., Dietrich,N., Dubuque,T., Favello,A., Gish,W.,
            Hawkins,M., Hultman,M., Kucaba,T., Lacy,M., Le,M., Le,N.,
            Mardis,E., Moore,B., Morris,M., Parsons,J., Prange,C., Rifkin,L.,
            Rohlfing,T., Schellenberg,K., Soares,M.B., Tan,F., Thierry-Mieg,J.,
            Trevaaskis,E., Underwood,K., Wohlmann,P., Waterston,R., Wilson,R.
            and Marra,M.
TITLE       Generation and analysis of 280,000 human expressed sequence tags
JOURNAL     Genome Res. 6 (9), 807-828 (1996)
MEDLINE     97044478
PUBMED     8889549
COMMENT     Contact: Wilson RK
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: est@watson.wustl.edu
            Insert Size: 26
            High quality sequence starts: 1 High quality sequence stops: 1
            Source: IMAGE Consortium, LNL This clone is available royalty-free
            through LNL; contact the IMAGE Consortium (info@image.llnl.gov)
            for further information. Trace considered overall poor quality
            Seq primer: -21m13
            High quality sequence stop: 1.
FEATURES    source
            Location/Qualifiers
                1..40
                /organism="Homo sapiens"
                /mol_type="mRNA"
                /db_xref="GDB:502531"
                /db_xref="taxon:9606"
                /clone="IMAGE:85474"
                /sex="male"
                /dev_stage="49 years old"
                /lab_host="SOLR cells (kanamycin resistant)"
                /clone_lib="Stratagene liver (#937224)"
                /note="Organ: liver; Vector: pBluescript SK; Site 1:
            EcoRI; Site 2: XhoI; Cloned unidirectionally. Primer:
            Oligo dT. Hepatectomy from normal male caucasian. Average
            insert size: 1.1 kb; Uni-ZAP XR Vector; ~5' adaptor
            sequence: 5' GAATTCGACGAG 3' -3' adaptor sequence: 5'
            CTCGAGTGTGTTTTTTTTTTT 3'"
Query Match      2.4%; Score 39; DB 1; Length 40;
Best Local Similarity 97.5%; Pred. No. 1; Indels 0; Gaps 0;
Matches 39; Conservative 0; Mismatches 1;

Qy 1512 CTCAGGCCCCCACTCGCCGAGCTCTCCCGCTCTGG 1551
      |||||
Db 40 CTCAGGCCCCCACTCGCCGAGCTCTCCCGCTCTGG 1

RESULT 6
LOCUS       H93557
DEFINITION  yv14dl1.r1 Soares fetal liver spleen lNFLS Homo sapiens cDNA clone
            IMAGE:242709 5' similar to gb:xl14723 CLUSTERIN PRECURSOR (HUMAN);
            mRNA sequence.
ACCESSION   H93557
VERSION     H93557.1 GI:1099885
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
            1 (bases 1 to 39)
REFERENCE   1 (bases 1 to 39)
AUTHORS    NIH-MGC http://mgc.nci.nih.gov/
            National Institutes of Health, Mammalian Gene Collection (MGC)
            Unpublished (1999)
            Unpublished (1999)

```

```

KEYWORDS    EST.
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
            1 (bases 1 to 48)
REFERENCE   1 (bases 1 to 48)
AUTHORS    Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
            Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
            Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
            Trevaaskis,E., Waterston,R., Williamson,A., Wohlmann,P. and
            Wilson,R.
            The WashU-Merck EST Project
            Unpublished (1995)
            Contact: Wilson RK
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: est@watson.wustl.edu
            High quality sequence starts: 1
            High quality sequence stops: 1
            Source: IMAGE Consortium, LNL
            This clone is available royalty-free through LNL; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            Trace considered overall poor quality
            Seq primer: M13RPI
            High quality sequence stop: 1.
FEATURES    source
            Location/Qualifiers
                1..48
                /organism="Homo sapiens"
                /mol_type="mRNA"
                /db_xref="GDB:3791842"
                /db_xref="taxon:9606"
                /clone="IMAGE:242709"
                /sex="male"
                /dev_stage="20 week-post conception.fetus"
                /lab_host="DHI0B (ampicillin resistant)"
                /clone_lib="Soares fetal liver spleen lNFLS"
                /note="Organ: Liver and Spleen; Vector: pT7T3D (Pharmacia)
            with a modified polylinker; Site 1: Pac I; Site 2: Eco RI;
            1st strand cDNA was primed with a Pac I - oligo(dT) primer
            [5' AACCTGGAGATTAATTAAGATCTTTTCTTTTCTTTT 3'],
            double-stranded cDNA was ligated to Eco RI adaptors
            (Pharmacia), digested with Pac I and cloned into the Pac I
            and Eco RI sites of the modified pT7T3 vector. Library
            went through one round of normalization. Library
            constructed by Bento Soares and M.Fatima Bonaldo."
Query Match      1.0%; Score 16; DB 1; Length 48;
Best Local Similarity 66.7%; Pred. No. 9;
Matches 22; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

Qy 627 AGTTCTTACCCGGGAGCCCGAGTACCTAC 659
      |||||
Db 36 AGGTTTNCAGCCGGGACACCCAGTTAAACTGC 4

RESULT 7
LOCUS       BF339449/c
DEFINITION  602039103F1 NCI CGAP_Brn64 Homo sapiens cDNA clone IMAGE:4186752
            5', mRNA sequence.
ACCESSION   BF339449
VERSION     BF339449.1 GI:11285904
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
            1 (bases 1 to 39)
REFERENCE   1 (bases 1 to 39)
AUTHORS    NIH-MGC http://mgc.nci.nih.gov/
            National Institutes of Health, Mammalian Gene Collection (MGC)
            Unpublished (1999)
            Unpublished (1999)

```

## COMMENT

Contact: Robert Strausberg, Ph.D.  
 Email: cgaaps-r@mail.nih.gov  
 Tissue Procurement: David N. Louis, M.D.  
 cDNA Library Preparation: Life Technologies, Inc.  
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
 DNA Sequencing by: Incyte Genomics, Inc.  
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>  
 Plate: LHAM9508 row: f column: 01  
 High quality sequence stop: 38.  
 Location/Qualifiers  
 1. .39  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:4186752"  
 /tissue\_type="glioblastoma with EGFR amplification"  
 /lab\_host="DH10B (T1 phage-resistant)"  
 /clone\_lib="NCI CGAP Brn64"  
 /notes="Organ: brain; Vector: pCMV-SPORT6; Site 1: NotI; Site 2: SalI; Cloned unidirectionally. Primer: Oligo dt. Average insert size 1.57 Kb. Constructed by Life Technologies. Note: this is a NCI\_CGAP Library."

## Query Match

Best Local Similarity 0.8%; Score 12.8; DB 1; Length 39;  
 Matches 17; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy

415 AGTTCTACGACGCGTCTGCAGAA 438

Db

25 ACTTCTGCAGACGCGTGCGTAGAA 2

## RESULT 8

BF342092/c

LOCUS

DEFINITION 602012848F1 NCI CGAP\_Brn64 Homo sapiens cDNA clone IMAGE:4148962  
 5', mRNA sequence.

ACCESSION

BF342092

VERSION

BF342092.1 GI:11288842

KEYWORDS

EST.

SOURCE

Homo sapiens (human)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 39)

NIH-MGC <http://mgc.nci.nih.gov/>.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

JOURNAL

Contact: Robert Strausberg, Ph.D.

Email: cgaaps-r@mail.nih.gov

Tissue Procurement: David N. Louis, M.D.

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>

Plate: LHAM9409 row: o column: 11

High quality sequence stop: 37.

Location/Qualifiers

1. .39

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="IMAGE:4148962"

/tissue\_type="glioblastoma with EGFR amplification"

/lab\_host="DH10B (T1 phage-resistant)"

/clone\_lib="NCI CGAP Brn64"

/notes="Organ: brain; Vector: pCMV-SPORT6; Site 1: NotI; Site 2: SalI; Cloned unidirectionally. Primer: Oligo dt. Average insert size 1.57 Kb. Constructed by Life

Technologies. Note: this is a NCI\_CGAP Library."

## Query Match

Best Local Similarity 0.8%; Score 12.8; DB 1; Length 39;  
 Matches 17; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy

415 AGTTCTACGACGCGTCTGCAGAA 438

Db

25 ACTTCTGCAGACGCGTGCGTAGAA 2

## FEATURES

source

RESULT 9

T74174

LOCUS

DEFINITION T74174 46 bp mRNA linear EST 02-MAR-1995  
 yc6b12.s1 Stratagene liver (#937224) Homo sapiens cDNA clone  
 IMAGE:85055 3' similar to gb:U14723 CLUSTERIN PRECURSOR (HUMAN);  
 mRNA sequence.

ACCESSION

T74174

VERSION

T74174.1 GI:690849

KEYWORDS

EST.

SOURCE

Homo sapiens (human)

ORGANISM

Homo sapiens

REFERENCE

1 (bases 1 to 46)

AUTHORS

Hillier, L., Lennon, G., Becker, M., Bonaldo, M.F., Chiapelli, B.,

Chisoe, S., Dietrich, N., Dubuque, T., Pavello, A., Gish, W.,

Hawkins, M., Hultman, M., Kucaba, T., Lacy, M., Le, M., Le, N.,

Mardis, E., Moore, B., Morris, M., Parsons, J., Prange, C., Rifkin, L.,

Rohlfing, T., Schellenberg, K., Soares, M.B., Tan, P., Thierry-Mieg, J.,

Trevaskis, E., Underwood, K., Wohlmann, P., Waterston, R., Wilson, R.

and Marra, M.

Generation and analysis of 280,000 human expressed sequence tags

Genome Res. 6 (9), 807-828 (1996)

97044478

8889549

Contact: Wilson RK

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800

Fax: 314 286 1810

Email: est@watson.wustl.edu

High quality sequence starts: 1

High quality sequence stops: 1

Source: IMAGE Consortium, LLNL

This clone is available royalty-free through LLNL; contact the

IMAGE Consortium ([info@image.llnl.gov](mailto:info@image.llnl.gov)) for further information.

Trace considered overall poor quality

Seq primer: -21mi3

High quality sequence stop: 1.

FEATURES

source

1. .46

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="GDB:502112"

/db\_xref="taxon:9606"

/clone="IMAGE:85055"

/sex="male"

/dev\_stage="49 years old"

/lab\_host="SOLR cells (kanamycin resistant)"

/clone\_lib="Stratagene liver (#937224)"

/note="Organ: liver; Vector: pBluescript SK; Site 1:

EcoRI; Site 2: XhoI; Cloned unidirectionally. Primer:

Oligo dt. Hepatectomy from normal male caucasian. Average

insert size: 1.1 kb; Uni-ZAP XR Vector; -5' adaptor

sequence: 5' GAATTCGGCAGG 3' -3' adaptor sequence: 5'

CTCAGTTTTTTTTTTTTTTT 3'

## Query Match

Best Local Similarity 0.8%; Score 12.8; DB 1; Length 46;  
 Matches 23; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

Qy

1573 CTCTGCTGCTCAGGAGACAGAAATTCCTCTCGATGCA 1613



Fax: 82 31 321 6355  
Email: [bhnaahm@qgbio.com](mailto:bhnaahm@qgbio.com), [bhnaahm@bio.myongji.ac.kr](mailto:bhnaahm@bio.myongji.ac.kr).

```

FEATURES
source
  Location/Qualifiers
  1..14
  /organism="Oryza sativa (japonica cultivar-group)"
  /mol_type="mRNA"
  /cultivar="Nackdong"
  /db_xref="taxon:39947"
  /clone="14ETL--04-D06"
  /tissue_type="leaf"
  /dev_stage="14 days after germination"
  /lab_host="E.coli DH10B"
  /clone_lib="Rice etiolated leaf plasmid cDNA library (14ETL)"
  /notes="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match      0.7%; Score 11.4; DB 1; Length 14;
Best Local Similarity 92.3%; Pred. No. 14;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 272 AGAAGCCAGAG 284
Db 14 AGAAGCCAGAG 2

RESULT 13
LOCUS CN752857/c
DEFINITION APhL3LD-VII-F11 APhL3LD Acyrthosiphon pisum cDNA clone
ACCESSION CN752857
VERSION 1
KEYWORDS EST.
SOURCE Acyrthosiphon pisum (pea aphid)
ORGANISM Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Paraneoptera; Hemiptera; Sternorrhyncha; Aphidiformes; Aphidoidea; Aphididae; Macrosiphini; Acyrthosiphon.
REFERENCE 1 (bases 1 to 12)
AUTHORS Hunter,W., Martinez-Torres,D., Rahbe,Y., Sabater-Munoz,B., Stern,D., Tagu,D. and Wincker,P.
TITLE An expressed sequence tags database for the pea aphid Acyrthosiphon pisum
JOURNAL Unpublished (2004)
COMMENT Contact: D. Tagu
INRA Rennes
UMR BIO3P, BP 35327, F-35653 Le Rheu Cedex France
Tel: +33.2.23.48.51.65
Fax: +33.2.23.48.51.50
Risk of contamination by bacterial sequences from obligatory (Buchnera) or facultative endosymbionts.
PCR Primers
FORWARD: GCCGCATAACTTCGTATAGCA
Plate: VII row: F column: 11.

FEATURES
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  /cultivar="yr2"
  /db_xref="taxon:7029"
  /clone="APHL3LDVIIIF11"
  /tissue_type="head"
  /dev_stage="third instar nymph (L3)"
  /lab_host="TOP10"
  /clone_lib="APHL3LD"
  /note="Vector: pDNR-LIB; Site 1: SfiIA; Site 2: SfiIB; Sample name: APhL3LD ; Plant growth place: INRA-Rennes, UMR BIO3P, BP 35327, 35653 Le Rheu cedex, France ; Soil conditions: peat ; Sowing date: 18/01/2003 ; Harvesting date: 03/02/2003 ; Stress date: no stress ; Description: aphids inoculated on one-week old Vicia faba germinations under non sterile conditions. ; experimental condition: long photoperiod (16-hr light/8-hr dark at 18 c)"

Query Match      0.5%; Score 9; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 698 CTCTCTCTT 706
Db 3 CTCTCTCTT 11

RESULT 15
LOCUS CW020522
DEFINITION GC0792 TIGEM gene trap library Mus musculus cDNA clone m4.E4.D08, mRNA sequence.

```

ACCESSION CW020522  
 VERSION GSS.  
 KEYWORDS Mus musculus (house mouse)  
 SOURCE Mus musculus  
 ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 REFERENCE 1 (bases 1 to 13)  
 AUTHORS Cobellis, G., Nicolaus, G., Marra, E., Barbarisi, M., Sardiello, M., Di Giorgio, F.P., Iovino, N., Zollo, M., Ballabio, A. and Cortese, R.  
 TITLE Tagging genes with cassette-exchange sites  
 JOURNAL Unpublished (2004)  
 COMMENT Contact: TIGEM  
 107

TIGEM  
 Via P. Castellino, 111, 80131 NAPOLI, ITALY  
 Tel: +390816132205  
 Fax: +390815790919  
 Email: cobellis@tigem.it  
 Sequence tag generated by 5' RACE of total RNA from gene trap ES cell line. ES cell lines harboring insertion mutation of target gene are available upon request from TIGEM. Annotation information available from TIGEM

Class: Gene Trap.

Location/Qualifiers

1. .13  
 /organism="Mus musculus"  
 /mol\_type="mRNA"  
 /strain="129 Ola"  
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 /clone="m4.E4.D08"  
 /sex="male"  
 /cell\_type="Embryonic stem cell"  
 /cell\_lines="E14"  
 /clone\_lib="TIGEM gene trap library"  
 /note="Vector: pFLIP1"

Query Match 0.5%; Score 8.2; DB 1; Length 13;  
 Best Local Similarity 76.9%; Pred. No. 18;  
 Matches 10; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 443 CTCAGGCTGGTT 455

Db 1 CTGGACCTGGTT 13

RESULT 16  
 CF278327 14 bp mRNA linear EST 14-AUG-2003  
 LOCUS 14ETL--04-D06.b1 Rice etiolated leaf plasmid cDNA library (14ETL)  
 DEFINITION Oryza sativa (japonica cultivar-group) cDNA clone 14ETL--04-D06, mRNA sequence.

ACCESSION CF278327  
 VERSION CF278327.1 GI:33655713  
 KEYWORDS EST.  
 SOURCE Oryza sativa (japonica cultivar-group)  
 ORGANISM Oryza sativa (japonica cultivar-group)  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.

REFERENCE 1 (bases 1 to 14)  
 AUTHORS Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.  
 TITLE Large-scale Sequencing Analysis of Rice ESTs  
 JOURNAL Unpublished (2003)  
 COMMENT Contact: Nahm B.H.

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 Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES

Location/Qualifiers

source

1. .14  
 /organism="Oryza sativa (japonica cultivar-group)"  
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 /cultivar="Nackdong"  
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 /clone="14ETL--04-D06"  
 /tissue\_type="leaf"  
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 /note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 0.5%; Score 8.2; DB 1; Length 14;  
 Best Local Similarity 76.9%; Pred. No. 18;  
 Matches 10; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 697 ACTCTTCTTTCC 709

Db 1 ACTTCTTCGCTTC 13

Search completed: September 13, 2005, 10:53:12  
 Job time : 0.001 secs

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